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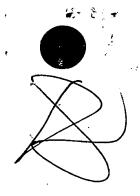
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PROVISIONAL SPECIFICATION

Invention Title:

EGF RECEPTOR AGONISTS AND ANTAGONISTS

The invention is described in the following statement:

EGF RECEPTOR AGONISTS AND ANTAGONISTS

Field of the Invention

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This invention relates to the field of epidermal growth factor (EGF) receptor structure and EGF receptor/ligand interactions. In particular, it relates to the field of using the EGF receptor structure to select and screen for agonists and antagonists of the polypeptide ligands.

Background of the Invention

Epidermal growth factor is a small polypeptide cytokine that stimulates marked proliferation of epithelial tissues and is a member of a larger family of structurally related cytokines such as transforming growth factor α (TGFα), amphiregulin, betacellulin, heparin-binding EGF and some viral gene products. Abnormal EGF family signalling is a characteristic of certain cancers (Soler, C. & Carpenter, G., 1994 In Nicola, N. (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp194-197; Walker, F. & Burgess, A. W., 1994, In Nicola, N. (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp198-201).

The epidermal growth factor receptor (EGFR) is the cell membrane receptor for EGF (Ullrich, A., and Schlessinger, J. (1990) Cell 61, 203-212). The EGFR also binds other ligands that contain amino acid sequences classified as the EGF-like motif. Among these ligands, the three-dimensional structures of EGF and TGF α have been determined by NMR (Montelione, G.T.; Wuthrich, K.; Nice, E.C., Burgess, A.W. and Scheraga, H.A. (1986) PNAS 83(22): 8594-8; Campbell, I.D., Cooke, R.M., Baron, M., Harvey, T.S., and Tappin, M.J. (1989) Prog. Growth Factor Res. 1, 13-22). Upon binding of the ligand to the extracellular domain, the EGFR undergoes dimerization, which eventually leads to the activation of its cytoplasmic protein tyrosine kinase (Ullrich, A., and Schlessinger, J. (1990) Cell 61, 203-212). The EGFR is also known as the ErbB-1 receptor and belongs to the type I family of receptor tyrosine kinases (Ullrich, A., and Schlessinger, J. (1990) Cell 61, 203-212). This group also includes the ErbB-2, ErbB-3 and ErbB-4 receptors. The ligand of ErbB-2 is still unknown but it is clear that heregulin is binding to ErbB-3 and ErbB-4 (Plowman, G.D., Green, J.M., Calouscou, J.M., Carlton, G.W., Rothwell, V.M., and Buckley, S. (1993) Nature 366, 473-475). One of the heregulins is known as neuregulin or NDF and contains an EGF-like sequence that was found to fold into an EGF-like fold by NMR (Nagata, K., Kohda, D., Hatanska, H., Ichikawa, S., Matsuda, S., Yamamoto, T., Suzuki,

A., and Inagaki, F. (1994) *EMBO J.* 13, 3517-3523 and Jacobson, N.E., Abadl, N., Sliwkowski, M.X., Reilly, D., Skelton, N.J., and Fairbrother, W.J. (1996) *Biochemistry* 36, 3402-3417).

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The type II family of receptor tyrosine kinases consists of the insulin receptor (INSR), the insulin-like growth factor I receptor, and the insulin receptor-related receptor (Ullrich, A., and Schlessinger, J. (1990) Cell 61, 203-212). Although the type II receptors consist of four chains $(\alpha_2\beta_2)$, both the extracellular portions of the receptors from the two families, as well as the tyrosine kinase portions, share significant sequence homology, suggesting a common evolutionary origin (Ullrich, A., and Schlessinger, J. (1990) Cell 61, 203-212, and Bajaj, M., Waterfield, M.D., Schlessinger, J., Taylor, W.R., and Blundell, T. (1987) Biochim. Biophys. Acta 916, 220-226).

The 621 amino acid residues of the extracellular domain of the human EGFR (sEGFR) can be subdivided into four domains as follows: L1, S1, L2 and S2, where L and S stand for "large" and "small" domains, respectively (Bajaj, M., Waterfield, M.D., Schlessinger, J., Taylor, W.R., and Blundell, T. (1987) *Biochim. Biophys. Acta* 916, 220-226, see Fig. 2). The L1 and L2 domains are homologous, as are the S1 and S2 domains.

Ligand-induced dimerization was first reported for the EGF receptor (Schlessinger, J. (1980) Trends Biochem Sci 13, 443-447) and now is widely accepted as a general mechanism for the transmission of growth stimulatory signals across the cell membrane. Although many biochemical experiments have been performed to reveal the molecular mechanism of receptor dimerization (Lemmon, M.A., Bu, Z., Ladbury, J.E., Zhou, M., Pinchasi, D., Lax, L., Engelman, D.M., and Schlessinger, J. (1997) EMBO J. 16, 281-294 and Tzabar, E., Pinkas-Kramarski, R., Moyer, J.D., Klapper, D.N., Alroy, L., Levkowitz, G., Shelly, M., Henis, S., Eisenstein, M., Ratzkin, B.J., Sela, M., Andrews, G.C., and Yarden, Y. (1997) EMBO J. 16, 4938-4950 and Lax, L., Mitra, A.K., Ravern, C., Hurwitz, D.R., Rubinstein, M., Ullrich, A., Stroud, R.M., and Schlessinger, J. (1991), J. Biol. Chem. 266, 13828-13833), the molecular mechanism by which monomeric ligands induce dimerization is still unknown for members of the EGFR family. Single particle averaging of electron microscopic images suggests that the overall shape of the sEGFR is four-lobed and doughnut-like (Lax, L., Mitra, A.K., Ravern, C., Hurwitz, D.R., Rubinstein, M., Ullrich, A., Stroud, R.M., and Schlessinger, J. (1991), J. Biol. Chem. 266, 13828-13833). Small angle x-ray scattering also indicate that the

sEGFR is a flattened sphere with long diameters of 110 Å and a short diameter of 20 Å (Lemmon, M.A., Bu, Z., Ladbury, J.E., Zhou, M., Pinchasi, D., Lax, L., Engelman, D.M., and Schlessinger, J. (1997) *EMBO J.* 16, 281-294). The crystallization of sEGFR in complex with EGF has been published (Günther, N., Betzel, C., and Weber, W. (1990) *J. Biol. Chem.* 265, 22082-22085), but the structure has not yet been reported, despite a decade of effort by many groups.

The EGF receptor ligand, TGF-α has been observed to be overproduced in keratinocyte cells which are subject to psoriasis (Turbitt, M.L. et al., 1990, J. Invest. Dermatol. 95(2), 229-232; Higashimyama, M. et al., 1991, J. Dermatol., 18(2), 117-119; Elder, J.T. et al, 1990, 94(1), 19-25). The overproduction of at least one other EGF receptor ligand, amphiregulin, has also been implicated in psoriasis. (Piepkorn, M. 1996, Am. J. Dermatopath., 18(2), 165-171). Molecules that inhibit the EGF receptor have been shown to inhibit the proliferation of both normal keratinocytes (Dvir, A. et al, 1991, J. Cell Biol., 113(4), 857-865) and psoriatic keratinocytes. (Ben-Bassat, H. et al., 1995, Exp. Dermatol., 4(2), 82-88). These findings indicate that EGF receptor antagonists may be useful in the treatment of psoriasis.

Many cancer cells express constitutively active EGFR (Sandgreen, E. P., et al., 1990, Cell, 61:1121-135; Karnes, W. E. J., et al., 1992, Gastroenterology, 102:474-485) or other EGFR family members (Hynes, N. E.,1993, Semin. Cancer Biol. 4:19-26). Elevated levels of activated EGFR occur in bladder, breast, lung and brain tumours (Harris, A. L., et al., 1989, In Furth & Greaves (eds) The Molecular Diagnostics of human cancer. Cold Spring Harbor Lab. Press, CSH, NY, pp353-357). Antibodies to EGFR can inhibit ligand activation of EGFR (Sato, J. D., et al., 1983 Mol. Biol. Med. 1:511-529) and the growth of many epithelial cell lines (Aboud-Pirak E., et al., 1988, J. Natl Cancer Inst. 85:1327-1331). Patients receiving repeated doses of a humanised chimeric anti-EGFR monoclonal antibody (Mab) showed signs of disease stabilization. The large doses required and the cost of production of humanised Mab is likely to limit the application of this type of therapy. These findings indicate that the development of EGF receptor antagonists will be attractive anticancer agents.

Summary of the Invention

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The present inventors have now obtained 3-dimensional structural information concerning the epidermal growth factor receptor (EGFR). This structural information was obtained by comparative modelling based on the 3D structure of the IGF-1 receptor as described in PP0585 and PP2598 (a copy of which is annexed hereto as Annexure A). The information presented in the present application provides the opportunity for the development of specific antagonists and agonists of EGFR for therapeutic applications.

Accordingly, in a first aspect the present invention provides a method of screening for, or designing, an agonist of the EGF receptor which method includes

- (i) selecting or designing a substance which possesses stereochemical complementarity to the EGF receptor site, wherein the receptor site is characterised by
- (a) amino acids 1-474 of the EGF receptor positioned at atomic coordinates substantially as shown in Figure 6 and 7 or a subset thereof; and
- (ii) testing the substance for the ability to act as an agonist of the EGF receptor.

In a second aspect the present invention provides a method of screening for, or designing, an antagonist of the EGF receptor which method includes

- (i) selecting or designing a substance which possesses stereochemical complementarity to the EGF receptor site, wherein the receptor site is characterised by
- (a) amino acids 1-474 of the EGF receptor positioned at atomic coordinates substantially as shown in Figures 6 and 7 or a subset thereof; and
- (ii) testing the substance for the ability to act as an antagonist of the EGF receptor.

The EGF receptor site defined in the first and second aspects of the present invention comprises the L1, S1 and L2 domains (residues 1-474) of the ectodomain of EGFR. At the centre of this structure is a cavity, bounded by all three domains, of sufficient size to accommodate a ligand molecule. By "stereochemical complementarity" we mean that the substance or a portion thereof correlates, in the manner of the classic "lock-and-key" visualisation of ligand-receptor interaction, with the cavity in the receptor site. Preferably, the stereochemical complementarity is such that the

substance has a K_I for the receptor site of less than $10^{-6}M$. More preferably, the K_I value is less than $10^{-8}M$ and more preferably less than $10^{-9}M$.

In preferred embodiments of the first and second aspects of the present invention, the method further involves selecting or designing a substance which has portions that match residues positioned on the surface of the receptor site which faces the cavity. By "match" we mean that the identified portions interact with the surface residues, for example, via hydrogen bonding or by enthalpy-reducing Van der Waals interactions which promote desolvation of the biologically active substance within the site, in such a way that retention of the substance within the cavity is favoured energetically.

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In a preferred embodiment of the first aspect of the present invention, the method includes screening for, or designing, a substance which possesses a stereochemistry and/or geometry which allows it to interact with both the L1 and L2 domains of the EGF receptor site. It is believed that EGFR monomers dimerise in nature in such a manner that the cavities of each monomer may face each other. Accordingly, the method of the first aspect of the present invention may involve screening for, or designing, a biologically active substance which interacts with the L1 domain of one monomer and the L2 domain of the other monomer.

In a third aspect the present invention provides a method of selecting or designing an agonist of the EGF receptor which method includes

- (i) selecting or designing a substance which interacts with
- (a) a fragment of the EGF receptor characterised by amino acids 1-474 positioned at atomic coordinates substantially as shown in Figures 6 and 7 or a subset thereof;

wherein the interaction of the substance with the fragment alters the position of at least one of the L1, L2 or S1 domains of the fragment relative to the position of at least one of the other domains; and

(ii) testing the substance for the ability to act as an agonist of the EGF receptor.

In a preferred embodiment of the third aspect of the present invention the substance interacts with the fragment in the region of the L1 domain-S1 domain interface, causing the L1 and S1 domains to move away from each other. In a further preferred embodiment the substance interacts with the hinge region between the L2 domain and the S1 domain causing an alteration in the positions of the domains relative to each other. In a further preferred

embodiment the substance interacts with the β sheet of the L1 domain causing an alteration in the position of the L1 domain relative to the position of the S1 domain or L2 domain.

In a fourth aspect the present invention provides an agonist of the EGF receptor obtained by a method according to the first or third aspects of the present invention.

In a fifth aspect the present invention provides an antagonist of the EGF receptor obtained by a method according to the second aspect of the present invention.

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The agonists or antagonists of the fourth and fifth aspects of the present invention may be mutant EGFR ligands where at least one mutation occurs in the region of the ligand which interacts with residues on the surface of the receptor site facing toward the cavity. For example, the residues Arg 41 and Tyr 13 in EGF are conserved in other members of the EGF receptor family of ligands (a Phe residue may be substituted for Tyr 13). Structures of several EGF family members show the two residues to be in close proximity. This portion of EGF may interact with a hydrophobic portion of the EGF receptor which contains one or more negatively charged residues such as the lower β sheet of the L1 domain. Mutants of EGF which show altered activity may be generated by introducing modifications to Arg 41 or Tyr 13 or other nearby residues. Alternatively, mutants of EGF may be generated by introducing modifications to residues on the opposite side of the ligand which may interact with a second receptor molecule in the unmodified ligand.

In a sixth aspect the present invention provides a substance which possesses stereochemical complementarity to the EGF receptor site, wherein the receptor site is characterised by

(a) amino acids 1-474 of the EGF receptor positioned at atomic coordinates substantially as shown in Figures 6 and 7 or a subset thereof;

with the proviso that the substance is not a naturally occurring ligand of the EGF receptor or a mutant thereof.

By "mutant" we mean a ligand which has been modified by one or more point mutations, insertions of amino acids or deletions of amino acids.

In a preferred embodiment of the sixth aspect of the present invention, the stereochemical complementarity is such that the compound has a $K_{\rm I}$ for

the receptor site of less than $10^{-6}M$. More preferably, the K_I value is less than $10^{-8}M$ and more preferably less than $10^{-9}M$.

The 3 dimensional structure of the EGF receptor elucidated by the present inventors also shows that the L2 and S2 domains are positioned such that they form a "corner" structure. It is envisaged that this corner structure provides a further binding site for ligands of the EGF receptor.

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Accordingly, in a seventh aspect the present invention provides a method of screening for, or designing, an agonist of the EGF receptor which method includes

- (i) selecting or designing a substance which binds simultaneously to the L2 and S2 domains of the EGF receptor, wherein the L2 and S2 domains are positioned substantially according to the atomic coordinates of amino acids 313-621 as shown in Figure 7, and
- (ii) testing the substance for the ability to act as an agonist of the EGF receptor.

In an eighth aspect the present invention provides a method of screening for, or designing, an antagonist of the EGF receptor which method includes

- (i) selecting or designing a substance which binds simultaneously to the L2 and S2 domains of the EGF receptor, wherein the L2 and S2 domains are positioned substantially according to the atomic coordinates of amino acids 313-621 as shown in Figure 7, and
- (ii) testing the substance for the ability to act as an antagonist of the EGF receptor.

In preferred embodiments of the seventh and eighth aspects of the present invention, the method involves selecting or designing a substance which has portions that match residues positioned on the inner surface of the corner structure. By "match" we mean that the identified portions interact with the surface residues, for example, via hydrogen bonding or by enthalpy-reducing Van der Waals interactions in such a way that retention of the substance within the corner structure is favoured energetically.

Preferably, the substance matches the residues positioned on the inner surface such that the substance has a K_I for the corner structure of less than $10^{-6}M$. More preferably, the K_I value is less than $10^{-8}M$ and more preferably less than $10^{-9}M$.

In a ninth aspect the present invention provides a method of selecting or designing an agonist of the EGF receptor which method includes

(i) selecting or designing a substance which interacts with

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(a) a fragment of the EGF receptor characterised by amino acids 313-621 positioned at atomic coordinates substantially as shown in Figure 7 or a subset thereof:

wherein the interaction of the substance with the fragment alters the relative positions of the L2 and S2 domains of the fragment with respect to each other; and

(ii) testing the substance for the ability to act as an agonist of the EGF receptor.

In a tenth aspect the present invention provides an agonist of the EGF receptor obtained by a method according to the seventh or ninth aspects of the present invention.

In an eleventh aspect the present invention provides an antagonist of the EGF receptor obtained by a method according to the eighth aspect of the present invention.

In a twelfth aspect the present invention provides a pharmaceutical composition for preventing or treating a disease which would benefit from increased signalling by the EGF receptor, which includes an agonist obtained by a method according to the first, third, seventh or ninth aspects of the present invention and a pharmaceutically acceptable carrier or diluent.

In an thirteenth aspect the present invention provides a pharmaceutical composition for preventing or treating a disease associated with signalling by the EGF receptor which includes an antagonist obtained by a method according to the second or eighth aspects of the present invention and a pharmaceutically acceptable carrier or diluent.

In a fourteenth aspect the present invention provides a method of preventing or treating a disease which would benefit from increased signalling by the EGF receptor which method includes administering to a subject in need thereof an agonist obtained by a method according to the first, third, seventh or ninth aspects of the present invention.

Diseases which may be treated by administration of EGFR agonists include wound healing and gastric ulcers.

In a fifteenth aspect the present invention provides a method of preventing or treating a disease associated with signalling by the EGF

receptor which method includes administering to a subject in need thereof an antagonist obtained by a method according to the second or eighth aspects of the present invention.

Diseases associated with signalling by the EGF receptor include psoriasis and many types of tumour states including but not restricted to cancer of the breast, brain, ovary, cervix, pancreas, lung, head and neck, and melanoma, rhabdomyosarcoma, mesothelioma and glioblastoma.

Brief Description of the Drawings

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Figure 1: Sequence alignment of human EGF receptor family proteins with IGF-1 receptor sequences and insulin receptor sequence for the first two domains of the EGF receptor. The alignment of EGF receptor and the various IGF-1 receptor sequences were used by the MODELLER program to create a model of the EGF receptor domains L1 and S1. Residues which are underlined were used to create additional $C\alpha$ - $C\alpha$ restraints for the construction of the EGF receptor model. IGF-1 receptor residues colored in magenta form part of helical secondary structures. Residues colored in light blue, light green and dark yellow reside in one of the three β -sheets (colored light blue, light green and dark yellow respectively) which make up part of the L1 β -helix. Residues colored in dark blue and dark green form part of a β -strand in the β -fingers. The residues in red are also in β -strands. Each cysteine residue in the S1 domain are numbered according to the module that it is a part of.

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Figure 2: Sequence alignment of human EGF receptor family proteins with IGF-1 receptor sequences and insulin receptor sequence for the third and fourth domains of the EGF receptor. The labelling scheme of the residues is the same as for Figure 1.

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Figure 3: Model polypeptide fold of the L1 and S1 domains of the EGF receptor. The L1 domain is at the left hand side of the structure with the N-terminus facing the front. The secondary structure elements are coloured in the same manner as in Figure 1.

Figure 4: Model polypeptide fold of the L2 and S2 domains of the EGF receptor. The L2 domain is at the bottom with its N-terminus facing the front. The secondary structure elements are coloured in the same manner as in Figure 1.

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Figure 5: Superpostion of the two models (of L1 and S1 domains and of L2 and S2 domains) onto structure of first three domains of IGF-1 receptor. The residues have been colored according to an estimate of the accuracy of the model cooridinates. Residues colored in yellow are judged to be well-modelled. Residues colored in orange are judged to have a moderate possibility of error. The coordinates or residues colored in red are believed to be inaccurate.

Figure 6: Coordinates of the model of the EGF receptor domains L1 and S1.

The coordinates are in relation to a Cartesian set of orthogonal axes. The final column contains the number 20, 40 or 60 depending on whether the residue containing the atom is judged to be well modelled, have a moderate possibility of error or is believed to be inaccurate respectively.

Figure 7: Coordinates of the model of the EGF receptor domains L2 and S2. The coordinates are in relation to a Cartesian set of orthogonal axes which are independent of the coordinate frame used for the EGF receptor model for L1 and S1 domains. The number in the final column is assigned in the same manner as for Figure 6.

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Detailed description of the Invention

Comparative modelling

The comparative modelling method exploits the observation that proteins with more than 25% amino acid identity will almost always have a similar protein backbone (Sander, C. And Schneider, R., 1991, Proteins: Structure Function and Genetics, 9, 56-68). In some cases, proteins will have similar backbone structures with a lower proportion of identical amino acids. By aligning the sequence of a (target) protein which is to be modelled with the sequences with known structures (the templates), a model of the protein can be obtained. Where a region of the target sequence follows the sequences

of a template, the backbone of the target is built to follow that of the template. Where the target sequence can not be aligned to a target sequence, the so-called insertion must be constructed by other means (Greer, J., 1991, Meth. Enzym. pp 239-252).

The MODELLER program (Šali, A and Blundell, T.L., 1993, J. Mol. Biol. 234, 779-815) is a semi-automated approach to building models of proteins given the structures of one or more template structures and an alignment between the sequences of the target protein and the templates. Based on the sequence alignment and a set of rules derived from the analysis of sets of aligned structure, the program generates a series of restraints for variables such as $C\alpha$ - $C\alpha$ distances, main chain and side chain dihedral angles for the target structure. The restraints are expressed in terms of probability density functions (PDFs). The PDFs are combined to yield an expression for the most probable structure as a function of the variables ($C\alpha$ - $C\alpha$ distances etc). The program then attempts to find structures to maximise the value of this function. In effect, the program attempts to minimise a transformed version of this function.

While some comparative modelling approaches involve the explicit building of regions of the model for which there is no sequence alignment with a template, the MODELLER program constructs PDFs for these regions, thus including them in the consideration of constructing a comparative model. It is conceivable that once a comparative model has been constructed using MODELLER that an algorithm to build the structures of these regions is applied.

The MODELLER program was used to build the structures of the extracellular portion of the EGF receptor using the 3D structure of the IGF-1 receptor (as described in PP0585 and PP2598) as a template. The description of the generation of these models is outlined below.

Construction of the alignment

The sequence of the EGF receptor extracellular domain can be divided into four domains, L1, S1, L2 and S2 on the basis of internal homology and homology with the insulin receptor family (Ward, C.W. et al., 1995, Proteins: Structure Function and Genetics 22: 141-153; Bajaj, M. et al., 1987, Biochim. Biophys. Acta 916: 220-226). At least two important sequence motifs are found in the EGF receptor sequence which are conserved in other EGF receptor homologues. The first motif is the sequence CXXXXXXW which is

found towards the end of both L1 and L2 of EGFR (C is cysteine, W is tryptophan and X is any residue). The second motif is the sequence CW where C is the third cysteine of both S1 and S2 (using the assignment of domain boundaries from Ward, C.W. et al., 1995, Proteins: Structure Function and Genetics 22: 141-153). The first motif is found in L1 but not L2 of the insulin receptor family. The second motif is found in the cysteine-rich domain of the insulin receptor family. These motifs are found in L1 and the cysteine-rich domain of the insulin receptor family. Structurally, the first motif corresponds to part of the L1 domain which allows penetration of the tryptophan residue of the second motif into the β -helix. As the first sequence motif is absent from L2 of the IGF-1 receptor, only the L1 and cysteine rich domains of the IGF-1 receptor were used as templates for the building of the EGF receptor extracellular domain models.

Construction of the alignment of L1 and S1

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There are two loops in the structure of the L1 domain which emerge from the breadloaf structure. The second loop (residues 86-93 in EGFR L1, 79-85 in IGF-1R L1) is structurally conserved in the L2 domain and differs by one amino acid residue in length. A region of the L2 domain corresponding to the loop was used as an additional template for this region. The sequence of the EGF receptor which corresponds to the first loop is of a different length and does not seem to be consistent with the loop of the IGF-1 receptor. The latter half of the region of EGF receptor sequence can be aligned to a region of sequence in the IGF-1 receptor's L2 domain. A portion of the IGF-1 receptor structure corresponding to this region of sequence plus the structure of flanking sequences was used as an additional template.

The alignment of the S1 domain of the EGF receptor to the IGF-1 receptor used the same combination of modules but involved the use of other modules from the cysteine-rich domain as additional templates. The first and second modules of the EGF module used the third module of the IGF-1 receptor cysteine-rich domain as additional templates. (This module contains two cysteines in disulfide bonds in a 1-3, 2-4 arrangement.) The sixth module of the EGF receptor can be modelled by the fifth module of the IGF-1 receptor, a β -finger.

Construction of the alignment of L2 and S2

The alignment of the EGF receptor sequence for the L2 domain to the L1 domain of the IGF-1 receptor sequence was similar to that of the L1

alignment. There is a 16 amino acid region which occurs roughly in the same region as the first loop in the IGF-1 receptor L1 domain. This region of sequence, which exhibits sequence homology amongst the EGF receptor family of proteins, can not be aligned with any region of the IGF-1 receptor sequence.

The sequence of the S2 domain was found to differ significantly from the S1 domain and suggested that the pattern of disulfide bonds may be different.

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An analysis of the β -finger structures in the IGF-1 receptor, TNF receptor and laminin- γ structures revealed that the β -fingers could be classed into three types exhibiting some structural and sequence conservation. Two of the structural types are relevent to the IGF-1 and EGF receptors. The first type of β -finger is characterised by structural conservation of the C-terminal portion of the module and also of the linker region after the module. The sequence signature is C...CXXC where the third cysteine residue is the start of another β -finger module. The second type of β -finger is characterised by structural conservation of the N-terminal portion of the module and also of the linker region after the module. The sequence signature is C...CXXXC where the third cysteine is the start of a module whose disufide bonding pattern is 1-3,2-4. The fifth module of the IGF-1 receptor cysteine-rich domain has some structural conservation with both types of β -finger.

The regions of the IGF receptor structure which were used as templates were identified as follows. The structure of IGF-1 receptor from the start of the L1 domain to the end of the first module of the cysteine-rich domain (which contains the conserved tryptophan residue which intercalates into the L1 β -helix) was used to model the corresponding regions of L2 and the start of S2 of the EGF receptor. Additional templates were used and "joined" to other templates by virtue of overlap in the sequence alignment.

The fourth and fifth modules of the IGF-1 receptor cysteine-rich domain were found to align with the sequences of the first and second and also the fourth and fifth putative modules of the S2 domain. The seventh module is the second last module of the S2 domain. The eighth module is neither a β -finger nor a module with the 1-3, 2-4 pattern of disulfide bonds. By elimination and use of the information described in the preceding paragraph, the third and sixth modules were assigned to be β -fingers of the second type. Two parts of the IGF-1 receptor structure were used to model

these two β -fingers. The fifth and seventh modules were used to model the β -finger modules. The linker region after the seventh module was also used. Additional residues after the linker were included to guide the placement of the next module. The positioning of the next module (modules 4 and 7 in S2) is essentially arbitrary and the use the extra residues offers a way of obtaining a plausible placement of the module.

Construction of the model

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Version 3 of the MODELLER program (Modeler User Guide, October 1996, San Diego Molecular Simulations Inc) was used to build models of the EGF receptor. Models of the L1 and S1 domains were constructed from the alignment shown in Figure 1 using the IGF-1 receptor templates shown and the EGF receptor sequence. Additional distance restraints were generated between $C\alpha$ atoms of selected residues. The restraints were generated as follows. The small IGF-1 receptor templates were superimposed into the structure of the first two domains of the IGF-1 receptor using the $C\alpha$ atoms of the residues which are aligned in Figure 1. Using the Homology module of the Insight II program (Homology User Guide, October 1995, San Diego BIOSYM/MSI) coordinates were built for the EGF receptor residues which are aligned to the IGF-1 receptor coordinates which are in bold typeface. From these coordinates, distance restraints in the form of Gaussian curves were constructed for pairs of $C\alpha$ atoms with a distance less than 50Å. The sigma value of the Gaussian curves was set to be 2Å. A MODELLER run was submitted using the alignment in Figure 1. The built models of proteins attempt to satisfy these restraints in addition to the restraints the program derives from the alignment.

To build models of the L2 and S2 domains, a similar process to that described in the preceding paragraph was used. The alignment used to build the models is shown in Figure 2. Two separate sets of additional restraints were used. The first set of restraints were derived from the IGF-1 receptor templates which are aligned with the first, second and third modules of the EGF receptor S2 domain. The second set of restraints were derived from the IGF-1 receptor templates which were aligned with the fourth, fifith and sixth modules of the EGF receptor S2 domain. Only those residues which are underlined in Figure 2 were used to generate the restraints. The sigma value of the Gaussian curves used to construct the additional restraints was 1Å.

For both sets of models, the MODELLER program constructed 20 models whose coordinates were perturbed from an initial structure by a random value of maximum distance 4Å. The refinement level used was the 'refine1' option in the MODELLER program.

Structure of the EGF receptor model

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The structure of the L1 and S1 domains of the EGF receptor as determined by the modelling described above is shown in Figure 3, while the structure of the L2 and S2 domains is shown in Figure 4. The superposition of these two models onto the structure of the extracellular domains of the IGF-1 receptor is shown in Figure 5.

The coordinates of the EGF receptor domains L1 and S1 are shown in Figure 6. The coordinates of the EGF receptor domains L2 and S2 are shown in Figure 7.

The structures of the L1 and S1 domains are similar to those of the IGF-1 receptor structure, as expected. There are two major differences in the S1 domain from the structure of the cysteine-rich region of the IGF-1 receptor structure. The sixth module of S2 is smaller that of the IGF-1 receptor and occupies less of the region between the two L domains. The fifth module, another β -finger, contains a large insertion which points away from the L1 domain. The structure of the end of the EGF receptor S1 domain is similar to that of the IGF-1 receptor cysteine-rich domain and is postulated to contain a hinge region between the last module of the S1 domain and the L2 domain.

A region of EGF receptor in L2 which could not be aligned with the IGF-1 receptor sequence includes the amino acids Trp-Pro which are conserved in the EGF receptor family of structure. This sequence motif is not found in the insulin receptor family and may represent a region of novel structure. This region of sequence could not be modelled on the corresponding region of the IGF-1 structure since none of the amino acids of the sequence Glu-Asn-Arg could be placed such that their side chains are in the interior of the β -helix. The asparagine has been observed to be glycosylated (Smith, K.D. et al, 1996, Growth-Factors, 13(1-2), 121-132) and therefore must point out of the structure. The charged residues glutamate and arginine are also expected to point out from the β -helix.

The amino acids 352-367 correspond to a large insertion in the third domain of the EGF receptor. The amino acids 351-364 have been identified as the epitope for several antibodies against the EGF receptor (Wu, D.G et al,

J. Biol. Chem. 1989 264(29):17469-17475). That this region forms a loop which sticks out of the structure is consistent with this region being accessible to the antibodies. The structure itself is difficult to model accurately since its sequence does not correspond to any part of the IGF-1 receptor sequence. The position of this insertion is in approximately the same region where the structures of IGF-1 receptor L1 and L2 domain differ.

The S2 domain adopts a different shape to the S1 domain. The S2 domain adopts a rod-like shape similar to that of the laminin γ-chain (Stetefeld, J. et al., 1996, J. Mol. Biol., 257(3): 644-657). Like the first half of the receptor model, the S2 domain contacts the L2 domain with the first module (this module contains the conserved tryptophan which intercalates into the breadloaf). Unlike S1, the rest of the S2 domain does not make any more contact with the L2 domain. The S2 domain points out from the L2 domain with a different geometry to the manner in which the S1 domain points out from L1.

Putative binding sites of the EGF receptor

From the IGF-1 receptor structure and a number of insulin receptor mutants, one of the regions of insulin binding was proposed to be the lower β sheet of the L1 domain. This surface is characterised by a number of hydrophobic residues which point out of the structure and also the presence of a structurally conserved loop. By analogy, we propose that the analogous β sheets of the L1 and L2 are potential binding sites. These sheets contain a number of hydrophobic residues, conserved amongst EGF receptor family members, which point away from the core of the β -helix structure. Residue 45 of a mutant EGF has been cross-linked to the residue Lysine 465 which is in the last strand of the lower β sheet of the L2 domain. (Summerfield, AE et al, J Biol Chem, 1996, 271(33), 19656-19659). Tyrosine 101 has been cross-linked to the N-terminus of EGF (Woltjer, RL et al, PNAS, 1992, 89(16), 7801-7805). This residue is in the portion of sequence which immediately follows a strand in the lower β sheet of L1.

The side chain of asparagine 1 of EGF has been cross-linked to lysine 336 of the EGF receptor (Wu, DG et al, PNAS, 1990, 87(8), 3151-3155). The latter residue is in the N-terminal helix of the L2 domain and points towards the cavity which is formed when the two halves of the EGF receptor are postioned in a similar arrangement to the first three domains of the IGF-1 receptor. Two nearby residues, Asn 328 and Asn 337 are glycosylated. This

mutation is in a similar position to the insulin receptor mutant S323L which has aberrent insulin binding.

Several insertional mutants of the EGF receptor extracellular domain have been constructed to probe the role of several regions of the receptor (Harte, M.T. and Gentry, L.E., 1995, Arch. Biochem. Biophys. 322(2), 387-389). EGF receptor mutants with insertions at residues 162, 169, 174 and 220 bound EGF with a similar affinity to wild-type EGF receptor but bound TGF- α with a lower affinity than wild-type receptor. The first insertion was located in the region near the end of the L1 domain and the first cysteine of the first module in S1. The second and third insertions were present in the first module of S1 and the fourth insertion was present in the third module of S1. EGF receptor mutants with insertions at postions at 251 and 574 (both in large β -finger modules, the first in S1 and the second in S2) bound twice as much EGF as the wild type receptor. Two insertional mutants which showed reduced EGF receptor binding contained insertions at postions 291 and 474. The former insertion is contained in the seventh module of S1 which is a β -finger. The latter insertion is near the end of the L2 domain.

Another EGF receptor mutant which shows altered ligand binding behaviour is the R497K mutant. The site of this mutation in the first module of the S2 domain and faces the side of the L2 domain opposite to that containing residue 465. This mutant binds EGF in a similar fashion as wild-type receptor but abolishes the high affinity binding site for TGF- α (Moriai, T. et al, 1994, PNAS 91(21), 10217-10221).

It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Dated this twenty ninth day of May 1998

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BIOMOLECULAR RESEARCH
INSTITUTE LTD
Patent Attorneys for the Applicant:

F B RICE & CO

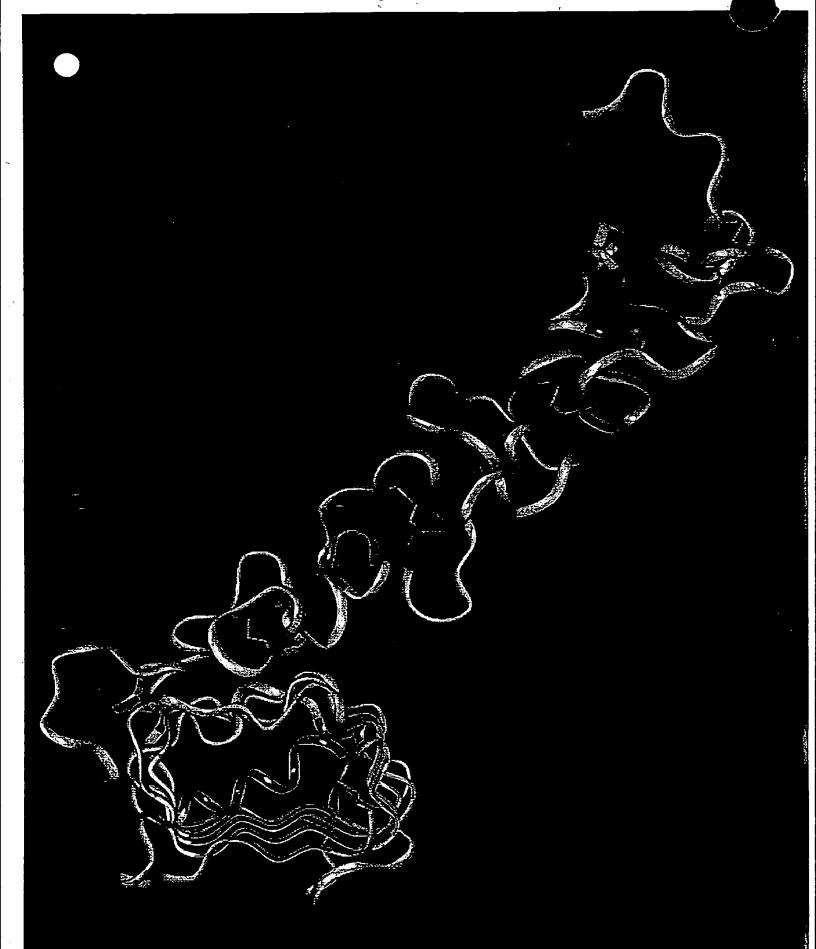
Figure 1

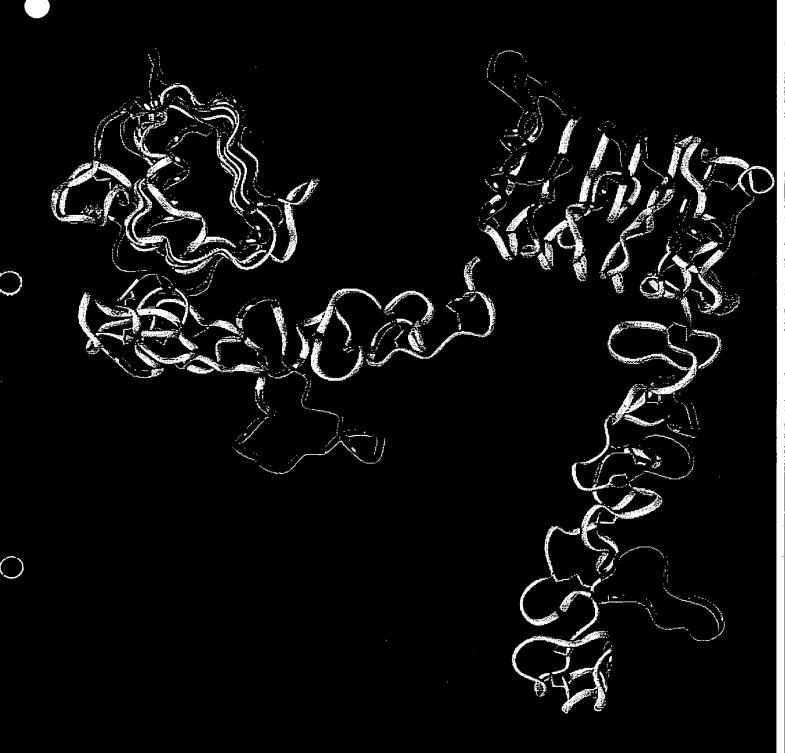
IGF1R	YVKIR
IGF1R	EICGPGIDIRNDYQQLKRLEN-CTVIEGYLHILLISKAEDYRSY
	lypgevc-pgmdirnnltrlhelen-csvieghlqillmfktrpedfrdl
InsR	Typgeve-pgmatrix
EGFR	leekkvc-qgtsnkltqlgtfedhflslqrmfnncevvlgnleityvqrny
ErbB2	c-tgtdmklrlpaspethldmlrhlyqgcqvvqgnleltylptna
ErbB3	c-pgtlnglsvtgdaenqyqtlyklyercevvmgnleivltghna
	c-agtenklsslsdleqqyral kyyencevvmgnleitsiehnr
ErbB4	C-agcentissisdicadital vilonoe,
IGF1R	HSHALVSLSFLKNLRLIL ILGEEQLEGNYSF
	RFPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFY-NYALVIF
IGF1R	REP. RELIVITED TO A STATE OF THE PROPERTY OF T
InsR	sfpklimitdylllfrvygleslkdlfpnltvirgsrlff-nyalvif
EGFR	dlsflktiqevagyvlia-Intveriplenlqiirgnmyyensyalavl
ErbB2	slsflqdiqevqgyvlia-hnqvrqvplqrlrivrgtqlfednyalavl
ErbB3	dlsflqwirevtgyvlva-mnefstlplpnlrvvrgtqvydgkfaifvm
	dlsflrsvrevtgyvlva-lnqfrylplenlriirgtklyedryalaif
ErbB4	indiana indian
IGF1R	
IGF1R	EMTNLKDIGLYNLRNITRGAIRIEKNADLCYLSTVDWSLILDA
	emvhlkelglynlmnitrgsvrieknnelcylatidwsrilds
InsR	emvinkeligiyilimiltigsvilekimeteyidatidadi
EGR_19	snydanktglkelpmrnlqeilhgavrfsnnpalcnvesiqwrdivssdf
ErbB2	dngdplnnttpvtgaspgglrelqlrslteilkggvliqrnpqlcyqdtilwkdifhknn
ErbB3	lnyntnsshalrqlrltqlteilsggvyiekndklchmdtidwrdivrdrd
ErbB4	lnyrkdgnfglqelglknlteilnggvyvdqnkflcyadtihwqdivrnpw
EIDB4	Invitagni gideraimizerinaa i edimerelamente
	•
IGF1R	CHPECL-GSCSAPDNDTA
IGF1R	VSNNYIV-GNK-PPKECGDLCPGTMEEKPMCEKTTINNEYNYRCWTTNR
	vednhiv-lnkddneecgdicpgtakgktncpatvingqfvercwthsh
InsR	Vednitv-Inkadneecgarc - pgtakgkthep atvingation agent
EGFR	lsnmsmdfqnh-lg-scq-kcdpscpngscwga-geen
ErbB2	qlaltlidtnr-sr-ach-pcspmckgsrcwge-ssed
ErbB3	aeivvkdngr-scp-pchevck-grcwgp-gsed
ErbB4	psnltlvstng-ss-gcg-rchksct-grcwgp-tenh
21221	1 1 1
IGF1R	C CHPECLGS CSAPDNDT AC
IGF1R	CQKMCPSTCGKRACTENNECCHPECLGSCSAPDNDTACVACRHYY
	cqkvcptickshgctaeglcchseclgncsqpddptkcvacrnfy
InsR	eq-1-1-1 keeper and an adaption and are declarated
EGFR	cqkltkiicaqqcsgrcrgk-spsdcchnqcaagctgp-resdclvcrkfr
ErbB2	cqsltrtvcaggca-rckgp-lptdccheqcaagctgp-khsdclaclhfn
ErbB3	cqtltkticapqcnghcfgp-npnqcchdecaggcsgp-qdtdcfacrhfn
ErbB4	cqtltrtvcaeqcdgrcygp-yvsdcchrecaggcsgp-kdtdcfacmnfn
	1 2 2 2 2 23 3 3 3 4
IGF1R	CVPA CPPN
IGF1R	YAGVCVPACPPNTYRFEGWRCVDRDFCANILSAES
InsR	ldgrcvetcpppyyhfqdwrcvnfsfcqdlhhkcknsr
	deatckdtcpplmlynpttyqmdvnpegkysfg-atcvkkcprn
EGFR	hsgicelhcpalvtyntdtfesmpnpegrytfg-ascvtacpyn
ErbB2	hsgiceIncpairtyntatiesmpnpegiytig-ascrta-cpyn
ErbB3	dsgacvprcpqplvynkltfqlepnphtkyqyg-gvcvascphn
ErbB4	dsgacvtqcpqtfvynpttfqlehnfnakytyg-afcvkkcphn
	4 5
IGF1R	<u>TYRFEGWRC</u>
IGF1R	SDSEGFVIHD-GECMQECPSGFIRNG-SQ-SMYCIPCEGPCPKV
InsR	rqqchqyvihnnkcipecpsgytmns-snllctpclgpcpkv
EGFR	yvvtdhgscvracgadsyeme-edgvrkckkcegpcrkv
ErbB2	ylstdvgsctlvcplhnqevtaedgtqrcekcskpcarv
ErbB3	fvvdq-tscvracppdkmevd-knglkmcepcgglcpka
ErbB4	fvvds-sscvracpsskmeve-engikmckpctdicpka
	6 7 7 8 8

Figure 2

IGF1R IGF1R InsR EGFR ErbB2 ErbB3 ErbB4	EICGPGIDIRNDYQQLKRLENCTVIEGYLHILLIS
IGF1R IGF1R InsR EGFR ErbB2 ErbB3 ErbB4	ILGEEQLEGNKAEDYRSYR-FPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFY-Nktrpedfrdls-fpklimitdylllfrvygleslkdlfpnltvirgsrlff-n qeldilktvkeitgflliqawpenrtdl-hafenleiirgrtkqhgq eqlqvfetleeitgylyisawpdslpdl-svfqnlqvirgrilhnga eklnvfrtvreitgylniqswpphmhnf-svfsnlttiggrslynrg eklnvfrtvreitgflniqswppnmtdf-svfsnlvtiggrvlys-g
IGF1R IGF1R InsR EGFR ErbB2 ErbB3 ErbB4	YSF YALVIFEMTNLKDIGLYNLRNITRGAIRIEKNADLCYLSTVDWSLILDAVSNNYIVGN yalvifemvhlkelglynlmnitrgsvrieknnelcylatidwsrildsvednhivln fslavvsl-nitslglrslkeisdgdviisgnknlcyantinwkklfgt-sgqktkiisn ysltlqgl-giswlglrslrelgsglalihhnthlcfvhtvpwdqlfrn-phqallhtan fsllimknlnvtslgfrslkeisagriyisanrqlcyhhslnwtkvlrgpteerldikhn lslilkqq-gitslqfqslkeisagniyitdnsnlcyyhtinwttlfst-inqrivirdn
IGF1R IGF1R InsR EGFR ErbB2 ErbB3 ErbB4	CHPECLGSCSAPDNDTACVACRHY K-PPKECGDLCPGTMEEKPMCEKTTINNEYNYRCWTTNRC kddneecgdicpgtakgktncpatvingqfvercwthshc r-gensckatgqvchalcspegcwgp-eprdcvscrnv r-pedecvgeglachql
IGF1R IGF1R EGFR ErbB2 ErbB3 ErbB4	YYAGVCVPACPPNTYRFEGWRC CHPECLGSCSAPDNDTAC CPSGFIRNGSQSMYCIPCEG srgrecvdkckllegeprefvenseciqchpeclpqa-mnitctgr-gpdnc lrgqecveecrvlqglpreyvnarhclpchpecqpqn-gsvtcfgp-eadqc srggvcvthcnflngeprefaheaecfschpecqpme-gtatcngs-gsdtc srgriciescnlydgefrefengsicvecdpqcekmedglltchgp-gpdnc 2 3 3 4 4 4 4
IGF1R IGF1R EGFR ErbB2 ErbB3 ErbB4	VACRHYYYAGVCVPACPPNTYRFEGWRC CHPECLGSCSA CPSGFIRNGSQSMYCIPCEG iqcahyidgphcvktcpagvmgenntl-vwkyadaghvchlchpnctygctg vacahykdppfcvarcpsgvkpdlsympiwkfpdeegacqpcpincthscvd aqcahfrdgphcvsscphgvlgakgpiykypdvqnecrpchenctqgckg tkcshfkdgpncvekcpdglqgansfifkyadpdrechpchpnctqgcng 5 5 6 6 7 7 7
IGF1R IGF1R EGFR ErbB2 ErbB3 ErbB4	PDNDTAC p-glegcptngpkips 1-ddkgc p-elqdc p-tshdc 7







MOTA	3	N	LEU	1	60.296	19.487	71.703	1.00 60.00
MOTA	5	CA	LEU	1	59.489	18.323	71.270	1.00 60.00
MOTA	6	CB	LEU	1	59.216	18.373	69.755	1.00 60.00
MC	7	CG	LEU	1	58.289	19.520	69.302	1.00 60.00
MO LA	8	CD1	LEU	1	56.879	19.357	69.888	1.00 60.00
MOTA	9	CD2	LEU	1	58.903	20.902	69.580	1.00 60.00
MOTA	10	С	LEU	1	60.208	17.051	71.563	1.00 60.00
MOTA	11	0	LEU	1	61.087	16.999	72.421	1.00 60.00
MOTA	12	N	GLU	2	59.824	15.976	70.853	1.00 60.00
MOTA	14	CA	GLU	2	60.463	14.712	71.045	1.00 60.00
MOTA	15	CB	GLU	2	59.551	13.646	71.675	1.00 60.00
MOTA	16	CG	GLU	2	59.244	13.895	73.153	1.00 60.00
ATOM	17	CD	GLU	2	60.480	13.515	73.955	1.00 60.00
MOTA	18	OE1	GLU	2	60.436	13.645	75.208	1.00 60.00
MOTA	19	OE2	GLU	2	61.485	13.084	73.327	1.00 60.00
ATOM	20	С	GLU	2	60.842	14.217	69.692	1.00 60.00
ATOM	21	0	GLU	2	60.830	14.962	68.714	1.00 60.00
ATOM	22	N	GLU	3	61.212	12.928	69.615	1.00,60.00
MOTA	24	CA	GLU	3	61.583	12.345	68.364	1.00 60.00
ATOM	25	CB	GLU	3	62.012	10.876	68.513	1.00 60.00
ATOM	26	CG	GLU	3	60.926	9.981	69.116	1.00 60.00
ATOM	27	CD	GLU	3	61.538	8.616	69.395	1.00 60.00
MOTA	28	OE1	GLU	3	62.780	8.481	69.232	1.00 60.00
ATOM	29	OE2	GLU	3	60.774	7.691	69.781	1.00 60.00
ATOM	30	С	GLU	3	60.382	12.401	67.479	1.00 60.00
MOTA	31	0	GLU	3	60.473	12.789	66.316	1.00 60.00
ATOM	32	N	LYS	4	59.209	12.029	68.025	1.00 60.00
ATOM	34	CA	LYS	4	58.014	12.055	67.238	1.00 60.00
ATOM	35	CB	LYS	4	56.883	11.191	67.818	1.00 60.00
ATOM	36	CG	LYS	4	55.752	10.920	66.828	1.00 60.00
ATOM	37	CD	LYS	4	56.125	9.887	65.766	1.00 60.00
ATOM	38	CE	LYS	4	56.026	8.449	66.279	1.00 60.00
MOTA	39	NZ	LYS	4	56.881	8.282	67.477	1.00 60.00
MOTA	43	С	LYS	4	57.530	13.466	67.246	1.00 60.00
ATOM	44	0	LYS	4	57.866	14.236	68.144	1.00 60.00
MOTA	45	N	LYS	5	56.738	13.855	66.229	1.00 40.00
MOTA	47	CA	LYS	5	56.253	15.201	66.238	1.00 40.00
MOTA	48	СВ	LYS	5	57.260	16.226	65.673	1.00 40.00
MOTA	49	CG	LYS	5	56.923	17.682	66.018	1.00 40.00
ATOM	50	CD	LYS	5	58.055	18.677	65.752	1.00 40.00
ATOM	51	CE	LYS	5	57.687	20.121	66.109	1.00 40.00
ATOM	52	NZ	LYS	5	58.848	21.016	65.897	1.00 40.00
ATOM	56	C	LYS	5	55.006	15.267	65.418	1.00 40.00
ATOM	57	0	LYS	5	54.478	14.249	64.973	1.00 40.00
ATOM	58	N	VAL	6	54.492	16.496	65.229	1.00 40.00
MOTA	60	CA	VAL	6	53.310	16.742	64.461	1.00 40.00
MOTA	61	CB	VAL	6	52.718	18.092	64.761	1.00 40.00
MOTA	62	CG1		6	51.500	18.346	63.858	1.00 40.00
MOTA	63		VAL	6	52.397	18.149	66.263	1.00 40.00
ATOM	64	С	VAL	6	53.718	16.713	63.024	1.00 40.00
MOTA	65	0	VAL	6	54.901	16.835	62.709	1.00 40.00
MOTA	66	N	CYS	7	52.749	16.513	62.107	1.00 40.00
MOTA	68	CA	CYS	7	53.077	16.507	60.711	1.00 40.00
ATOM	69	CB	CYS	7	53.033	15.116	60.050	1.00 40.00
MOTA	70	SG	CYS	7	51.430	14.278	60.192	1.00 40.00
ATOM	71	С	CYS	7	52.115	17.399	59.995	1.00 40.00
MOTA	72	0	CYS	7	51.133	17.864	60.567	1.00 40.00
MOTA	73	N	GLN	8	52.398	17.681	58.711	1.00 40.00
MOTA	75	CA	GLN	8	51.565	18.559	57.947	1.00 40.00
ATOM	76	СВ	GLN	8	52.249	19.057	56.664	1.00 40.00
ATOM	77	CG	GLN	8	52.592	17.934	55.683	1.00 40.00
MOTA	78	CD	GLN	8	53.346	18.542	54.510	1.00 40.00
MOTA	79	OE1	GLN	8	54.534	18.846	54.609	1.00 40.00
MOTA	80	NE2	GLN	8	52.638	18.727	53.364	1.00 40.00

Figure 6

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I A	83	С	GLN	8	50.310	17.853	57.564		40.00
ATOM	84	0	GLN	8	50.163	16.646	57.754		40.00
MOTA	85	N	GLY	9	49.354	18.626	57.021		40.00
OM.	87	CA	GLY	9 9	48.094 47.630	18.108 19.103	56.597 55.597	1.00	40.00
WO W	88 89	С 0	GLY GLY	9	46.441	19.207	55.311		40.00
MOTA MOTA	90	N	THR	10	48.583	19.883	55.052		40.00
ATOM	92	CA	THR	10	48.228	20.808	54.023		40.00
MOTA	93	СВ	THR	10	49.373	21.659	53.561	1.00	40.00
ATOM	94	OG1	THR	10	49.884	22.424	54.644		40.00
MOTA	96	CG2	THR	10	48.875	22.586	52.440	1.00	
MOTA	97	С	THR	10	47.861	19.897	52.908	1.00	
MOTA	98	0	THR	10	48.727	19.416	52.179	1.00	40.00
ATOM	99	N	SER	11 11	46.547 46.075	19.653 18.684	52.754 51.822		40.00
MOTA	101 102	CA CB	SER SER	11	46.073	19.088	50.356		40.00
ATOM ATOM	102	OG	SER	11	45.542	20.251	50.051		40.00
ATOM	105	C	SER	11	46.842	17.433	52.099		40.00
ATOM	106	ō	SER	11	47.460	16.877	51.193	1.00	40.00
MOTA	107	N	ASN	12	46.840	16.960	53.368		40.00
MOTA	109	CA	ASN	12	47.566	15.750	53.624	1.00	
MOTA	110	CB	ASN	12	47.743	15.405	55.113	1.00	
ATOM	111	CG	ASN	12	48.722	14.241 13.628	55.199 54.189		40.00
ATOM	112	ND2	ASN ASN	12 12	49.066 49.182	13.020	56.438		40.00
ATOM ATOM	113 116	C ND2	ASN	12	46.715	14.696	53.020		40.00
ATOM	117	0	ASN	12	45.802	14.172	53.657		40.00
ATOM	118	N	LYS	13	46.993	14.364	51.749	1.00	40.00
ATOM	120	CA	LYS	13	46.144	13.421	51.104		40.00
ATOM	121	CB	LYS	13	45.416	14.008	49.884		40.00
ATOM	122	CG	LYS	13	46.363	14.573	48.825		40.00
ATOM	123	CD	LYS	13	45.675	14.921 15.551	47.505 46.477		40.00
ATOM	124	CE NZ	LYS LYS	13 13	46.617 45.877	15.863	45.233		40.00
ATOM ATOM	125 129	C	LYS	13	46.913	12.234	50.648		40.00
ATOM	130	0	LYS	13	47.735	12.310	49.737		40.00
ATOM	131	N	LEU	14	46.652	11.096	51.310	1.00	40.00
ATOM	133	CA	LEU	14	47.211	9.852	50.895		40.00
ATOM	134	CB	LEU	14	46.976	8.748	51.947		40.00
ATOM	135	CG	LEU	14			51.598		40.00
MOTA	136		LEU	14	46.871 49.076	6.739 7.413	50.371 51.504		40.00
ATOM	137 138	CD2	LEU LEU	14 14	46.341	9.560	49.715		40.00
ATOM ATOM	139	0	LEU	14	45.124	9.706	49.797		40.00
ATOM	140	N	THR	15	46.926	9.175	48.565	1.00	20.00
ATOM	142	CA	THR	15	46.046	8.932	47.460		20.00
ATOM	143	CB	THR	15	45.720	10.173	46.680		20.00
ATOM	144	OG1		15	44.734	9.894	45.699		20.00
ATOM	146	CG2	THR	15	47.008	10.693	46.016		20.00
ATOM	147	C	THR	15 15	46.662 47.882	7.957 7.845	46.516 46.427		20.00
ATOM ATOM	148 149	O N	THR GLN	16	45.812	7.213	45.784		20.00
MOTA	151	CA	GLN	16	46.308	6.267	44.830		20.00
ATOM	152	СВ	GLN	16	45.194	5.417	44.193	1.00	20.00
АТОМ	153	CG	GLN	16	45.677	4.384	43.166		20.00
ATOM	154	CD	GLN	16	45.903	5.076	41.826		20.00
ATOM	155		GLN	16	46.999	5.031	41.269		20.00
MOTA	156		GLN	16	44.838	5.737	41.296		20.00
MOTA	159	С О	GLN GLN	16 16	46.943 48.054	7.055 6.749	43.737 43.312		20.00
ATOM ATOM	160 161	N	LEU	17	46.034	8.105	43.312		20.00
ATOM	163	CA	LEU	17	46.700	8.915	42.189		20.00
ATOM	164	СВ	LEU	17	45.794	10.142	41.941		20.00
ATOM	165	CG	LEU	17	46.211	11.086	40.792	1.00	20.00

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MOTA	166		LEU	17	47.470	11.904	41.126	1.00 20.00
ATOM	167	CD2	LEU	17	46.324	10.326	39.462	1.00 20.00
MOTA	168	С	LEU	17	48.081	9.372	42.501	1.00 20.00
MC	169	0	LEU	17	48.436	9.591	43.657	1.00 20.00
PT-OW	170	N	GLY	18	48.912	9.499	41.455	1.00 20.00
MOTA	172	CA	GLY	18	50.262	9.939	41.643	1.00 20.00
MOTA	173	С	GLY	18	51.057	9.374	40.516	1.00 20.00
MOTA	174	0	GLY	18	50.876	8.222	40.127	1.00 20.00
MOTA	175	N	THR	19	51.972	10.189	39.961	1.00 20.00
MOTA	177	CA	THR	19	52.782	9.709	38.886	1.00 20.00
MOTA	178	CB	THR	19	53.666	10.769	38.292	1.00 20.00
ATOM	179	OG1		19	54.347	10.254	37.158 39.347	1.00 20.00 1.00 20.00
MOTA	181	CG2	THR	19 10	54.670	11.258 8.619	39.436	1.00 20.00
ATOM	182	С	THR	19 19	53.635 53.833	7.588	38.796	1.00 20.00
ATOM	183	O N	THR	20	54.148	8.817	40.664	1.00 20.00
ATOM	184 186	N CA	PHE PHE	20	54.987	7.834	41.278	1.00 20.00
ATOM ATOM	187	CB	PHE	20	55.635	8.347	42.579	1.00 20.00
ATOM	188	CG	PHE	20	56.659	7.367	43.040	1.00 20.00
ATOM	189	CD1		20	57.923	7.381	42.496	1.00 20.00
ATOM	190	CD2		20	56.398	6.515	44.089	1.00 20.00
ATOM	191	CE1	PHE	20	58.900	6.537	42.967	1.00 20.00
ATOM	192	CE2	PHE	20	57.373	5.673	44.569	1.00 20.00
ATOM	193	CZ	PHE	20	58.627	5.682	44.007	1.00 20.00
ATOM	194	C	PHE	20	54.090	6.693	41.619	1.00 20.00
ATOM	195	0	PHE	20	52.871	6.793	41.490	1.00 20.00
ATOM	196	N	GLU	21	54.671	5.558	42.047	1.00 20.00
ATOM	198	CA	GLU	21	53.833	4.450	42.396	1.00 20.00
ATOM	199	СВ	GLU	21	54.593	3.121	42.541	1.00 20.00
ATOM	200	CG	GLU	21	55.122	2.564	41.219	1.00 20.00
ATOM	201	CD	GLU	21	55.844	1.259	41.522	1.00 20:00
ATOM	202	OE1	GLU	21	56.277	0.584	40.550	1.00 20.00
MOTA	203	OE2	GLU	21	55.970	0.918	42.729	1.00 20.00
ATOM	204	С	GLU	21	53.254	4.782	43.725	1.00 20.00
ATOM	205	0	GLU	21	53.828	4.458	44.764	1.00 20.00
ATOM	206	N	ASP	22	52.087	5.454	43.721	1.00 20.00
ATOM	208	CA	ASP	22	51.483	5.831	44.961	1.00 20.00
MOTA	209	CB	ASP	22	50.885	7.248	44.940	1.00 20.00
MOTA	210	CG	ASP	22	50.624	7.676	46.376	1.00 20.00
MOTA	211		ASP	22	50.950	8.847	46.707	1.00 20.00 1.00 20.00
MOTA	212		ASP	22	50.091	6.845	47.159	1.00 20.00
ATOM	213	С	ASP	22	50.379	4.864	45.231 44.357	1.00 20.00
MOTA	214	0	ASP	22	49.567	4.565 4.335	44.337	1.00 20.00
ATOM	215	N	HIS	23	50.341 49.347	3.384	46.853	1.00 40.00
ATOM	217 218	CA CB	HIS HIS	23 23	49.761	1.915	46.649	1.00 40.00
ATOM ATOM	219		HIS	23	49.838	1.473	45.220	1.00 40.00
MOTA MOTA	220		HIS	23	50.917	1.323	44.403	1.00 40.00
ATOM	221		HIS	23	48.750	1.052	44.486	1.00 40.00
ATOM	223		HIS	23	49.222	0.673	43.271	1.00 40.00
ATOM	224		HIS	23	50.530	0.820	43.174	1.00 40.00
ATOM	226	C	HIS	23	49.165	3.538	48.323	1.00 40.00
ATOM	227	o	HIS	23	49.412	4.596	48.899	1.00 40.00
MOTA	228	N	PHE	24	48.700	2.447	48.952	1.00 40.00
ATOM	230	CA	PHE	24	48.497	2.366	50.365	1.00 40.00
ATOM	231	СВ	PHE	24	47.878	1.032	50.798	1.00 40.00
ATOM	232	CG	PHE	24	47.619	1.074	52.265	1.00 40.00
ATOM	233	CD1		24	46.418	1.545	52.742	1.00 40.00
ATOM	234	CD2		24	48.565	0.632	53.162	1.00 40.00
ATOM	235	CE1		24	46.157	1.564	54.092	1.00 40.00
ATOM	236		PHE	24	48.312	0.655	54.513	1.00 40.00
ATOM	237	CZ	PHE	24	47.105	1.118	54.981	1.00 40.00
ATOM	238	С	PHE	24	49.858	2.476	50.972	1.00 40.00
ATOM	239	0	PHE	24	50.016	2.876	52.124	1.00 40.00

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A .	554	С	LEU	55	48.807	3.909	63.695	1.00 40.00
ATOM	555	0	LEU	55	47.740	4.362	64.108	1.00 40.00
MOTA	556	N	LYS	56	49.696	3.297	64.498	1.00 40.00
MC	558	CA	LYS	56	49.497	3.101	65.901 66.506	1.00 40.00 1.00 40.00
A r OM	559	CB	LYS	56	50.576	2.185	68.008	1.00 40.00
MOTA	560	CG	LYS	56 56	50.417 51.365	1.939 0.867	68.554	1.00 40.00
MOTA	561	CD CE	LYS LYS	56	52.806	1.355	68.725	1.00 40.00
ATOM	562 563	NZ	LYS	56	53.656	0.266	69.255	1.00 40.00
ATOM ATOM	567	C	LYS	56	49.574	4.403	66.636	1.00 40.00
ATOM	568	0	LYS	56	48.753	4.684	67.506	1.00 40.00
ATOM	569	N	THR	57	50.566	5.235	66.273	1.00 20.00
ATOM	571	CA	THR	57	50.892	6.456	66.958	1.00 20.00
ATOM	572	СВ	THR	5 7	52.151	7.079	66.433	1.00 20.00
MOTA	573	OG1	THR	57	52.558	8.147	67.275	1.00 20.00
MOTA	575	CG2	THR	57	51.890	7.590	65.006	1.00 20.00
MOTA	576	С	THR	57	49.837	7.520	66.919 67.911	1.00 20.00 1.00 20.00
MOTA	577	0	THR	57	49.634 49.134	8.217 7.669	65.781	1.00 20.00
MOTA	578	N	ILE	58 58	49.134	8.749	65.585	1.00 20.00
ATOM	580	CA CB	ILE ILE	58	47.381	8.578	64.339	1.00 20.00
ATOM ATOM	581 582	CG2	ILE	58	46.356	9.724	64.289	1.00 20.00
ATOM	583	CG1	ILE	58	48.286	8.508	63.097	1.00 20.00
ATOM	584	CD1	ILE	58	49.117	9.770	62.877	1.00 20.00
ATOM	585	С	ILE	58	47.233	8.931	66.716	1.00 20.00
ATOM	586	0	ILE	58	46.204	8.260	66.774	1.00 20.00
ATOM	587	N	GLN	59	47.579	9.822	67.672	1.00 20.00
ATOM	589	CA	GLN	59	46.734	10.199	68.773	1.00 20.00
MOTA	590	CB	GLN	59	47.517	10.863	69.915	1.00 20.00 1.00 20.00
ATOM	591	CG	GLN	59	48.143	12.195	69.501 70.736	1.00 20.00
MOTA	592	CD	GLN	59 59	48.757 49.685	12.832 12.297	71.340	1.00 20.00
ATOM	593 594	OE1 NE2	GLN	59	48.215	14.014	71.129	1.00 20.00
ATOM ATOM	597	C	GLN	59	45.679	11.189	68.377	1.00 20.00
ATOM	598	0	GLN	59	44.530	11.095	68.808	1.00 20.00
ATOM	599	N	GLU	60	46.048	12.190	67.550	1.00 20.00
MOTA	601	CA	GLU	60	45.095	13.224	67.262	1.00 20.00
ATOM	602	CB	GLU	60	45.290	14.461	68.155	1.00 20.00
MOTA	603	CG	GLU	60	44.250	15.563	67.946	1.00 20.00
MOTA	604	CD	GLU	60	44.647	16.742	68.822 69.530	1.00 20.00 1.00 20.00
ATOM	605		GLU	60	43.756	17.283 17.123	68.787	1.00 20.00
ATOM	606		GLU	60 60	45.848 45.206	13.695	65.848	1.00 20.00
MOTA	607 608	С 0	GLU GLU	60	46.181	13.420	65.153	1.00 20.00
MOTA ATOM	609	N	VAL	61	44.145	14.383	65.381	1.00 20.00
ATOM	611	CA	VAL	61	44.109	15.031	64.104	1.00 20.00
ATOM	612	СВ	VAL	61	43.283	14.315	63.069	1.00 20.00
ATOM	613	CG1	VAL	61	41.843	14.146	63.582	1.00 20.00
ATOM	614	CG2	VAL	61	43.376	15.105	61.752	1.00 20.00
ATOM	615	С	VAL	61	43.469	16.347	64.419	1.00 20.00
ATOM	616	0	VAL	61	42.399	16.407	65.018	1.00 20.00 1.00 20.00
MOTA	617	N	ALA	62	44.133	17.447	64.037 64.335	1.00 20.00
MOTA	619	CA	ALA	62 62	43.683 44.789	18.774 19.827	64.147	1.00 20.00
ATOM	620	CB	ALA ALA	62	42.528	19.201	63.488	1.00 20.00
ATOM ATOM	621 622	С О	ALA	62	42.002	20.294	63.685	1.00 20.00
ATOM ATOM	623	N	GLY	63	42.161	18.409	62.461	1.00 20.00
ATOM	625	CA	GLY	63	41.087	18.809	61.595	1.00 20.00
ATOM	626	C	GLY	63	40.025	17.758	61.501	1.00 20.00
ATOM	627	0	GLY	63	39.332	17.458	62.470	1.00 20.00
ATOM	628	N	TYR	64	39.856	17.187	60.289	1.00 20.00
ATOM	630	CA	TYR	64	38.849	16.189	60.073	1.00 20.00
MOTA	631	СВ	TYR	64	37.728	16.639	59.114	1.00 20.00 1.00 20.00
MOTA	632	CG	TYR	64	38.295	16.800	57.741	1.00 20.00

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ATOM	633	CD1	TYR	64	38.320	15.737	56.867	1.00 20.00
MOTA	634	CE1		64	38.835	15.874	55.599	1.00 20.00
MOTA	635	CD2	TYR	64	38.791	18.013	57.320	1.00 20.00
MC	636	CE2		64	39.310	18.157	56.054	1.00 20.00
OM	637	CZ	TYR	64	39.335	17.086	55.193	1.00 20.00
MOTA	638	OH	TYR	64	39.880	17.228	53.899	1.00 20.00
ATOM	640	С	TYR	64	39.501	14.990	59.462	1.00 20.00
ATOM	641	0	TYR	64	40.654	15.050	59.040	1.00 20.00
ATOM	642	N	VAL	65	38.779	13.849	59.438	1.00 20.00
ATOM	644	CA	VAL	65	39.311	12.653	58.845	1.00 20.00
ATOM	645	CB	VAL	65	39.362	11.494	59.793	1.00 20.00
ATOM	646		VAL	65	39.871	10.259	59.032	1.00 20.00
ATOM	647		VAL	65	40.235	11.888	60.997	1.00 20.00
ATOM	648	С	VAL	65	38.415	12.249	57.708	1.00 20.00
MOTA	649	0	VAL	65	37.194	12.259	57.835	1.00 20.00
АТОМ	650	N	LEU	66	39.004	11.884	56.549	1.00 20.00
ATOM	652	CA	LEU	66	38.207	11.501	55.412	1.00 20.00
ATOM	653	СВ	LEU	66	38.272	12.530	54.268	1.00 20.00
ATOM	654	CG	LEU	66	37.431	12.161	53.034	1.00 20.00
MOTA	655		LEU	66	35.934	12.089	53.374	1.00 20.00
MOTA	656		LEU	66	37.726	13.110	51.858	1.00 20.00
MOTA	657	С	LEU	66	38.691	10.186	54.867	1.00 20.00
ATOM	658	0	LEU	66	39.892	9.925	54.848	1.00 20.00
MOTA	659	N	ILE	67	37.758	9.312	54.410	1.00 20.00 1.00 20.00
MOTA	661	CA	ILE	67 67	38.160	8.028 6.965	53.887 54.942	1.00 20.00
ATOM	662	CB	ILE	67 67	38.248	7.382	55.955	1.00 20.00
ATOM	663	CG2		67	39.328	6.722	55.570	1.00 20.00
MOTA	664	CG1		67 67	36.866	5.463	56.434	1.00 20.00
ATOM	665	CD1	ILE	67	36.803		52.835	1.00 20.00
MOTA	666	C	ILE	67 67	37.214	7.495 7.879	52.768	1.00 20.00
ATOM	667	0	ILE	67 69	36.047 37.738	6.584	51.975	1.00 40.00
MOTA	668	N	ALA	68 68	37.736	5.902	50.920	1.00 40.00
ATOM	670	CA CB	ALA ALA	68	36.603	6.825	49.767	1.00 40.00
ATOM	671 672	СВ	ALA	68	38.026	4.927	50.364	1.00 40.00
ATOM	673	0	ALA	68	38.926	5.308	49.616	1.00 40.00
ATOM ATOM	674	N	LEU	69	37.895	3.634	50.721	1.00 40.00
ATOM	676	CA	LEU	69	38.868	2.675	50.282	1.00 40.00
ATOM	677	СВ	LEU	69	39.908	2.322	51.360	1.00 40.00
ATOM	678	CG	LEU	69	40.796	3.485	51.840	1.00 40.00
MOTA	679		LEU	69	39.979	4.582	52.541	1.00 40.00
MOTA	680		LEU	69	41.929	2.963	52.738	1.00 40.00
MOTA	681	С	LEU	69	38.173	1.386	49.995	1.00 40.00
MOTA	682	0	LEU	69	36.949	1.285	50.065	1.00 40.00
ATOM	683	N	ASN	70	38.970	0.364	49.626	1.00 20.00
ATOM	685	CA	ASN	70	38.448	-0.949	49.395	1.00 20.00
ATOM	686	СВ	ASN	70	38.493	-1.389	47.922	1.00 20.00
ATOM	687	CG	ASN	70	37.404	-0.633	47.175	1.00 20.00
ATOM	688	OD1	ASN	70	36.218	-0.806	47.450	1.00 20.00
ATOM	689	ND2	ASN	70	37.813	0.230	46.207	1.00 20.00
ATOM	692	С	ASN	70	39.314	-1.885	50.172	1.00 20.00
ATOM	693	0	ASN	70	40.387	-1.505	50.640	1.00 20.00
ATOM	694	N	THR	71	38.830	-3.132	50.348	1.00 20.00
ATOM	696	CA	THR	71	39.493	-4.195	51.056	1.00 20.00
ATOM	697	СВ	THR	71	40.639	-4.813	50.298	1.00 20.00
ATOM	698	OG1	THR	71	41.089	-5.980	50.970	1.00 20.00
ATOM	700	CG2	THR	71	41.786	-3.803	50.147	1.00 20.00
ATOM	701	С	THR	71	39.925	-3.813	52.440	1.00 20.00
ATOM	702	0	THR	71	40.538	-4.614	53.145	1.00 20.00
MOTA	703	N	VAL	72	39.580	-2.590	52.888	1.00 20.00
ATOM	705	CA	VAL	72	39.932	-2.171	54.215	1.00 20.00
MOTA	706	CB	VAL	72	40.149	-0.691	54.328	1.00 20.00
MOTA	707	CG1	VAL	72	40.470	-0.349	55.792	1.00 20.00
MOTA	708	CG2	VAL	72	41.247	-0.280	53.333	1.00 20.00

F	709	С	VAL	72	38.758	-2.514	55.074	1.00 20.00
ATOM	710	0	VAL	72	37.671	-1.965	54.911	1.00 20.00
ATOM	711	N	GLU	73	38.955	-3.480	55.988	1.00 20.00
MC	713	CA	GLU	73	37.923	-3.967	56.856	1.00 20.00
MOLA	714	CB	GLU	73	38.349	-5.279	57.534	1.00 20.00
ATOM	715	CG	GLU	73	38.561	-6.403	56.516	1.00 20.00
MOTA	716	CD	GLU	73	39.076	-7.630	57.251	1.00 20.00
MOTA	717	OE1		73	39.263	-7.542	58.493	1.00 20.00
MOTA	718	OE2	GLU	73	39.289	-8.674	56.578	1.00 20.00
MOTA	719	С	GLU	73	37.499	-3.001	57.921	1.00 20.00
ATOM	720	0	GLU	73	36.306	-2.829	58.162	1.00 20.00 1.00 20.00
ATOM	721	N	ARG	74	38.454	-2.328	58.590	1.00 20.00
MOTA	723	CA	ARG	74	38.077	-1.471	59.680 61.043	1.00 20.00
ATOM	724	СВ	ARG	74	38.258	-2.160	61.198	1.00 20.00
ATOM	725	CG	ARG	74	37.398 37.779	-3.418 -4.286	62.399	1.00 20.00
ATOM	726	CD	ARG	74	39.121	-4.200	62.119	1.00 20.00
ATOM	727	NE	ARG	74 74	40.196	-4.529	62.887	1.00 20.00
MOTA	729	CZ	ARG	74 74	40.190	-3.644	63.915	1.00 20.00
MOTA	730	NH1	ARG ARG	74 74	41.422	-5.075	62.631	1.00 20.00
ATOM	733	NH2 C	ARG	74 74	38.988	-0.290	59.663	1.00 20.00
MOTA	736 737	0	ARG	74	39.927	-0.235	58.875	1.00 20.00
MOTA	738	N	ILE	75	38.743	0.708	60.536	1.00 20.00
ATOM	740	CA	ILE	75	39.646	1.827	60.611	1.00 20.00
ATOM ATOM	741	CB	ILE	75	38.942	3.150	60.486	1.00 20.00
ATOM	742	CG2	ILE	75	39.993	4.273	60.555	1.00 20.00
ATOM	743	CG1	ILE	75	38.138	3.193	59.175	1.00 20.00
ATOM	744	CD1	ILE	75	39.003	3.053	57.923	1.00 20.00
ATOM	745	С	ILE	75	40.260	1.740	61.980	1.00 20.00
ATOM	746	0	ILE	75	40.265	2.684	62.765	1.00 20.00
ATOM	747	N	PRO	76	40.856	0.609	62.211	1.00 20.00
ATOM	748	CD	PRO	76	41.577	-0.084	61.161	1.00 20.00
ATOM	749	CA	PRO	76	41.328	0.159	63.486	1.00 20.00
ATOM	750	CB	PRO	76	41.810	-1.276	63.244	1.00 20.00
ATOM	751	CG	PRO	76	41.661	-1.506	61.724	1.00 20.00
ATOM	752	С	PRO	76	42.464	0.947	64.063	1.00 20.00
ATOM	753	0	PRO	76	43.009	0.430	65.036	1.00 20.00
ATOM	754	N	LEU	77	42.891	2.094	63.463	1.00 20.00
ATOM	756	CA	LEU	77	43.941	2.919	64.023	1.00 20.00 1.00 20.00
MOTA	757	CB	LEU	77	43.971	4.354	63.475	1.00 20.00
MOTA	758	CG	LEU	77 .	44.267	4.436	61.970 61.153	1.00 20.00
MOTA	759	CD1		77	43.148	3.768 5.887	61.547	1.00 20.00
MOTA	760	CD2		77	44.552 43.653	3.019	65.485	1.00 20.00
ATOM	761	C	LEU	77 77	42.773	3.760	65.919	1.00 20.00
ATOM	762 763	O N	LEU GLU	78	44.422	2.245	66.273	1.00 20.00
ATOM	765	CA	GLU	78	44.154	2.030	67.661	1.00 20.00
MOTA MOTA	766	CB	GLU	78	45.215	1.126	68.313	1.00 20.00
	767	CG	GLU	78	45.162		.67.872	1.00 20.00
ATOM ATOM	768	CD	GLU	78	44.210	-1.063	68.810	1.00 20.00
ATOM	769	OE1		78	43.065	-0.569	68.991	1.00 20.00
ATOM	770	OE2		78	44.620	-2.117	69.367	1.00 20.00
ATOM	771	C	GLU	78	44.131	3.271	68.485	1.00 20.00
ATOM	772	0	GLU	78	43.173	3.510	69.214	1.00 20.00
ATOM	773	N	ASN	79	45.182	4.097	68.380	1.00 20.00
ATOM	775	CA	ASN	79	45.370	5.233	69.236	1.00 20.00
ATOM	776	СВ	ASN	79	46.830	5.720	69.251	1.00 20.00
ATOM	777	CG	ASN	79	47.647	4.686	70.016	1.00 20.00
ATOM	778	OD1		79	48.858	4.827	70.181	1.00 20.00
ATOM	779	ND2	ASN	79	46.968	3.609	70.494	1.00 20.00
ATOM	782	С	ASN	79	44.505	6.442	69.057	1.00 20.00
ATOM	783	0	ASN	79	44.285	7.157	70.033	1.00 20.00
MOTA	784	N	LEU	80	44.011	6.718	67.831	1.00 20.00
ATOM	786	CA	LEU	80	43.334	7.957	67.532	1.00 20.00

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ATOM	787	CB	LEU	80	42.657	7.950	66.151	1.00 20.00
ATOM	788	CG	LEU	80	42.050	9.307	65.757	1.00 20.00
MOTA	789	CD1	LEU	80	43.147	10.376	65.627	1.00 20.00
)M	790	CD2	LEU	80	41.188	9.195	64.492	1.00 20.00
A'1'OM	791	С	LEU	80	42.315	8.342	68.565	1.00 20.00
ATOM	792	0	LEU	80	41.225	7.776	68.629	1.00 20.00
ATOM	793	N	GLN	81	42.728	9.271	69.461	1.00 20.00
ATOM	795	CA	GLN	81	41.964	9.831	70.544	1.00 20.00
ATOM	796	СВ	GLN	81	42.877	10.381	71.654	1.00 20.00
ATOM	797	CG	GLN	81	43.812	9.339	72.267	1.00 20.00
ATOM	798	CD	GLN	81	42.971	8.360	73.071	1.00 20.00
ATOM	799	OE1		81	41.955	8.730	73.659	1.00 20.00
ATOM	800	NE2		81	43.406	7.072	73.096	1.00 20.00
АТОМ	803	С	GLN	81	40.993	10.945	70.241	1.00 20.00
MOTA	804	0	GLN	81	39.869	10.940	70.741	1.00 20.00
ATOM	805	N	ILE	82	41.401	11.959	69.443	1.00 20.00
ATOM	807	CA	ILE	82	40.535	13.097	69.267	1.00 20.00
ATOM	808	СВ	ILE	82	40.842	14.181	70.259	1.00 20.00
MOTA	809	CG2		82	39.994	15.403	69.898	1.00 20.00
ATOM	810	CG1		82	40.626	13.682	71.699	1.00 20.00
ATOM	811	CD1	ILE	82	39.183	13.280	72.002	1.00 20.00
ATOM	812	C	ILE	82	40.686	13.698	67.897	1.00 20.00
ATOM	813	ō	ILE	82	41.764	13.658	67.307	1.00 20.00
ATOM	814	N	ILE	83	39.580	14.259	67.352	1.00 20.00
ATOM	816	CA	ILE	83	39.588	14.935	66.082	1.00 20.00
ATOM	817	СВ	ILE	83	38.670	14.293	65.081	1.00 20.00
ATOM	818	CG2	ILE	83	38.638	15.171	63.821	1.00 20.00
ATOM	819	CG1	ILE	83	39.099	12.841	64.812	1.00 20.00
ATOM	820	CD1	ILE	83	38.048	12.026	64.060	1.00 20.00
ATOM	821	C	ILE	83	39.032	16.298	66.376	1.00 20.00
ATOM	822	ō	ILE	83	37.822	16.488	66.434	1.00 20.00
ATOM	823	N	ARG	84	39.907	17.309	66.484	1.00 20.00
ATOM	825	CA	ARG	84	39.536	18.627	66.922	1.00 20.00
ATOM	826	СВ	ARG	84	40.749	19.570	66.962	1.00 20.00
ATOM	827	CG	ARG	84	41.796	19.151	67.993	1.00 20.00
MOTA	828	CD	ARG	84	43.065	20.005	67.955	1.00 20.00
ATOM	829	NE	ARG	84	42.674	21.408	68.266	1.00 20.00
ATOM	831	CZ	ARG	84	42.606	21.830	69.563	1.00 20.00
ATOM	832	NH1	ARG	84	42.894	20.965	70.579	1.00 20.00
ATOM	835	NH2	ARG	84	42.252	23.118	69.842	1.00 20.00
ATOM	838	С	ARG	84	38.485	19.300	66.091	1.00 20.00
ATOM	839	Ó	ARG	84	37.694	20.079	66.618	1.00 20.00
ATOM	840	N	GLY	85	38.462	19.077	64.768	1.00 20.00
ATOM	842	CA	GLY	85	37.451	19.713	63.971	1.00 20.00
ATOM	843	С	GLY	85	37.729	21.178	63.827	1.00 20.00
ATOM	844	0	GLY	85	36.814	21.971	63.607	1.00 20.00
ATOM	845	N	ASN	86	39.009	21.579	63.922	1.00 20.00
ATOM	847	CA	ASN	86	39.344	22.971	63.806	1.00 20.00
ATOM	848	СВ	ASN	86	40.860	23.225	63.837	1.00 20.00
ATOM	849	CG	ASN	86	41.372	22.841	65.216	1.00 20.00
ATOM	850		ASN	86	40.593	22.557	66.124	1.00 20.00
ATOM	851		ASN	86	42.722	22.838	65.381	1.00 20.00
ATOM	854	С	ASN	86	38.845	23.418	62.473	1.00 20.00
ATOM	855	0	ASN	86	38.279	24.503	62.339	1.00 20.00
ATOM	856	N	MET	87	39.054	22.584	61.441	1.00 20.00
ATOM	858	CA	MET	87	38.530	22.905	60.148	1.00 20.00
ATOM	859	СВ	MET	87	39.596	23.081	59.054	1.00 20.00
ATOM	860	ÇG	MET	87	40.482	21.853	58.857	1.00 20.00
ATOM	861	SD	MET	87	41.713	21.605	60.170	1.00 20.00
ATOM	862	CE	MET	87	42.788	22.960	59.615	1.00 20.00
ATOM	863	С	MET	87	37.681	21.741	59.775	1.00 20.00
ATOM	864	0	MET	87	38.064	20.591	59.980	1.00 20.00
АТОМ	865	N	TYR	88	36.497	22.022	59.204	1.00 20.00
ATOM	867	CA	TYR	88	35.560	20.985	58.901	1.00 20.00

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A	868	СВ	TYR	88	34.142	21.317	59.393	1.00 20.00	
ATOM	869	CG	TYR	88	33.731	22.569	58.691	1.00 20.00	
ATOM	870	CD1	TYR	88	34.124	23.798	59.169	1.00 20.00	
MC	871	CE1	TYR	88	33.792	24.953	58.499	1.00 20.00	
A·1·OM	872	CD2	TYR	88	32.989	22.515	57.532	1.00 20.00	
ATOM	873	CE2	TYR	88	32.653	23.666	56.858	1.00 20.00	
ATOM	874	CZ	TYR	88	33.059	24.887	57.339	1.00 20.00	
ATOM	875	OH	TYR	88	32.726	26.069	56.643	1.00 20.00 1.00 20.00	
ATOM	877	С	TYR	88	35.452	20.773 21.643	57.431 56.625	1.00 20.00	
ATOM	878	0	TYR	88	35.783	19.565	57.059	1.00 20.00	
ATOM	879	N	TYR	89	34.990 34.771	19.303	55.689	1.00 20.00	
MOTA	881	CA	TYR	.89 89	34.771	17.713	55.436	1.00 20.00	
ATOM	882	CB CG	TYR TYR	89	34.869	17.477	53.966	1.00 20.00	
MOTA	883 884	CD1	TYR	89	36.035	17.628	53.253	1.00 20.00	
ATOM	885	CE1	TYR	89	36.078	17.349	51.908	1.00 20.00	
ATOM ATOM	886	CD2	TYR	89	33.745	17.019	53.320	1.00 20.00	
MOTA	887	CE2	TYR	89	33.781	16.737	51.975	1.00 20.00	
ATOM	888	cz	TYR	89	34.949	16.901	51.269	1.00 20.00	
ATOM	889	ОН	TYR	89	34.989	16.606	49.890	1.00 20.00	
ATOM	891	С	TYR	89	33.357	19.658	55.493	1.00 20.00	
ATOM	892	0	TYR	89	32.594	19.687	56.458	1.00 20.00	
ATOM	893	N	GLU	90	32.995	20.007	54.240	1.00 20.00	
ATOM	895	CA	GLU	90	31.712	20.544	53.872	1.00 20.00	
ATOM	896	CB	GLU	90	31.383	20.403	52.373	1.00 20.00	
MOTA	897	CG	GLU	90	32.243	21.273	51.449	1.00 20.00	
MOTA	898	CD	GLU	90	33.488	20.498	51.031	1.00 20.00 1.00 20.00	
ATOM	899	OE1	GLU	90	33.999	19.684 20.710	51.845 49.875	1.00 20.00	
MOTA	900	OE2	GLU	90	33.942 30.596	19.920	54.637	1.00 20.00	
ATOM	901	С	GLU	90 90	30.590	18.760	55.034	1.00 20.00	
MOTA	902	N O	GLU ASN	91	29.540	20.711	54.890	1.00 20.00	
MOTA	903 905	CA	ASN	91	28.425	20.266	55.671	1.00 20.00	
ATOM ATOM	906	CB	ASN	91	27.743	19.004	55.118	1.00 20.00	
ATOM	907	CG	ASN	91	26.376	18.884	55.782	1.00 20.00	
ATOM	908		ASN	91	26.067	19.584	56.745	1.00 20.00	
ATOM	909		ASN	91	25.526	17.968	55.247	1.00 20.00	•
ATOM	912	С	ASN	91	28.955	19.976	57.037	1.00 20.00	
MOTA	913	0	ASN	91	28.340	19.265	57.830	1.00 20.00	
ATOM	914	N	SER	92	30.120	20.575	57.343	1.00 20.00	
MOTA	916	CA	SER	92	30.775	20.462	58.611	1.00 20.00	
MOTA	917	CB	SER	92	30.121	21.328	59.705	1.00 20.00 1.00 20.00	
MOTA	918	OG	SER	92	28.804	20.867	59.972 59.117	1.00 20.00	
MOTA	920	C	SER	92 92	30.861 30.223	19.058 18.715	60.111	1.00 20.00	
ATOM	921	O N	SER TYR	93	31.668	18.203	58.453	1.00 20.00	
ATOM	922 924	CA	TYR	93	31.828	16.876	58.966	1.00 20.00	
ATOM ATOM	925	CB	TYR	93	31.560	15.753	57.946	1.00 20.00	
ATOM	926	CG	TYR	93	30.103	15.728	57.618	1.00 20.00	
ATOM	927		TYR	93	29.612	16.358	56.497	1.00 20.00	
ATOM	928		TYR	93	28.270	16.311	56.196	1.00 20.00	
ATOM	929			93	29.220	15.080	58.452	1.00 20.00	
ATOM	930	CE2	TYR	93	27.876	15.039	58.163	1.00 20.00	
ATOM	931	CZ	TYR	93	27.400	15.650	57.028	1.00 20.00	
MOTA	932	OH	TYR	93	26.023	15.603	56.722	1.00 20.00	
ATOM	934	С	TYR	93	33.237	16.716	59.448	1.00 20.00	
ATOM	935	0	TYR	93	34.195	17.026	58.744	1.00 20.00	
MOTA	936	N	ALA	94	33.384	16.307	60.722	1.00 20.00 1.00 20.00	
ATOM	938	CA	ALA	94	34.651	16.026	61.332 62.866	1.00 20.00	
ATOM	939	CB	ALA	94	34.568 35.172	15.964 14.706	60.866	1.00 20.00	
MOTA	940	C	ALA ALA	94 94	35.172	14.706	60.696	1.00 20.00	
ATOM	941 942	O N	LEU	95	34.266	13.724	60.696	1.00 20.00	
ATOM ATOM	944	CA	LEU	95	34.661	12.411	60.279	1.00 20.00	
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MOTA	945	CB	LEU	95	34.488	11.374	61.403	1.00 20.00
MOTA	946	CG	LEU	95	34.889	9.936	61.030	1.00 20.00
MOTA	947	CD1	LEU	95	36.389	9.831	60.704	1.00 20.00
MC	948	CD2	LEU	95	34.445	8.947	62.122	1.00 20.00
OM	949	С	LEU	95	33.775	12.005	59.148	1.00 20.00
ATOM	950	0	LEU	95	32.580	11.774	59.326	1.00 20.00
MOTA	951	N	ALA	96	34.344	11.901	57.934	1.00 20.00
ATOM	953	CA	ALA	96	33.529	11.501	56.828	1.00 20.00
MOTA	954	CB	ALA	96	33.592	12.471	55.636	1.00 20.00
MOTA	955	С	ALA	96	34.041	10.183	56.352	1.00 20.00
MOTA	956	0	ALA	96	35.222	10.053	56.040	1.00 20.00
MOTA	957	N	VAL	97	33.165	9.160	56.327	1.00 20.00
MOTA	959	CA	VAL	97	33.548	7.887	55.793	1.00 20.00
ATOM	960	CB	VAL	97	33.554	6.778	56.812	1.00 20.00
ATOM	961		VAL	97	34.698	7.057	57.803 57.507	1.00 20.00 1.00 20.00
MOTA	962		VAL	97 07	32.183	6.709 7.591	54.706	1.00 20.00
ATOM	963	C	VAL	97 07	32.560 31.395	7.287	54.700	1.00 20.00
MOTA	964	0	VAL	97 98	33.010	7.671	53.443	1.00 20.00
ATOM	965	N CA	LEU LEU	98	32.089	7.495	52.359	1.00 20.00
MOTA	967 968	CB	LEU	98	32.012	8.718	51.428	1.00 20.00
MOTA MOTA	969	CG	LEU	98	31.150	8.489	50.171	1.00 20.00
ATOM	970		LEU	98	29.683	8.208	50.525	1.00 20.00
ATOM	971	CD2		98	31.312	9.645	49.170	1.00 20.00
ATOM	972	C	LEU	98	32.469	6.338	51.501	1.00 20.00
ATOM	973	ō	LEU	98	33.649	6.086	51.273	1.00 20.00
ATOM	974	N	SER	99	31.427	5.622	51.017	1.00 20.00
ATOM	976	CA	SER	99	31.533	4.513	50.113	1.00 20.00
ATOM	977	СВ	SER	99	31.565	4.948	48.637	1.00 20.00
ATOM	978	OG	SER	99	31.664	3.812	47.792	1.00 20.00
MOTA	980	С	SER	99	32.738	3.676	50.385	1.00 20.00
MOTA	981	0	SER	99	33.741	3.777	49.679	1.00 20.00
MOTA	982	N	ASN	100	32.683	2.847	51.441	1.00 40.00
MOTA	984	CA	ASN	100	33.796	1.990	51.716	1.00 40.00
MOTA	985	CB	ASN	100	34.171	1.941	53.206	1.00 40.00
MOTA	986	CG	ASN	100	34.709	3.304	53.612	1.00 40.00
MOTA	987	OD1		100	34.075	4.033	54.371	1.00 40.00
MOTA	988		ASN	100	35.912	3.661	53.088	1.00 40.00
MOTA	991	C	ASN	100	33.361	0.605	51.348 52.172	1.00 40.00 1.00 40.00
MOTA	992	0	ASN	100	32.801 33.630	-0.113 0.186	50.097	1.00 40.00
ATOM	993	N CA	TYR TYR	101 101	33.830	-1.112	49.639	1.00 40.00
MOTA	995 996	CB	TYR	101	32.957	-1.200	48.122	1.00 40.00
ATOM ATOM	997	CG	TYR	101	31.781	-0.366	47.741	1.00 40.00
ATOM	998		TYR	101	30.502	-0.820	47.972	1.00 40.00
ATOM	999		TYR	101	29.415	-0.125	47.495	1.00 40.00
ATOM	1000		TYR	101	31.958	0.775	46.992	1.00 40.00
ATOM	1001		TYR	101	30.875	1.470	46.507	1.00 40.00
ATOM	1002	CZ	TYR	101	29.601	1.021	46.761	1.00 40.00
ATOM	1003	ОН	TYR	101	28.489	1.723	46.251	1.00 40.00
ATOM	1005	С	TYR	101	34.312	-2.096	49.893	1.00 40.00
ATOM	1006	0	TYR	101	35.170	-1.894	50.752	1.00 40.00
ATOM	1007	N	ASP	102	34.256	-3.225	49.153	1.00 60.00
MOTA	1009	CA	ASP	102	35.256	-4.250	49.221	1.00 60.00
MOTA	1010	CB	ASP	102	34.979	-5.334	50.276	1.00 60.00
ATOM	1011	CG	ASP	102	36.283	-6.075	50.550	1.00 60.00
MOTA	1012		ASP	102	37.327	-5.662	49.979	1.00 60.00
MOTA	1013		ASP	102	36.252	-7.065	51.329	1.00 60.00
MOTA	1014	С	ASP	102	35.215	-4.938	47.893	1.00 60.00
MOTA	1015	0	ASP	102	34.499	-4.515	46.986	1.00 60.00
MOTA	1016	N	ALA	103	36.007	-6.017	47.742	1.00 60.00
MOTA	1018	CA	ALA	103	36.008	-6.756	46.516	1.00 60.00
ATOM	1019	CB	ALA	103	37.015	-7.919 -7.347	46.523	1.00 60.00
ATOM	1020	С	ALA	103	34.647	-7.347	46.359	1.00 60.00

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<i>P</i> i	1021	0	ALA	103	34.	025	-7.233	45.304	1.00	60.00
ATOM	1022	N	ASN	104	34.	138	-7.984	47.430	1.00	60.00
ATOM	1024	CA	ASN	104	32.	835	-8.569	47.350	1.00	60.00
M	1025	СВ	ASN	104	32.	720	-9.946	48.030	1.00	60.00
MOLA	1026	CG	ASN	104	32.	998	-9.784	49.516	1.00	60.00
ATOM	1027	OD1	ASN	104	32.	112	-9.433	50.294	1.00	60.00
ATOM	1028	ND2	ASN	104	34.	266 -	-10.058	49.926		60.00
ATOM	1031	С	ASN	104	31.	884	-7.637	48.020		60.00
ATOM	1032	0	ASN	104	32.		-6.462	48.219		60.00
ATOM	1033	N	LYS	105	30.		-8.148	48.379		60.00
ATOM	1035	CA	LYS	105	29.		-7.312	48.989		60.00
MOTA	1036	CB	LYS	105	28.		-7.937	48.947		60.00
MOTA	1037	ÇG	LYS	105	27.		-6.984	49.345		60.00
MOTA	1038	CD	LYS	105	25.		-7.506	48.968		60.00
MOTA	1039	ÇE	LYS	105	25.		-7.581	47.458		60.00
MOTA	1040	NZ	LYS	105	24.		-8.102	47.179		60.00 60.00
MOTA	1044	С	LYS	105	30.		-7.109	50.420		60.00
ATOM	1045	0	LYS	105	29.		-7.823	51.301		60.00
MOTA	1046	N	THR	106	30.		-6.121	50.683 52.027		60.00
MOTA	1048	CA	THR	106	31.		-5.845			60.00
MOTA	1049	CB	THR	106	31.		-7.084	52.771 54.151		60.00
MOTA	1050		THR	106	31.		-6.802 -7.635	52.145		60.00
ATOM	1052		THR	106	33. 32.		-4.897	51.936		60.00
ATOM	1053	C	THR	106 106	32.		-4.105	51.000		60.00
MOTA	1054	0	THR	107	33.		-4.946	52.930		40.00
ATOM	1055	N	GLY GLY	107	34.		-4.142	52.938		40.00
MOTA	1057	CA	GLY	107	34.		-3.603	54.311		40.00
MOTA	1058	С 0	GLY	107	35.		-4.153	55.094		40.00
MOTA	1059 1060	N	LEU	108	34.		-2.527	54.668		20.00
MOTA	1062	CA	LEU	108	34.		-1.977	55.974		20.00
ATOM ATOM	1063	CB	LEU	108	34.		-0.453	56.025		20.00
MOTA	1064	CG	LEU	108	34.		0.161	57.420		20.00
MOTA	1065		LEU	108	35.		-0.006	57.885	1.00	20.00
MOTA	1066		LEU	108	33.		1.625	57.463	1.00	20.00
ATOM	1067	C	LEU	108	33.		-2.598	56.868	1.00	20.00
ATOM	1068	0	LEU	108	32.	105	-2.259	56.795	1.00	20.00
ATOM	1069	N	LYS	109	33.	711	-3.570	57.691	1.00	20.00
ATOM	1071	CA	LYS	109	32.	849	-4.236	58.625		20.00
ATOM	1072	СВ	LYS	109	33.	493	-5.499	59.220		20.00
ATOM	1073	CG	LYS	109	33.	728	-6.599	58.181		20.00
ATOM	1074	CD	LYS	109	34.		-6.233	57.124		20.00
ATOM	1075	CE	LYS	109	35.		-7.330	56.084		20.00
ATOM	1076	NZ	LYS	109	35.		-8.503	56.719		20.00
ATOM	1080	С	LYS	109	32.		-3.335	59.761		20.00
ATOM	1081	0	LYS	109	31.		-3.352	60.243		20.00
MOTA	1082	N	GLU	110	33.		-2.532	60.241		20.00
ATOM	1084	CA	GLU	110	33.		-1.699	61.375		20.00
ATOM	1085	СВ	GLU	110	33.		-2.506	62.686 62.753		20.00
ATOM	1086	CG	GLU	110	34.		-3.458	64.072		20.00
MOTA	1087	CD	GLU	110	34.		-4.215 -4.770	64.393		20.00
ATOM	1088		GLU	110	33.		-4.770 -4.249	64.776		20.00
MOTA	1089		GLU	110	35.		-0.592	61.413		20.00
MOTA	1090	C	GLU	110	34.		-0.516	60.570		20.00
ATOM	1091	0	GLU	110	35. 33.		0.344	62.363		20.00
MOTA	1092	N C2	LEU	111 111	34.		1.475	62.663		20.00
MOTA	1094	CA	LEU LEU	111	34.		2.581	63.358		20.00
MOTA	1095	CB CG	LEU	111	34.		3.839	63.700		20.00
ATOM	1096 1097		LEU	111	35.		4.544	62.419		20.00
ATOM	1097		LEU	111	34.		4.771	64.638		20.00
ATOM ATOM	1098	CDZ	LEU	111	36.		1.204	63.522		20.00
ATOM	1100	0	LEU	111	37.		1.894	63.330		20.00
ATOM	1101	N	PRO	112	36.		0.168	64.355		20.00
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ATOM	1102	CD	PRO	112	36.108	-1.117	63.673	1.00 20.00
MOTA	1103	CA	PRO	112	36.946	0.092	65.507	1.00 20.00
MOTA	1104	CB	PRO	112	37.607	-1.286	65.523	1.00 20.00
M	1105	CG	PRO	112	37.399	-1.812	64.107	1.00 20.00
MOLA	1106	С	PRO	112	37.924	1.181	65.815	1.00 20.00
MOTA	1107	0	PRO	112	39.116	0.935	65.971	1.00 20.00
MOTA	1108	N	MET	113	37.371	2.381	66.007	1.00 20.00
MOTA	1110	CA	MET	113	37.969	3.619	66.401	1.00 20.00
MOTA	1111	CB	MET	113	37.208	4.872	65.938	1.00 20.00
MOTA	1112	CG	MET	113	37.357	5.147	64.443	1.00 20.00
MOTA	1113	SD	MET	113	39.035	5.590	63.905	1.00 20.00
MOTA	1114	CE	MET	113	38.968	7.272	64.579	1.00 20.00
MOTA	1115	С	MET	113	38.023	3.646	67.891	1.00 20.00 1.00 20.00
MOTA	1116	0	MET	113	38.035	4.725	68.468	
MOTA	1117	N	ARG	114	37.983	2.481	68.565	1.00 20.00 1.00 20.00
MOTA	1119	CA	ARG	114	37.744	2.375 1.019	69.983 70.550	1.00 20.00
ATOM	1120	CB	ARG	114	38.199	0.735	70.350	1.00 20.00
MOTA	1121	CG	ARG	114	39.689 39.990	-0.125	69.122	1.00 20.00
ATOM	1122	CD	ARG	114	39.362	-1.457	69.345	1.00 20.00
ATOM	1123	NE	ARG	114 114	39.850	-2.557	68.703	1.00 20.00
ATOM	1125	CZ	ARG	114	39.275	-3.778	68.906	1.00 20.00
MOTA	1126	NH1 NH2	ARG ARG	114	40.917	-2.437	67.859	1.00 20.00
ATOM	1129 1132	C	ARG	114	38.335	3.440	70.870	1.00 20.00
ATOM	1132	0	ARG	114	37.721	3.778	71.879	1.00 20.00
ATOM ATOM	1134	N	ASN	115	39.533	3.969	70.584	1.00 20.00
ATOM	1134	CA	ASN	115	40.116	5.009	71.396	1.00 20.00
ATOM	1137	CB	ASN	115	41.633	5.149	71.193	1.00 20.00
ATOM	1138	CG	ASN	115	42.267	3.951	71.883	1.00 20.00
ATOM	1139		ASN	115	41.577	3.133	72.489	1.00 20.00
ATOM	1140		ASN	115	43.619	3.851	71.812	1.00 20.00
ATOM	1143	С	ASN	115	39.483	6.371	71.233	1.00 20.00
ATOM	1144	0	ASN	115	39.737	7.272	72.029	1.00 20.00
MOTA	1145	N	LEU	116	38.690	6.577	70.164	1.00 20.00
MOTA	1147	CA	LEU	116	38.092	7.838	69.813	1.00 20.00
ATOM	1148	CB	LEU	116	37.302	7.771	68.493	1.00 20.00
MOTA	1149	CG	LEU .	116	36.636	9.094	68.073	1.00 20.00
MOTA	1150		ĻEU	116	37.689	10.176	67.784	1.00 20.00
MOTA	1151	CD2	LEU	116	35.666	8.886	66.901	1.00 20.00
MOTA	1152	С	LEU	116	37.155	8.329	70.876	1.00 20.00
MOTA	1153	0	LEU	116	36.014	7.880	70.973	1.00 20.00
MOTA	1154	N	GLN	117	37.673	9.215	71.750	1.00 20.00
MOTA	1156	CA	GLN	117	36.955	9.843	72.820	1.00 20.00 1.00 20.00
MOTA	1157	СВ	GLN	117	37.897	10.308	73.944 74.599	1.00 20.00
ATOM	1158	CG	GLN	117	38.698 37.734	9.182 8.298	75.375	1.00 20.00
ATOM	1159	CD OF1	GLN	117 117	36.848	7.672	74.795	1.00 20.00
ATOM	1160		GLN GLN	117	37.907	8.244	76.724	1.00 20.00
ATOM	1161 1164	C	GLN	117	36.146	11.051	72.455	1.00 20.00
ATOM	1165	0	GLN	117	35.059	11.239	72.993	1.00 20.00
MOTA	1166	N	GLU	118	36.662	11.951	71.587	1.00 20.00
ATOM ATOM	1168	CA	GLU	118	35.860	13.113	71.321	1.00 20.00
ATOM	1169	CB	GLU	118	35.913	14.183	72.424	1.00 20.00
ATOM	1170	CG	GLU	118	34.858	15.275	72.226	1.00 20.00
ATOM	1171	CD	GLU	118	34.975	16.291	73.350	1.00 20.00
ATOM	1172		GLU	118	33.956	16.974	73.630	1.00 20.00
ATOM	1173		GLU	118	36.084	16.402	73.940	1.00 20.00
ATOM	1174	C	GLU	118	36.217	13.797	70.043	1.00 20.00
MOTA	1175	0	GLU	118	37.375	13.829	69.629	1.00 20.00
ATOM	1176	N	ILE	119	35.185	14.358	69.380	1.00 20.00
ATOM	1178	CA	ILE	119	35.360	15.138	68.194	1.00 20.00
ATOM	1179	СВ	ILE	119	34.474	14.698	67.059	1.00 20.00
ATOM	1180	CG2	ILE	119	34.603	15.722	65.922	1.00 20.00
ATOM	1181	CG ₁	ILE	119	34.829	13.264	66.628	1.00 20.00

<i>H</i> 1	1182	CD1	ILE	119	33.826	12.644	65.654		20.00
ATOM	1183	С	ILE	119	34.944	16.515	68.607	1.00	20.00
MOTA	1184	0	ILE	119	33.767	16.862	68.525	1.00	20.00
MC	1185	N	LEU	120	35.925	17.373	68.955		20.00
OM	1187	CA	LEU	120	35.647	18.662	69.531		20.00
ATOM	1188	CB	LEU	120	36.861	19.604	69.661		20.00
MOTA	1189	CG	LEU	120	37.871	19.235	70.761		20.00
ATOM	1190	CD1	LEU	120	38.609	17.938	70.424		20.00
ATOM	1191	CD2	LEU	120	38.825	20.404	71.057	1.00	20.00
MOTA	1192	С	LEU	120	34.660	19.438	68.726		20.00
ATOM	1193	0	LEU	120	33.852	20.172	69.292		20.00
ATOM	1194	N	HIS	121	34.699	19.344	67.387	1.00	20.00
ATOM	1196	CA	HIS	121	33.731	20.124	66.677	1.00	20.00
ATOM	1197	СВ	HIS	121	34.231	21.527	66.296		20.00
ATOM	1198	CG	HIS	121	33.162	22.376	65.673		20.00
MOTA	1199	CD2	HIS	121	32.867	22.598	64.363		20.00
ATOM	1200	ND1	HIS	121	32.234	23.095	66.393		20.00
ATOM	1202	CE1	HIS	121	31.430	23.713	65.490	1.00	20.00
ATOM	1203	NE2	HIS	121	31.776	23.441	64.245		20.00
MOTA	1205	С	HIS	121	33.334	19.442	65.411		20.00
ATOM	1206	0	HIS	121	34.098	18.668	64.840		20.00
ATOM	1207	N	GLY	122	32.099	19.720	64.947		20.00
ATOM	1209	CA	GLY	122	31.633	19.168	63.714		20.00
ATOM	1210	С	GLY	122	30.940	17.873	63.991		20.00
ATOM	1211	0	GLY	122	31.039	17.322	65.086		20.00
MOTA	1212	N	ALA	123	30.204	17.370	62.978		20.00
MOTA	1214	CA	ALA	123	29.471	16.140	63.080		20.00
ATOM	1215	CB	ALA	123	28.040	16.233	62.527		20.00
ATOM	1216	С	ALA	123	30.174	15.063	62.315		20.00
ATOM	1217	0	ALA	123	31.321	15.229	61.909		20.00
ATOM	1218	N	VAL	124	29.500	13.906	62.126		20.00
ATOM	1220	CA	VAL	124	30.075	12.810	61.392		20.00
MOTA	1221	CB	VAL	124	30.249	11.569	62.219		20.00
ATOM	1222		VAL	124	28.855	11.048	62.614		20.00
MOTA	1223	CG2		124	31.094	10.562	61.420		20.00
MOTA	1224	С	VAL	124	29.175	12.455	60.246		20.00
MOTA	1225	0	VAL	124	28.001	12.822	60.226		20.00
ATOM	1226	N	ARG	125	29.718	11.762	59.223		20.00
ATOM	1228	CA	ARG	125	28.902	11.392 12.269	58.101 56.870		20.00
ATOM	1229	CB	ARG	125	29.175 28.335	11.918	55.646		20.00
MOTA	1230	CG	ARG	125	28.619	12.837	54.459		20.00
ATOM	1231	CD	ARG	125 125	27.732	12.408	53.345		20.00
ATOM	1232	NE	ARG	125	26.442	12.852	53.316		20.00
ATOM	1234	CZ NH1	ARG	125	25.626	12.509	52.278		20.00
ATOM	1235 1238	NH2		125	25.966	13.637	54.325		20.00
ATOM	1236	C	ARG	125	29.243	9.985	57.723		20.00
ATOM	1242	0	ARG	125	30.297	9.728	57.145		20.00
ATOM	1242	N	PHE	126	28.354	9.023	58.025		20.00
ATOM	1245	CA	PHE	126	28.636	7.664	57.661		20.00
MOTA MOTA	1246	CB	PHE	126	28.341	6.650	58.781		20.00
ATOM	1247	CG	PHE	126	29.317	6.817	59.893		20.00
ATOM	1248	CD1		126	30.518	6.145	59.875		20.00
ATOM	1249	CD2		126	28.994	7.566	61.000		20.00
ATOM	1250	CE1		126	31.389	6.236	60.934		20.00
ATOM	1251	CE2		126	29.861	7.662	62.062		20.00
ATOM	1252	CZ	PHE	126	31.060	6.993	62.033		20.00
ATOM	1253	C	PHE	126	27.707	7.295	56.548		20.00
ATOM	1254	0	PHE	126	26.558	6.923	56.781		20.00
ATOM	1255	N	SER	127	28.193	7.340	55.295		20.00
ATOM	1257	CA	SER	127	27.298	7.056	54.219		20.00
MOTA	1258	СВ	SER	127	26.962	8.291	53.365		20.00
ATOM	1259	OG	SER	127	28.137	8.806	52.760		20.00
ATOM	1261	C	SER	127	27.798	5.986	53.302		20.00
ATOM	1201	_						•	

ATOM	1262	0	SER	127	28.995	5.712	53.212	1.00 20.00
ATOM	1263	N	ASN	128	26.840	5.341	52.604	1.00 20.00
MOTA	1265	CA	ASN	128	27.126	4.347	51.610	1.00 20.00
MC	1266	СВ	ASN	128	27.619	4.946	50.280	1.00 20.00
MO'	1267	CG	ASN	128	26.461	5.697	49.637	1.00 20.00
MOTA	1268	OD1	ASN	128	25.444	5.108	49.275	1.00 20.00
ATOM	1269	ND2	ASN	128	26.617	7.041	49.494	1.00 20.00
ATOM	1272	С	ASN	128	28.134	3.339	52.055	1.00 20.00
ATOM	1273	0	ASN	128	29.252	3.306	51.542	1.00 20.00
ATOM	1274	N	ASN	129	27.778	2.502	53.050	1.00 20.00
MOTA	1276	CA	ASN	129	28.702	1.470	53.428	1.00 20.00
ATOM	1277	СВ	ASN	129	29.436	1.800	54.735	1.00 20.00
ATOM	1278	CG	ASN	129	30.295	3.030	54.482	1.00 20.00
ATOM	1279	OD1	ASN	129	31.229	2.993	53.682	1.00 20.00
ATOM	1280	ND2	ASN	129	29.965	4.156	55.170	1.00 20.00
ATOM	1283	С	ASN	129	27.923	0.211	53.673	1.00 20.00
MOTA	1284	0	ASN	129	27.696	-0.162	54.821	1.00 20.00
MOTA	1285	N	PRO	130	27.598	-0.495	52.620	1.00 20.00
ATOM	1286	CD	PRO	130	28.347	-0.415	51.380	1.00 20.00
ATOM	1287	CA	PRO	130	26.725	-1.646	52.666	1.00 20.00
АТОМ	1288	СВ	PRO	130	26.874	-2.340	51.311	1.00 20.00
ATOM	1289	CG	PRO	130	27.546	-1.292	50.404	1.00 20.00
ATOM	1290	С	PRO	130	27.007	-2.592	53.801	1.00 20.00
ATOM	1291	0	PRO	130	26.073	-2.963	54.510	1.00 20.00
ATOM	1292	N	ALA	131	28.280	-2.993	53.967	1.00 20.00
ATOM	1294	CA	ALA	131	28.763	-3.910	54.962	1.00 20.00
ATOM	1295	СВ	ALA	131	30.131	-4.505	54.587	1.00 20.00
ATOM	1296	С	ALA	131	28.907	-3.352	56.350	1.00 20.00
ATOM	1297	0	ALA	131	28.971	-4.114	57.312	1.00 20.00
ATOM	1298	N	LEU	132	29.031	-2.020	56.492	1.00 20.00
ATOM	1300	CA	LEU	132	29.337	-1.428	57.767	1.00 20.00
ATOM	1301	СВ	LEU	132	29.400	0.108	57.704	1.00 20.00
ATOM	1302	CG	LEU	132	29.742	0.793	59.038	1.00 20.00
ATOM	1303	CD1		132	31.129	0.382	59.549	1.00 20.00
ATOM	1304	CD2	LEU	132	29.586	2.318	58.928	1.00 20.00
ATOM	1305	С	LEU	132	28.388	-1.818	58.852	1.00 20.00
ATOM	1306	0	LEU	132	27.174	-1.653	58.743	1.00 20.00
ATOM	1307	N	CYS	133	28.965	-2.335	59.955	1.00 20.00
ATOM	1309	CA	CYS	133	28.236	-2.785	61.096	1.00 20.00
MOTA	1310	CB	CYS	133	28.392	-4.290	61.352	1.00 20.00
ATOM	1311	SG	CYS	133	27.437	-5.281	60.176	1.00 20.00
MOTA	1312	С	CYS	133	28.804	-2.090	62.292	1.00 20.00
MOTA	1313	0	CYS	133	29.656	-1.214	62.167	1.00 20.00
MOTA	1314	N	ASN	134	28.310	-2.460	63.488	1.00 20.00
MOTA	1316	CA	ASN	134	28.773	-1.887	64.715	1.00 20.00
MOTA	1317	CB	ASN	134	30.193	-2.332	65.107	1.00 20.00
MOTA	1318	CG	ASN	134	30.101	-3.784	65.561	1.00 20.00
MOTA	1319	OD1	ASN	134	30.893	-4.632	65.156	1.00 20.00
MOTA	1320	ND2	ASN	134	29.102	-4.078	66.436	1.00 20.00
ATOM	1323	С	ASN	134	28.729	-0.397	64.609	1.00 20.00
ATOM	1324	0	ASN	134	29.653	0.292	65.040	1.00 20.00
ATOM	1325	N	VAL	135	27.731	0.107	63.854	1.00 20.00
ATOM	1327	CA	VAL	135	27.391	1.500	63.755	1.00 20.00
MOTA	1328	CB	VAL	135	26.828	1.846	62.408	1.00 20.00
ATOM	1329	CG1	VAL	135	27.912	1.585	61.349	1.00 20.00
ATOM	1330	CG2	VAL	135	25.538	1.036	62.190	1.00 20.00
MOTA	1331	С	VAL	135	26.393	1.959	64.782	1.00 20.00
MOTA	1332	0	VAL	135	26.512	3.040	65.353	1.00 20.00
ATOM	1333	N	GLU	136	25.349	1.136	65.009	1.00 20.00
MOTA	1335	CA	GLU	136	24.252	1.436	65.892	1.00 20.00
MOTA	1336	CB	GLU	136	23.078	0.452	65.745	1.00 20.00
MOTA	1337	CG	GLU	136	21.911	0.768	66.680	1.00 20.00
ATOM	1338	CD	GLU	136	21.210	2.009	66.147	1.00 20.00
MOTA	1339	OE1	GLU	136	20.551	1.899	65.079	1.00 20.00

A C	1340	OE2	GLU	136	21.327	3.082	66.798	1.00 20.00		
ATOM	1341	С	GLU	136	24.708	1.359	67.305	1.00 20.00		
MOTA	1342	0	GLU	136	24.139	1.986	68.196	1.00 20.00		
M	1343	N	SER	137	25.749	0.542	67.513	1.00 20.00		
A . OM	1345	CA	SER	137	26.349	0.181	68.762	1.00 20.00		
MOTA	1346	СВ	SER	137	27.419	-0.903	68.574	1.00 20.00		
MOTA	1347	OG	SER	137	26.854	-2.020	67.907	1.00 20.00		
MOTA	1349	С	SER	137	27.023	1.314	69.462	1.00 20.00 1.00 20.00		
MOTA	1350	0	SER	137	27.244	1.223	70.667 68.753	1.00 20.00		
MOTA	1351	N	ILE	138	27.452	2.377 3.385	69.515	1.00 20.00		
MOTA	1353	CA	ILE	138	28.131 29.429	3.894	68.940	1.00 20.00		
MOTA	1354	CB	ILE	138 138	30.414	2.715	68.934	1.00 20.00		
ATOM	1355	CG2	ILE	138	29.257	4.560	67.568	1.00 20.00		
ATOM	1356 1357		ILE	138	28.957	3.567	66.454	1.00 20.00		
MOTA	1357	CDI	ILE	138	27.294	4.575	69.845	1.00 20.00		
ATOM ATOM	1359	0	ILE	138	26.422	4.989	69.082	1.00 20.00		
ATOM	1360	N	GLN	139	27.544	5.144	71.044	1.00 20.00		
MOTA	1362	CA	GLN	139	26.824	6.306	71.473	1.00 20.00		
MOTA	1363	CB	GLN	139	26.612	6.369	72.996	1.00 20.00		
ATOM	1364	CG	GLN	139	25.723	5.254	73.550	1.00 20.00		
ATOM	1365	CD	GLN	139	25.608	5.455	75.055	1.00 20.00		
ATOM	1366		GLN	139	26.228	6.352	75.625	1.00 20.00		
ATOM	1367		GLN	139	24.789	4.599	75.721	1.00 20.00		
ATOM	1370	С	GLN	139	27.653	7.494	71.108	1.00 20.00		
MOTA	1371	0	GLN	139	28.533	7.915	71.854	1.00 20.00		
MOTA	1372	N	TRP	140	27.351	8.092	69.948	1.00 20.00		
ATOM	1374	CA	TRP	140	28.071	9.224	69.450	1.00 20.00	•	
MOTA	1375	СВ	TRP	140	27.692	9.605	68.010	1.00 20.00		
MOTA	1376	CG	TRP	140	28.076	8.535	67.013	1.00 20.00 1.00 20.00		
MOTA	1377	CD2		140	29.428	8.220 7.119	66.635 65.780	1.00 20.00		
ATOM	1378		TRP	140	29.372 30.620	8.790	66.980	1.00 20.00		
MOTA	1379		TRP	140 140	27.281	7.613	66.398	1.00 20.00		
ATOM	1380		TRP TRP	140	28.048	6.762	65.638	1.00 20.00		
MOTA	1381 1383		TRP	140	30.508	6.574	65.251	1.00 20.00		
ATOM ATOM	1384		TRP	140	31.763	8.237	66.445	1.00 20.00		
ATOM	1385		TRP	140	31.709	7.152	65.595	1.00 20.00		
MOTA	1386	C	TRP	140	27.801	10.373	70.359	1.00 20.00		
ATOM	1387	Ō	TRP	140	28.476	11.394	70.301	1.00 20.00		
ATOM	1388	N	ARG	141	26.754	10.253	71.190	1.00 20.00		
ATOM	1390	CA	ARG	141	26.397	11.300	72.099	1.00 20.00		
ATOM	1391	СВ	ARG	141	25.226	10.879	73.005	1.00 20.00		
MOTA	1392	CG	ARG	141	24.596	12.002	73.831	1.00 20.00		
MOTA	1393	CD	ARG	141	23.535	11.481	74.804	1.00 20.00		
MOTA	1394	NE	ARG	141	22.804	12.651	75.364	1.00 20.00		
MOTA	1396	CZ	ARG	141	21.689	13.118	74.730 75.237	1.00 20.00 1.00 20.00		
MOTA	1397		ARG	141	21.013	14.190	73.591	1.00 20.00		
MOTA	1400		ARG	141	21.246 27.568	12.509 11.603	72.983	1.00 20.00		
MOTA	1403	С	ARG	`141 141	27.850	12.769	73.253	1.00 20.00		
MOTA	1404	O N	ARG ASP	141	28.270	10.571	73.493	1.00 20.00		
ATOM	1405 1407	N CA	ASP	142	29.398	10.884	74.323	1.00 20.00		
MOTA MOTA	1407	CB	ASP	142	29.869	9.726	75.243	1.00 20.00		
ATOM	1408	CG	ASP	142	30.337	8.470	74.513	1.00 20.00		
ATOM	1410		ASP	142	30.547	8.500	73.274	1.00 20.00		
ATOM	1411		ASP	142	30.493	7.437	75.218	1.00 20.00		
MOTA	1412	C	ASP	142	30.543	11.452	73.533	1.00 20.00		
ATOM	1413	o	ASP	142	31.222	12.373	73.987	1.00 20.00		
ATOM	1414	N	ILE	143	30.787	10.913	72.324	1.00 20.00		
ATOM	1416	CA	ILE	143	31.880	11.333	71.493	1.00 20.00		
AIOH	7410									
ATOM	1417	СВ	ILE	143	32.102	10.348	70.369	1.00 20.00		
		CG2	ILE ILE ILE	143 143 143	32.102 30.926 33.460	10.348 10.462 10.541	70.369 69.391 69.684	1.00 20.00 1.00 20.00 1.00 20.00		

MOTA	1420	CD1	ILE	143	33.543	11.814	68.850	1.00 20.00
MOTA	1421	С	ILE	143	31.688	12.725	70.950	1.00 20.00
MOTA	1422	0	ILE	143	32.602	13.546	70.998	1.00 20.00
MC	1423	N	VAL	144	30.480	13.041	70.442	1.00 20.00
WO.T.	1425	CA	VAL	144	30.207	14.324	69.854	1.00 20.00
MOTA	1426	CB	VAL	144	29.753	14.239	68.426	1.00 20.00
ATOM	1427		VAL	144	30.892	13.642	67.582	1.00 20.00
MOTA	1428		VAL	144	28.449	13.425	68.377	1.00 20.00
MOTA	1429	С	VAL	144	29.090	14.942	70.630	1.00 20.00
MOTA	1430	0	VAL	144	28.288	14.241	71.240	1.00 20.00
ATOM	1431	N	SER	145	29.004	16.285	70.626	1.00 20.00
ATOM	1433	CA	SER	145	27.993	16.945	71.401	1.00 20.00
ATOM	1434	CB	SER	145	27.967	18.470	71.217	1.00 20.00 1.00 20.00
ATOM	1435	OG C	SER	145 145	29.188 26.640	19.039 16.424	71.669 71.040	1.00 20.00
MOTA	1437 1438	c o	SER SER	145	26.434	15.869	69.963	1.00 20.00
MOTA	1438	N	SER	146	25.678	16.577	71.968	1.00 40.00
MOTA MOTA	1433	CA	SER	146	24.344	16.120	71.722	1.00 40.00
ATOM	1442	CB	SER	146	23.417	16.297	72.935	1.00 40.00
ATOM	1443	OG	SER	146	23.868	15.487	74.011	1.00 40.00
MOTA	1445	C	SER	146	23.801	16.949	70.609	1.00 40.00
ATOM	1446	Ö	SER	146	23.167	16.436	69.688	1.00 40.00
ATOM	1447	N	ASP	147	24.059	18.268	70.664	1.00 40.00
ATOM	1449	CA	ASP	147	23.578	19.139	69.638	1.00 40.00
ATOM	1450	СВ	ASP	147	24.004	20.603	69.840	1.00 40.00
ATOM	1451	CG	ASP	147	23.299	21.444	68.785	1.00 40.00
ATOM	1452	OD1	ASP	147	22.361	20.911	68.135	1.00 40.00
ATOM	1453	OD2	ASP	147	23.693	22.629	68.613	1.00 40.00
ATOM	1454	С	ASP	147	24.208	18.667	68.373	1.00 40.00
ATOM	1455	0	ASP	147	23.561	18.599	67.329	1.00 40.00
ATOM	1456	N	PHE	. 148	25.502	18.307	68.448	1.00 40.00
MOTA	1458	CA	PHE	148	26.182	17.857	67.280	1.00 40.00
ATOM	1459	CB	PHE	148	27.692	17.655	67.485	1.00 40.00
MOTA	1460	CG	PHE	148	28.305	19.013	67.455	1.00 40.00
MOTA	1461		PHE	148	28.659	19.580	66.253	1.00 40.00
MOTA	1462		PHE	. 148	28.480	19.742	68.608	1.00 40.00
ATOM	1463	CE1	PHE	148	29.191	20.846	66.203	1.00 40.00
MOTA	1464	CE2	PHE	148	29.014	21.009 21.564	68.565 67.361	1.00 40.00
MOTA	1465 1466		PHE PHE	148 148	29.373 25.596	16.582	66.770	1.00 40.00
ATOM ATOM	1467	С 0	PHE	148	25.551	16.361	65.562	1.00 40.00
ATOM	1468	N	LEU	149	25.100	15.717	67.672	1.00 40.00
ATOM	1470	CA	LEU	149	24.608	14.440	67.240	1.00 40.00
ATOM	1471	CB	LEU	149	24.069	13.569	68.387	1.00 40.00
ATOM	1472	CG	LEU	149	23.546	12.205	67.900	1.00 40.00
MOTA	1473		LEU	149	24.670	11.377	67.254	1.00 40.00
MOTA	1474	CD2	LEU	149	22.825	11.446	69.023	1.00 40.00
MOTA	1475	С	LEU	149	23.505	14.619	66.249	1.00 40.00
MOTA	1476	0	LEU	149	23.379	13.843	65.303	1.00 40.00
MOTA	1477	N	SER	150	22.675	15.664	66.425	1.00 40.00
ATOM	1479	CA	SER	150	21.578	15.868	65.523	1.00 40.00
MOTA	1480	СВ	SER	150	20.763	17.128	65.857	1.00 40.00
ATOM	1481	OG	SER	150	21.564	18.288	65.698	1.00 40.00
MOTA	1483	С	SER	150	22.114	16.030	64.135	1.00 40.00
ATOM	1484	0	SER	150	21.501	15.583	63.167	1.00 40.00
MOTA	1485	N	ASN	151	23.286	16.678	64.015	1.00 40.00
ATOM	1487	CA	ASN	151	23.919	16.977	62.762	1.00 40.00
ATOM	1488	CB	ASN	151	25.177	17.844	62.937	1.00 40.00
ATOM	1489	CG	ASN	151	24.741	19.195	63.487	1.00 40.00
MOTA	1490		ASN	151 151	23.656	19.688 19.813	63.180 64.329	1.00 40.00
ATOM	1491		ASN	151 151	25.612 24.341	19.813	62.019	1.00 40.00
ATOM	1494	с 0	ASN ASN	151	24.341	15.743	60.790	1.00 40.00
MOTA MOTA	1495 1496	N	MET	151	24.686	14.664	62.747	1.00 40.00
MIUM	T#30	7.4	Lini	1.52	24.000	13.004	52.737	1.00 40.00

Z A	1498	CA	MET	152	25.193	13.461	62.147		40.00
ATOM	1499	CB	MET	152	25.308	12.309	63.162		40.00
MOTA	1500	CG	MET	152	25.897	11.013	62.602		40.00
MC	1501	SD	MET	152	26.051	9.686	63.835		40.00
P. OW	1502	CE	MET	152	26.754	8.460	62.697		40.00
MOTA	1503	С	MET	152	24.326	13.011	61.016		40.00
MOTA	1504	0	MET	152	23.101	13.009	61.115		40.00
MOTA	1505	N	SER	153	24.967	12.636	59.887		40.00
MOTA	1507	CA	SER	153	24.220 24.502	12.200 13.023	58.745 57.473		40.00
ATOM	1508	CB	SER	153 153	23.728	12.530	56.390		40.00
ATOM	1509	OG C	SER SER	153	24.586	10.788	58.441		40.00
MOTA	1511	0	SER	153	25.725	10.484	58.086		40.00
MOTA MOTA	1512 1513	N	MET	154	23.612	9.872	58.577		40.00
ATOM	1515	CA	MET	154	23.874	8.509	58.242		40.00
ATOM	1516	CB	MET	154	23.599	7.514	59.384		40.00
ATOM	1517	CG	MET	154	23.890	6.064	58.993	1.00	40.00
ATOM	1518	SD	MET	154	23.588	4.841	60.306	1.00	40.00
ATOM	1519	CE	MET	154	25.146	5.148	61.184	1.00	40.00
MOTA	1520	С	MET	154	22.942	8.173	57.137		40.00
ATOM	1521	0	MET	154	21.741	8.426	57.230	1.00	40.00
ATOM	1522	N	ASP	155	23.463	7.600	56.040		40.00
MOTA	1524	CA	ASP	155	22.536	7.273	55.010		40.00
ATOM	1525	CB	ASP	155	22.995	7.565	53.563		40.00
MOTA	1526	CG	ASP	155	24.145	6.657	53.156		40.00
ATOM	1527		ASP	155	24.405	6.563	51.927		40.00
MOTA	1528	OD2		155	24.773	6.038	54.051		40.00
ATOM	1529	С	ASP	155	22.264	5.822	55.133		40.00
MOTA	1530	0	ASP	155	23.085	5.059	55.646		40.00
ATOM	1531	N	PHE	156 156	21.080	5.440	54.628 54.646		40.00
ATOM	1533	CA	PHE	156	20.544 19.243	4.117 4.042	53.826		40.00
ATOM	1534	CB	PHE PHE	156 156	18.768	2.632	53.757		40.00
ATOM	1535	CG CD1		156	18.067	2.069	54.797		40.00
MOTA	1536 1537	CD1	PHE	156	18.934	1.913	52.596		40.00
ATOM ATOM	1537	CE1	PHE	156	17.563	0.794	54.688		40.00
ATOM	1539	CE2	PHE	156	18.435	0.637	52.482		40.00
ATOM	1540	CZ	PHE	156	17.747	0.076	53.531	1.00	40.00
ATOM	1541	С	PHE	156	21.540	3.207	54.022	1.00	40.00
ATOM	1542	0	PHE	156	21.535	2.002	54.267	1.00	40.00
ATOM	1543	N	GLN	157	22.447	3.768	53.207		40.00
MOTA	1545	CA	GLN	157	23.349	2.907	52.518		40.00
MOTA	1546	CB	GLN	157	24.276	3.608	51.518		40.00
MOTA	1547	CG	GLN	157	24.984	2.599	50.609		40.00
MOTA	1548	CD	GLN	157	23.914	1.839	49.835		40.00
MOTA	1549		GLN	157	22.728	2.158	49.910		40.00
ATOM	1550		GLN	157	24.342	0.797	49.072 53.456		40.00
MOTA	1553	C	GLN	157 157	24.172 24.886	2.079 1.187	53.430		40.00
ATOM	1554	O N	GLN	157 158	24.126	2.350	54.776		40.00
MOTA	1555	N CA	ASN ASN	158	24.120	1.507	55.675		40.00
MOTA	1557 1558	CB	ASN	158	25.044	2.095	57.084		40.00
MOTA MOTA	1559	CG	ASN	158	26.028	3.251	56.984		40.00
ATOM	1560		ASN	158	26.920	3.251	56.136		40.00
ATOM	1561		ASN	158	25.869	4.264	57.877	1.00	40.00
ATOM	1564	C	ASN	158	24.131	0.208	55.803	1.00	40.00
ATOM	1565	ō	ASN	158	23.093	0.012	55.175		40.00
ATOM	1566	N	HIS	159	24.671	-0.732	56.607		40.00
АТОМ	1568	CA	HIS	159	24.049	-2.020	56.748		40.00
ATOM	1569	CB	HIS	159	25.033	-3.127	57.165		40.00
MOTA	1570	CG	HIS	159	24.457	-4.507	57.054		40.00
ATOM	1571		HIS	159	24.069	-5.379	58.023		40.00
ATOM	1572		HIS	159	24.246	-5.157	55.858		40.00
MOTA	1574	CE1	HIS	159	23.740	-6.379	56.160	1.00	40.00

MOTA	1575		HIS	159	23.614		57.463	1.00 40.00
MOTA	1577	С	HIS	159	22.963		57 .7 79	1.00 40.00
MOTA	1578	0	HIS	159	22.940	-1.052	58.614	1.00 40.00
MC	1579	N	LEU	160	22.020	-2.922	57.735	1.00 40.00
OM	1581	CA	LEU	160	20.933	-2.939	58.671	1.00 40.00
MOTA	1582	CB	LEU	160	19.700	-3.721	58.183	1.00 40.00
MOTA	1583	CG	LEU	160	19.036	-3.116	56.933	1.00 40.00
ATOM	1584	CD1	LEU	160	19.969	-3.190	55.714	1.00 40.00
ATOM	1585	CD2	LEU	160	17.660	-3.751	56.672	1.00 40.00
ATOM	1586	С	LEU	160 .	21.396	-3.580	59.941	1.00 40.00
ATOM	1587	0	LEU	160	22.356	-4.345	59.956	1.00 40.00
MOTA	1588	N	GLY	161	20.671	-3.307	61.042	1.00 40.00
ATOM	1590	CA	GLY	161	20.984	-3.755	62.372	1.00 40.00
ATOM	1591	С	GLY	161	21.076	-5.247	62.474	1.00 40.00
MOTA	1592	0	GLY	161	21.366	-5.783	63.542	1.00 40.00
MOTA	1593	N	SER	162	20.837	-5.955	61.359	1.00 40.00
ATOM	1595	CA	SER	162	20.887	-7.388	61.308	1.00 40.00
ATOM	1596	СВ	SER	162	20.644	-7.945	59.896	1.00 40.00
ATOM	1597	OG	SER	162	20.708	-9.364	59.915	1.00 40.00
ATOM	1599	C	SER	162	22.260	-7.815	61.734	1.00 40.00
ATOM	1600	o	SER	162	22.481	-8.959	62.127	1.00 40.00
ATOM	1601	N	CYS	163	23.229	-6.888	61.661	1.00 40.00
ATOM	1603	CA	CYS	163	24.610	-7.156	61.943	1.00 40.00
ATOM	1604	CB	CYS	163	25.371	-5.859	62.222	1.00 40.00
ATOM	1605	SG	CYS	163	25.554	-4.822	60.750	1.00 40.00
ATOM	1606	C	CYS	163	24.886	-8.059	63.119	1.00 40.00
ATOM	1607	0	CYS	163	25.394	-9.158	62.913	1.00 40.00
ATOM	1608	N	GLN	164	24.587	-7.659	64.380	1.00 40.00
ATOM	1610	CA	GLN	164	24.973	-8.554	65.450	1.00 40.00
ATOM	1611	CB	GLN	164	26.484	-8.826	65.471	1.00 40.00
	1612	CG	GLN	164	27.309	-7.566	65.753	1.00 40.00
MOTA	1613	CD	GLN	164	28.783	-7.943	65.755	1.00 40.00
ATOM	1614	OE1		164	29.153	-9.070	65.434	1.00 40.00
MOTA		NE2	GLN	164	29.155	-6.968	66.131	1.00 40.00
ATOM	1615	C C	GLN	164	24.637	-8.001	66.809	1.00 40.00
MOTA	1618 1619	0	GLN	164	23.602	-7.363	66.996	1.00 40.00
MOTA			LYS	165	25.511	-8.286	67.811	1.00 40.00
ATOM ATOM	1620 1622	N CA	LYS	165	25.328	-7.828	69.167	1.00 40.00
ATOM	1623	CB	LYS	165	24.424	-8.751	70.000	1.00 40.00
ATOM	1623		LYS	165	22.993	-8.779	69.455	1.00 40.00
	1625	CG CD	LYS	165	22.111	-9.891	70.021	1.00 40.00
MOTA	1625	CE	LYS	165	20.752	-9.994	69.322	1.00 40.00
MOTA	1627	NZ	LYS	165	20.732	-8.724	69.468	1.00 40.00
ATOM				165	26.668	-7.709	69.849	1.00 40.00
MOTA	1631 1632	C	LYS	165	27.674	-8.220	69.358	1.00 40.00
MOTA		O N	LYS	166	26.712	-7.013	71.011	1.00 40.00
ATOM	1633 1635	N	CYS CYS	166	27.947	-6.772	71.718	1.00 20.00
ATOM	1636	CA	CYS	166	28.006	-5.409	72.445	1.00 20.00
MOTA		CB					71.364	1.00 20.00
MOTA	1637	SG	CYS	166	27.870 28.175	-3.949 -7.810		1.00 20.00
ATOM	1638	C	CYS	166			72.772	
ATOM	1639	0	CYS	166	27.458	-8.806	72.858	1.00 20.00
ATOM	1640	N	ASP	167	29.221	-7.588	73.598	1.00 20.00
ATOM	1642	CA	ASP	167	29.568	-8.493	74.655	1.00 20.00
ATOM	1643	СВ	ASP	167	31.034	-8.383	75.105	1.00 20.00
ATOM	1644	CG	ASP	167	31.911	-8.872	73.962	1.00 20.00
MOTA	1645	OD1		167	31.345	-9.325	72.932	1.00 20.00
MOTA	1646	OD2		167	33.160	-8.804	74.107	1.00 20.00
MOTA	1647	C	ASP	167	28.717	-8.188	75.845	1.00 20.00
ATOM	1648	0	ASP	167	28.188	-7.087	75.987	1.00 20.00
ATOM	1649	N	PRO	168	28.553	-9.167	76.691	1.00 20.00
MOTA	1650	CD	PRO	168		-10.545	76.233	1.00 20.00
ATOM	1651	CA	PRO	168	27.792	-8.962	77.891	1.00 20.00
ATOM	1652	CB	PRO	168		-10.352	78.468	1.00 20.00
ATOM	1653	CG	PRO	168	27.548	-11.259	77.224	1.00 20.00

	A L	1654	С	PRO	168	28.529	-8.037	78.800		20.00
	MOTA	1655	0	PRO	168	27.901	-7.408	79.651		20.00
	MOTA	1656	N	SER	169	29.863	-7.961 7.115	78.653		20.00
	MC	1658	CA	SER	169 169	30.671 32.175	-7.115 -7.337	79.481 79.251		20.00
	MOM	1659 1660	CB OG	SER SER	169	32.173	-6.474	80.089		20.00
	ATOM ATOM	1662	C	SER	169	30.385	-5.681	79.188		20.00
	ATOM	1663	0	SER	169	30.266	-4.860	80.096	1.00	20.00
	ATOM	1664	N	CYS	170	30.245	-5.338	77.893	1.00	20.00
	ATOM	1666	CA	CYS	170	30.047	-3.970	77.527		20.00
	ATOM	1667	CB	CYS	170	29.930	-3.734	76.011		20.00
	ATOM	1668	SG	CYS	170	31.315	-4.412	75.053		20.00
	ATOM	1669	С	CYS	170	28.745	-3.530 -4.316	78.102 78.647		20.00
	ATOM	1670	0	CYS	170 171	27.974 28.514	-2.253	78.002		20.00
	ATOM	1671 1672	N CD	PRO PRO	171	29.596	-1.292	78.150		20.00
	ATOM ATOM	1673	CA	PRO	171	27.261	-1.721	78.446		20.00
	ATOM	1674	СВ	PRO	171	27.450	-0.210	78.515	1.00	20.00
	ATOM	1675	CG	PRO	171	28.955	-0.053	78.798		20.00
	ATOM	1676	С	PRO	171	26.247	-2.180	77.457		20.00
	MOTA	1677	0	PRO	171 .	26.624	-2.504	76.332		20.00
	MOTA	1678	N	ASN	172	24.962	-2.223	77.846		20.00
)	MOTA	1680	CA	ASN	172	23.973	-2.748 -2.700	76.955 77.517		20.00
	ATOM	1681	CB CG	ASN ASN	172 172	22.449	-3.681	78.675		20.00
	ATOM ATOM	1682 1683	OD1	ASN	172	23.461	-4.092	79.240		20.00
	ATOM	1684	ND2	ASN	172	21.198	-4.074	79.036		20.00
	ATOM	1687	C	ASN	172	23.961	-2.023	75.651		20.00
	ATOM	1688	0	ASN	172	23.484	-0.894	75.552	1.00	
	ATOM	1689	N	GLY	173	24.513	-2.674	74.609	1.00	
	MOTA	1691	CA	GLY	173	24.434	-2.157	73.276	1.00	
	ATOM	1692	C	GLY	173	25.496 25.466	-1.168 -0.616	72.921 71.822	1.00	
	ATOM	1693	O N	GLY SER	173 174	26.471	-0.895	73.807	1.00	
	ATOM ATOM	1694 1696	CA	SER	174	27.427	0.082	73.367	1.00	
	ATOM	1697	СВ	SER	174	27.613	1.251	74.348	1.00	20.00
	ATOM	1698	OG	SER	174	26.414	2.007	74.427	1.00	
	ATOM	1700	С	SER	174	28.770	-0.540	73.156	1.00	
	MOTA	1701	0	SER	174	29.426	-0.961	74.108	1.00	20.00
	ATOM	1702	N	CYS	175	29.213 30.524	-0.629 -1.156	71.883 71.631		20.00
	ATOM	1704	CA	CYS CYS	175 175	30.524	-2.687	71.827		20.00
,	MOTA MOTA	1705 1706	CB SG	CYS	175	29.735	-3.685	70.593		20.00
	ATOM	1707	C	CYS	175	30.933	-0.843	70.226	1.00	20.00
	ATOM	1708	0	CYS	175	30.096	-0.687	69.339		20.00
	ATOM	1709	N	TRP	176	32.254	-0.693	70.011		20.00
	MOTA	1711	CA	TRP	176	32.809	-0.427	68.715		20.00
	MOTA	1712	CB	TRP	176	34.264 34.394	0.062 1.381	68.806 69.536		20.00
	ATOM	1713	CG	TRP	176 176	34.394	2.660	68.967		20.00
	ATOM	1714 1715	CD2 CE2	TRP TRP	176	34.267	3.619	69.961		20.00
	ATOM ATOM	1716		TRP	176	33.638	3.006	67.718		20.00
	ATOM	1717		TRP	176	34.748	1.618	70.833	1.00	20.00
	ATOM	1718		TRP	176	34.689	2.966	71.100		20.00
	ATOM	1720	CZ2	TRP	176	34.039	4.945	69.718		20.00
	MOTA	1721	CZ3	TRP	176	33.404	4.341	67.480		20.00
	ATOM	1722	CH2	TRP	176	33.601	5.292	68.458		20.00
	MOTA	1723	С	TRP	176	32.767	-1.662 -1.602	67.868 66.665		20.00
	ATOM	1724	N O	TRP GLY	176 177	32.515 33.028	-1.802	68.493		20.00
	ATOM ATOM	1725 1727	CA	GLY	177	33.027	-4.074	67.786		20.00
	ATOM	1728	C	GLY	177	32.794	-5.125	68.820	1.00	20.00
	ATOM	1729	0	GLY	177	32.595	-4.818	69.994		20.00
	ATOM	1730	N	ALA	178	32.791	-6.406	68.410	1.00	20.00

MOTA	1732	CA	ALA	178	32.582	-7.432	69.385	1.00 20.00
MOTA	1733	CB	ALA	178	32.153	-8.780	68.782	1.00 20.00
ATOM	1734	С	ALA	178	33.875	-7.645	70.100	1.00 20.00
MC	1735	0	ALA	178	34.887	-7.982	69.487	1.00 20.00
MO'LA	1736	N	GLY	179	33.868	-7.445	71.431	1.00 20.00
MOTA	1738	CA	GLY	179	35.059	-7.639	72.203	1.00 20.00
MOTA	1739	С	GLY	179	34.927	-6.812	73.439	1.00 20.00
MOTA	1740	0	GLY	179	34.295	-5.757	73.429	1.00 20.00
MOTA	1741	N	GLU	180	35.529	-7.282	74.546	1.00 20.00
MOTA	1743	CA	GLU	180	35.459	-6.562	75.782	1.00 20.00
MOTA	1744	СВ	GLU	180	36.109	-7.332	76.946	1.00 20.00
ATOM	1745	CG	GLU	180	35.881	-6.693	78.317	1.00 20.00 1.00 20.00
MOTA	1746	CD	GLU	180	36.375	-7.672 -8.780	79.373 78.984	1.00 20.00
MOTA	1747		GLU	180 180	36.831 36.297	-7.327	80.582	1.00 20.00
ATOM	1748	C	GLU	180	36.192	-5.273	75.597	1.00 20.00
ATOM	1749	0	GLU GLU	180	35.742	-4.217	76.036	1.00 20.00
ATOM	1750 1751	N	GLU	181	37.353	-5.343	74.924	1.00 20.00
ATOM ATOM	1753	CA	GLU	181	38.158	-4.188	74.662	1.00 20.00
ATOM	1754	СВ	GLU	181	39.505	-4.543	74.007	1.00 20.00
ATOM	1755	CG	GLU	181	40.467	-3.359	73.892	1.00 20.00
ATOM	1756	CD	GLU	181	41.744	-3.859	73.231	1.00 20.00
ATOM	1757		GLU	181	42.734	-3.080	73.194	1.00 20.00
ATOM	1758		GLU	181	41.750	-5.028	72.761	1.00 20.00
АТОМ	1759	С	GLU	181	37.399	-3.309	73.724	1.00 20.00
АТОМ	1760	0	GLU	181	37.473	-2.083	73.798	1.00 20.00
ATOM	1761	N	ASN	182	36.632	-3.946	72.821	1.00 20.00
ATOM	1763	CA	ASN	182	35.877	-3.278	71.806	1.00 20.00
ATOM	1764	CB	ASN	182	35.133	-4.250	70.876	1.00 20.00
MOTA	1765	CG	ASN	182	36.159	-4.895	69.958	1.00 20.00
MOTA	1766	OD1	ASN	182	36.626	-6.006	70.202	1.00.20.00
MOTA	1767	ND2		182	36.519	-4.174	68.863	1.00 20.00
ATOM	1770	С	ASN	182	34.862	-2.373	72.420	1.00 20.00
ATOM	1771	0	ASN	182	34.486	-1.378	71.802	1.00 20.00
ATOM	1772	N	CYS	183	34.385	-2.721	73.636	1.00 20.00 1.00 20.00
ATOM	1774	CA	CYS	183	33.391	-1.959	74.344 75.846	1.00 20.00
ATOM	1775	CB	CYS	183 183	33.302 32.927	-2.281 -4.017	76.211	1.00 20.00
ATOM	1776	SG C	CYS CYS	183	33.734	-0.519	74.270	1.00 20.00
ATOM	. 1777 1778	0	CYS	183	34.905	-0.150	74.228	1.00 20.00
MOTA MOTA	1779	N	GLN	184	32.705	0.341	74.212	1.00 60.00
ATOM	1781	CA	GLN	184	33.052	1.720	74.177	1.00 60.00
ATOM	1782	CB	GLN	184	31.868	2.667	73.922	1.00 60.00
ATOM	1783	CG	GLN	184	32.280	4.138	73.840	1.00 60.00
ATOM	1784	CD	GLN	184	31.040	4.956	73.509	1.00 60.00
ATOM	1785	OE1	GLN	184	30.966	5.609	72.468	1.00 60.00
ATOM	1786	NE2	GLN	184	30.032	4.919	74.420	1.00 60.00
ATOM	1789	С	GLN	184	33.564	1.942	75.554	1.00 60.00
MOTA	1790	0	GLN	184	32.819	1.836	76.528	1.00 60.00
ATOM	1791	N	LYS	185	34.872	2.229	75.669	1.00 60.00
ATOM	1793	CA	LYS	185	35.432	2.376	76.975	1.00 60.00
MOTA	1794	CB	LYS	185	36.970	2.443	77.002	1.00 60.00
MOTA	1795	CG	LYS	185	37.567	3.707	76.384	1.00 60.00
ATOM	1796	CD	LYS	185	39.064	3.845	76.667	1.00 60.00
ATOM	1797	CE	LYS	185	39.403	3.882	78.159	1.00 60.00
ATOM	1798	NZ	LYS	185	40.861	3.722	78.351	1.00 60.00 1.00 60.00
ATOM	1802	С	LYS	185	34.883	3.614	77.587 77.131	1.00 60.00
ATOM	1803	0	LYS	185 186	33.880	4.162	78.659	1.00 60.00
MOTA	1804	N Ca	LEU	186 186	35.533 34.995	4.091 5.238	79.314	1.00 60.00
MOTA	1806	CA CB	LEU LEU	186	35.506	5.439	80.750	1.00 60.00
ATOM	1807 1808	CG	LEU	186	35.069	4.350	81.745	1.00 60.00
ATOM ATOM	1809		LEU	186	35.653	2.978	81.374	1.00 60.00
ATOM	1810		LEU	186	35.392	4.768	83.189	1.00 60.00
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A	1811	С	LEU	186	35.332	6.483	78.571		60.00
ATOM	1812	0	LEU	186	36.484	6.913	78.546		60.00
ATOM	1813	N	THR	187	34.321	7.095	77.925		60.00
MC	1815	CA	THR	187	34.573	8.363 8.756	77.316 76.246		60.00
A I OM	1816	CB OG1	THR	187 187	33.595 34.062	9.910	75.563		60.00
MOTA	1817 1819	CG2	THR THR	187	32.231	9.048	76.894		60.00
ATOM ATOM	1820	C	THR	187	34.396	9.281	78.474		60.00
ATOM	1821	o	THR	187	33.991	8.833	79.544		60.00
ATOM	1822	N	LYS	188	34.687	10.584	78.305		60.00
АТОМ	1824	CA	LYS	188	34.575	11.445	79.444	1.00	60.00
ATOM	1825	СB	LYS	188	34.925	12.915	79.163		60.00
ATOM	1826	CG	LYS	188	33.900	13.660	78.310		60.00
ATOM	1827	CD	LYS	188	34.040	15.179	78.415		60.00
ATOM	1828	CE	LYS	188	33.643	15.726	79.789		60.00
MOTA	1829	ΝZ	LYS	188	33.913	17.179	79.862 79.909		60.00
ATOM	1833	С	LYS	188	33.160	11.416 11.311	81.104		60.00
ATOM	1834	0	LYS	188	32.887 32.213	11.488	78.959		60.00
MOTA	1835	N CA	ILE	189 189	30.839	11.477	79.346		60.00
MOTA	1837 1838	CB	ILE	189	29.899	11.547	78.180		60.00
ATOM ATOM	1839	CG2	ILE	189	28.472	11.349	78.715		60.00
ATOM	1840	CG1	ILE	189	30.091	12.869	77.420	1.00	60.00
ATOM	1841	CD1	ILE	189	29.811	14.102	78.279	1.00	60.00
ATOM	1842	C	ILE	189	30.579	10.189	80.048		60.00
ATOM	1843	0	ILE	189	30.049	10.175	81.158		60.00
ATOM	1844	N	ILE	190	30.968	9.063	79.422		60.00
ATOM	1846	CA	ILE	190	30.707	7.809	80.057		60.00
MOTA	1847	CB	ILE	190	30.069	6.798	79.136		60.00
MOTA	1848	CG2	ILE	190	30.963	6.582	77.901		60.00
ATOM	1849	CG1	ILE	190	29.724	5.515	79.908		60.00
ATOM	1850	CD1	ILE	190	28.793	4.578	79.140 80.652		60.00
MOTA	1851	C	ILE	190	31.955 32.644	7.237 6.419	80.050		60.00
ATOM	1852	0	ILE CYS	190 191	32.266	7.679	81.882	1.00	
ATOM ATOM	1853 1855	N CA	CYS	191	33.355	7.192	82.682		20.00
ATOM	1856	CB	CYS	191	34.411	8.248	83.072	1.00	
ATOM	1857	SG	CYS	191	35.657	8.621	81.806	1.00	20.00
ATOM	1858	C	CYS	191	32.642	6.902	83.953		20.00
ATOM	1859	0	CYS	191	31.452	6.592	83.949		20.00
ATOM	1860	N	ALA	192	33.354	6.979	85.089		20.00
ATOM	1862	CA	ALA	192	32.632	6.815	86.308		20.00
MOTA	1863	СВ	ALA	192	33.504	6.907	87.572		20.00
ATOM	1864	С	ALA	192	31.709	7.988	86.298 85.650		20.00
MOTA	1865	0	ALA	192	31.983 30.575	8.996 7.883	87.007		20.00
ATOM	1866	N Ca	GLN GLN	193 193	29.623	8.951	86.991		20.00
ATOM	1868 1869	CA CB	GLN	193	28.408	8.660	87.885		20.00
ATOM ATOM	1870	CG	GLN	193	27.614	7.421	87.466		20.00
ATOM	1871	CD	GLN	193	26.463	7.264	88.448	1.00	20.00
ATOM	1872		GLN	193	26.124	8.194	89.178	1.00	20.00
ATOM	1873	NE2	GLN	193	25.849	6.051	88.477		20.00
ATOM	1876	С	GLN	193	30.284	10.164	87.555		20.00
MOTA	1877	0	GLN	193	30.100	11.276	87.061		20.00
MOTA	1878	N	GLN	194	31.080	9.962	88.619		20.00
MOTA	1880	CA	GLN	194	31.727	11.025	89.328		20.00
MOTA	1881	CB	GLN	194	32.421	10.520	90.602		20.00
MOTA	1882	CG	GLN	194	31.452	9.916	91.618		20.00
ATOM	1883	CD OF1	GLN	194	32.266	9.456	92.816 93.761		20.00
ATOM	1884		GLN	194 194	31.735 33.600	8.876 9.717	93.761		20.00
MOTA	1885	NE2 C	GLN GLN	194	32.762	11.748	88.527		20.00
MOTA	1888 1889	0	GLN	194	32.822	12.976	88.557		20.00
ATOM ATOM	1890	N	CYS	195	33.601	11.012	87.775		20.00
MOTA	1030	**	-15		33.001				

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MOTA	1892	CA	CYS	195	34.677	11.669	87.090	1.00 20.00
MOTA	1893	CB.	CYS	195	35.560	10.744	86.234	1.00 20.00
ATOM	1894	SG	CYS	195	36.498	9.530	87.203	1.00 20.00
MC	1895	С	CYS	195	34.166	12.729	86.178	1.00 20.00
PT OW	1896	0	CYS	195	33.102	12.601	85.575	1.00 20.00
MOTA	1897	N	SER	196	34.923	13.837	86.088	1.00 20.00
ATOM	1899	CA	SER	196	34.550	14.887	85.197	1.00 20.00
MOTA	1900	CB	SER	196	34.101	16.172	85.910	1.00 20.00
ATOM	1901	OG	SER	196	32.911	15.924	86.644	1.00 20.00
ATOM	1903	С	SER	196	35.763	15.221	84.395	1.00 20.00
MOTA	1904	0	SER	196	36.859	15.369	84.932	1.00 20.00
MOTA	1905	N	GLY	197	35.597	15.299	83.064	1.00 20.00
MOTA	1907	ÇA	GLY	197	36.671	15.699	82.207	1.00 20.00
ATOM	1908	С	GLY	197	37.113	14.530	81.389	1.00 20.00
MOTA	1909	0	GLY	197	36.915	14.511	80.176	1.00 20.00
MOTA	1910	N	ARG	198	37.712	13.515	82.048	1.00 20.00
MOTA	1912	CA	ARG	198	38.178	12.340	81.363	1.00 20.00
MOTA	1913	CB	ARG	198	39.450	12.556	80.522	1.00 20.00
MOTA	1914	CG	ARG	198	39.207	13.349	79.238	1.00 20.00
MOTA	1915	CD	ARG	198	38.159	12.693	78.335	1.00 20.00
ATOM	1916	NE	ARG	198	37.917	13.606	77.184	1.00 20.00
MOTA	1918	CZ	ARG	198	36.929	13.329	76.284	1.00 20.00
MOTA	1919	NH1		198	36.724	14.156	75.219	1.00 20.00
MOTA	1922	NH2	ARG	198	36.145	12.222	76.452	1.00 20.00
MOTA	1925	С	ARG	198	38.529	11.321	82.396	1.00 20.00
ATOM	1926	0	ARG	198	38.423	11.580	83.594	1.00 20.00 1.00 20.00
ATOM	1927	N	CYS.	199	38.930	10.109	81.955	1.00 20.00 1.00 20.00
MOTA	1929	CA	CYS	199	39.312	9.139	82.937	1.00 20.00
MOTA	1930	CB	CYS	199	38.123	8.371	83.541 82.306	1.00 20.00
MOTA	1931	SG	CYS	199	37.204 40.245	7.408 8.116	82.374	1.00 20.00
MOTA	1932	C	CYS	199 199	40.245	7.815	81.181	1.00 20.00
MOTA	1933	O	CYS ARG	200	41.117	7.581	83.252	1.00 20.00
MOTA	1934 1936	N CA	ARG	200	42.032	6.538	82.900	1.00 20.00
ATOM ATOM	1937	CB	ARG	200	43.077	6.284	84.002	1.00 20.00
ATOM ATOM	1938	CG	ARG	200	44.151	5.262	83.625	1.00 20.00
ATOM	1939	CD	ARG	200	43.815	3.826	84.030	1.00 20.00
ATOM	1940	NE	ARG	200	44.952	2.965	83.598	1.00 20.00
ATOM	1942	CZ	ARG	200	44.960	2.419	82.346	1.00 20.00
ATOM	1943	NH1	ARG	200	43.921	2.651	81.491	1.00 20.00
ATOM	1946	NH2	ARG	200	46.010	1.641	81.951	1.00 20.00
ATOM	1949	С	ARG	200	41.239	5.282	82.719	1.00 20.00
ATOM	1950	0	ARG	200	41.464	4.523	81.778	1.00 20.00
MOTA	1951	N	GLY	201	40.266	5.045	83.622	1.00 20.00
MOTA	1953	CA	GLY	201	39.478	3.849	83.551	1.00 20.00
MOTA	1954	С	GLY	201	38.275	4.028	84.422	1.00 20.00
MOTA	1955	0	GLY	201	37.966	5.138	84.852	1.00 20.00
MOTA	1956	N	LYS	202	37.561	2.918	84.701	1.00 20.00
MOTA	1958	CA	LYS	202	36.372	2.971	85.502	1.00 20.00
MOTA	1959	CB	LYS	202	35.473	1.729	85.344	1.00 20.00
MOTA	1960	CG	LYS	202	34.536	1.759	84.136	1.00 20.00
MOTA	1961	CD	LYS	202	33.447	2.827	84.254	1.00 20.00
MOTA	1962	CE	LYS	202	32.464	2.569	85.398	1.00 20.00
MOTA	1963	NZ	LYS	202	31.492	3.680	85.500	1.00 20.00
MOTA	1967	С	LYS	202	36.702	3.052	86.956	1.00 20.00
ATOM	1968	0	LYS	202	36.693	2.042	87.657	1.00 20.00
MOTA	1969	N	SER	203	37.015	4.264	87.450	1.00 20.00
ATOM	1971	CA	SER	203	37.229	4.428	88.857	1.00 20.00
ATOM	1972	CB	SER	203	38.515	3.773	89.388	1.00 20.00
ATOM	1973	OG	SER	203	39.656	4.451	88.885	1.00 20.00
MOTA	1975	С	SER	203	37.339	5.895	89.101	1.00 20.00
ATOM	1976	0	SER	203 204	37.694 37.009	6.662 6.306	88.207 90.290	1.00 20.00 1.00 20.00
MOTA	1977	N	PRO	204	37.009	5.677	91.012	1.00 20.00
MOTA	1978	CD	PRO	203	22.714	2.077	J U . E	2.00 20.00

i 1	1979	CA	PRO	204	37.136	7.697	90.613	1.00 20.00		
MOTA	1980	СВ	PRO	204	36.361	7.894	91.912	1.00 20.00		
MOTA	1981	CG	PRO	204	35.277	6.800	91.847	1.00 20.00		
MC	1982	C	PRO	204	38.584	8.051	90.685	1.00 20.00		
MO. W	1983	0	PRO	204	38.925	9.227	90.563	1.00 20.00 1.00 20.00		
MOTA	1984	N	SER	205 205	39.445 40.861	7.045 7.250	90.920 90.973	1.00 20.00		
MOTA	1986 1987	CA CB	SER SER	205	41.623	5.985	91.400	1.00 20.00		
ATOM ATOM	1988	OG	SER	205	41.259	5.621	92.723	1.00 20.00		
MOTA	1990	C	SER	205	41.298	7.589	89.587	1.00 20.00		
ATOM	1991	Ō	SER	205	42.189	8.412	89.379	1.00 20.00		
ATOM	1992	N	ASP	206	40.643	6.948	88.604	1.00 20.00		
ATOM	1994	CA	ASP	206	40.948	7.079	87.212	1.00 20.00		
ATOM	1995	CB	ASP	206	40.180	6.094	86.316	1.00 20.00		
ATOM	1996	CG	ASP	206	40.887	4.749	86.409	1.00 20.00		
MOTA	1997		ASP	206	40.184	3.704	86.368	1.00 20.00 1.00 20.00		
MOTA	1998		ASP	206	42.142 40.703	4.751 8.452	86.518 86.687	1.00 20.00		
ATOM	1999	C	ASP ASP	206 206	41.286	8.800	85.661	1.00 20.00		
ATOM ATOM	2000 2001	O N	CYS	207	39.811	9.229	87.348	1.00 20.00		
ATOM	2003	CA	CYS	207	39.456	10.559	86.921	1.00 20.00		
ATOM	2004	CB	CYS	207	38.758	11.404	88.000	1.00 20.00		
ATOM	2005	SG	CYS	207	37.287	10.620	88.721	1.00 20.00		
ATOM	2006	С	CYS	207	40.702	11.297	86.535	1.00 20.00		
ATOM	2007	0	CYS	207	41.765	11.068	87.110	1.00 20.00		
ATOM	2008	N	CYS	208	40.612	12.192	85.530	1.00 20.00		
ATOM	2010	CA	CYS	208	41.814	12.830	85.073	1.00 20.00		
ATOM	2011	CB	CYS	208	42.132	12.584 12.887	83.584 83.236	1.00 20.00 1.00 20.00		
ATOM	2012	SG	CYS CYS	208 208	43.890 41.703	14.311	85.255	1.00 20.00		
ATOM ATOM	2013 2014	С О	CYS	208	40.680	14.824	85.707	1.00 20.00		
ATOM	2015	N	HIS	209	42.788	15.037	84.915	1.00 20.00		•
ATOM	2017	CA	HIS	209	42.827	16.460	85.083	1.00 20.00		
ATOM	2018	СВ	HIS	209	44.187	17.074	84.698	1.00 20.00		
MOTA	2019	CG	HIS	209	44.306	18.531	85.033	1.00 20.00		
MOTA	2020		HIS	209	44.765	19.137	86.163	1.00 20.00		
MOTA	2021		HIS	209	43.946	19.550	84.181 84.830	1.00 20.00 1.00 20.00		
ATOM	2023		HIS HIS	209 209	44.203 44.701	20.713 20.513	86.037	1.00 20.00		
ATOM ATOM	2024 2026	C	HIS	209	41.760	17.080	84.239	1.00 20.00		
ATOM	2027	0	HIS	209	41.311	16.503	83.251	1.00 20.00		
ATOM	2028	N	ASN	210	41.317	18.289	84.632	1.00 20.00		
ATOM	2030	CA	ASN	210	40.255	18.971	83.952	1.00 20.00		
ATOM	2031	CB	ASN	210	39.810	20.259	84.670	1.00 20.00		
MOTA	2032	CG	ASN	210	40.987	21.221	84.745	1.00 20.00		
ATOM	2033		ASN	210	41.375	21.838	83.754	1.00 20.00 1.00 20.00		
MOTA	2034		ASN	210	41.562 40.644	21.368 19.322	85.969 82.547	1.00 20.00		
MOTA	2037 2038	C	ASN ASN	210 210	39.809	19.322	81.644	1.00 20.00		
ATOM ATOM	2039	O N	GLN	211	41.920	19.698	82.340	1.00 20.00		
ATOM	2041	CA	GLN	211	42.433	20.094	81.056	1.00 20.00		
ATOM	2042	СВ	GLN	211	43.817	20.754	81.156	1.00 20.00		
ATOM	2043	CG	GLN	211	43.804	22.051	81.966	1.00 20.00		
MOTA	2044	CD	GLN	211	42.967	23.077	81.212	1.00 20.00	•	
MOTA	2045		GLN	211	42.714	22.936	80.016	1.00 20.00		
MOTA	2046		GLN	211	42.528	24.144	81.931	1.00 20.00	•	
ATOM	2049	С	GLN	211	42.545	18.956	80.093	1.00 20.00 1.00 20.00		
ATOM	2050	0	GLN	211	42.326	19.106	78.892 80.608	1.00 20.00		
ATOM	2051 2053	N CA	CYS CYS	212 212	42.911 43.108	17.779 16.604	79.822	1.00 20.00		
ATOM ATOM	2053	CB	CYS	212	43.100	15.421	80.762	1.00 20.00		
MOTA	2055	SG	CYS	212	44.657	15.757	81.777	1.00 20.00		
ATOM	2056	c	CYS	212	41.941	16.393	78.929	1.00 20.00		
ATOM	2057	0	CYS	212	40.802	16.652	79.309	1.00 20.00		

MOTA	2058	N	ALA	213	42.212	15.952	77.688	1.00 20.00
ATOM	2060	ÇA	ALA	213	41.143	15.660	76.792	1.00 20.00
MOTA	2061	СВ	ALA	213	41.084	16.582	75.562	1.00 20.00
MC	2062	С	ALA	213	41.425	14.273	76.320	1.00 20.00
AT-OM	2063	0	ALA	213	42.577	13.844	76.300	1.00 20.00
MOTA	2064	N	ALA	214	40.368	13.525	75.957	1.00 20.00
MOTA	2066	CA	ALA	214	40.528	12.175	75.504	1.00 20.00
ATOM	2067	CB	ALA	214	41.699	11.962	74.525	1.00 20.00
ATOM	2068	С	ALA	214	40.711	11.263	76.677	1.00 20.00
MOTA	2069	0	ALA	214	39.751	10.646	77.138	1.00 20.00
MOTA	2070	N	GLY	215	41.955	11.149	77.192	1.00 20.00
MOTA	2072	CA	GLY	215	42.196	10.264	78.303	1.00 20.00
ATOM	2073	С	GLY	215	43.502	10.625 11.754	78.944 78.818	1.00 20.00 1.00 20.00
ATOM	2074	O N	GLY	215	43.975 44.101	9.684	79.707	1.00 20.00
ATOM	2075	N	CYS	216 216	45.376	9.987	80.283	1.00 20.00
MOTA	2077	CA CB	CYS CYS	216	45.343	11.252	81.161	1.00 20.00
ATOM	2078	SG		216	44.623	11.038	82.816	1.00 20.00
ATOM	2079	C	CYS CYS	216	45.875	8.808	81.064	1.00 20.00
ATOM	2080 2081	0	CYS	216	45.119	7.884	81.362	1.00 20.00
ATOM	2081	N	THR	217	47.189	8.779	81.372	1.00 20.00
ATOM	2082	CA	THR	217	47.714	7.670	82.119	1.00 20.00
MOTA MOTA	2085	CB	THR	217	49.218	7.605	82.163	1.00 20.00
ATOM	2086	OG1	THR	217	49.627	6.333	82.641	1.00 20.00
ATOM	2088	CG2	THR	217	49.764	8.698	83.093	1.00 20.00
ATOM	2089	C	THR	217	47.201	7.681	83.529	1.00 20.00
ATOM	2090	ō	THR	217	46.827	6.639	84.065	1.00 20.00
ATOM	2091	N	GLY	218	47.162	8.869	84.167	1.00 20.00
ATOM	2093	CA	GLY	218	46.700	8.971	85.525	1.00 20.00
MOTA	2094	С	GLY	218	46.499	10.427	85.785	1.00 20.00
ATOM	2095	0	GLY	218	47.164	11.256	85.168	1.00 20.00
MOTA	2096	N	PRO	219	45.620	10.765	86.692	1.00 40.00
MOTA	2097	CD	PRO	219	45.358	9.917	87.844	1.00 40.00
ATOM	2098	CA	PRO	219	45.286	12.142	86.948	1.00 40.00
ATOM	2099	СВ	PRO	219	44.421	12.125	88.206	1.00 40.00
ATOM	2100	CG	PRO	219	44.931	10.884	88.961	1.00 40.00
ATOM	2101	С	PRO	219	46.484	13.028	87.106	1.00 40.00
ATOM	2102	0	PRO	219	47.146	12.971	88.140	1.00 40.00
ATOM	2103	N	ARG	220	46.763	13.856	86.079	1.00 40.00
ATOM	2105	CA	ARG	220	47.847	14.791	86.092	1.00 40.00
MOTA	2106	СВ	ARG	220	49.241	14.143	86.156	1.00 40.00
MOTA	2107	CG	ARG	220	50.377	15.168	86.169	1.00 40.00
ATOM	2108	CD	ARG	220	51.759	14.562	86.416	1.00 40.00
ATOM	2109	NE	ARG	220	51.806	14.132	87.842	1.00 40.00
MOTA	2111	CZ	ARG	220	51.345	12.899	88.204 89.515	1.00 40.00
MOTA	2112		ARG	220	51.379	12.520	87.262	1.00 40.00
ATOM	2115		ARG	220	50.852 47.752	12.044 15.546	84.804	1.00 40.00
ATOM	2118	C	ARG	220 220	47.752	15.067	83.839	1.00 40.00
ATOM	2119	O N	ARG GLU	221	48.316	16.765	84.767	1.00 20.00
MOTA	2120	N		221	48.290	17.606	83.602	1.00 20.00
MOTA	2122	CA CB	GLU GLU	221	48.797	19.024	83.910	1.00 20.00
MOTA	2123	CG	GLU	221	47.920	19.795	84.898	1.00 20.00
MOTA ATOM	2124 2125	CD	GLU .	221	48.628	21.101	85.230	1.00 20.00
MOTA			GLU	221	48.993	21.839	84.276	1.00 20.00
ATOM	2126 2127	OE2		221	48.817	21.375	86.446	1.00 20.00
ATOM	2127	C C	GLU	221	49.156	17.082	82.491	1.00 20.00
ATOM ATOM	2129	0	GLU	221	48.814	17.193	81.316	1.00 20.00
ATOM	2130	N	SER	222	50.334	16.539	82.848	1.00 20.00
ATOM	2130	CA	SER	222	51.324	16.099	81.902	1.00 20.00
MOTA	2132	CB	SER	222	52.691	15.855	82.565	1.00 20.00
ATOM	2133	OG	SER .	222	52.603	14.778	83.487	1.00 20.00
MOTA	2136	c	SER	222	50.999	14.860	81.120	1.00 20.00
ATOM	2137	0	SER	222	51.361	14.741	79.952	1.00 20.00
AIOM	217,	~				·-	·	

M	2138	N	ASP	223	50.342	13.881	81.759	1.00 20.00	
A1 OM	2140	CA	ASP	223	50.110	12.593	81.165	1.00 20.00	
MOTA	2141	CB	ASP	223	49.830	11.500	82.195	1.00 20.00	
Mι	2142	CG	ASP	223	48.518	11.829	82.857	1.00 20.00	
MOLA	2143		ASP	223	47.585	11.000	82.697	1.00 20.00	
MOTA	2144		ASP	223	48.422	12.888	83.529	1.00 20.00	
MOTA	2145	С	ASP	223	49.059	12.514	80.099	1.00 20.00	
MOTA	2146	0	ASP	223	48.972	11.524 13.518	79.377 80.001	1.00 20.00 1.00 20.00	
ATOM	2147	N	CYS	224 224	48.181 47.069	13.416	79.106	1.00 20.00	
MOTA	2149	CA	CYS CYS	224	46.143	14.588	79.372	1.00 20.00	
MOTA	2150 2151	CB SG	CYS	224	45.836	14.280	81.137	1.00 20.00	
ATOM ATOM	2152	C	CYS	224	47.403	13.115	77.677	1.00 20.00	
ATOM	2153	0	CYS	224	48.507	13.379	77.209	1.00 20.00	
ATOM	2154	N	LEU	225	46.474	12.399	77.001	1.00 20.00	
MOTA	2156	CA	LEU	225	46.601	12.001	75.627	1.00 20.00	
ATOM	2157	СВ	LEU	225	45.630	10.880	75.219	1.00 20.00	
MOTA	2158	CG	LEU	225	45.984	9.523	75.857	1.00 20.00	
ATOM	2159	CD1	LEU	225	45.831	9.559	77.387	1.00 20.00	
ATOM	2160	CD2	LEU	225	45.207	8.373	75.198	1.00 20.00	
MOTA	2161	С	LEU	225	46.402	13.160	74.708	1.00 20.00	
MOTA	2162	0	LEU	225	46.995	13.214	73.631	1.00 20.00	
MOTA	2163	N	VAL	226	45.504	14.090	75.082	1.00 20.00	
MOTA	2165	CA	VAL	226	45.314	15.266	74.290	1.00 20.00	
MOTA	2166	СВ	VAL	226	44.276	15.130	73.206	1.00 20.00	
MOTA	2167		VAL	226	42.883	14.999	73.839	1.00 20.00 1.00 20.00	
MOTA	2168		VAL	226	44.408	16.330 16.356	72.253 75.224	1.00 20.00	
ATOM	2169	С	VAL	226 226	44.898 44.618	16.330	76.395	1.00 20.00	
MOTA	2170 2171	O N	VAL CYS	227	44.864	17.613	74.730	1.00 20.00	
ATOM ATOM	2171	CA	CYS	227	44.543	18.697	75.608	1.00 20.00	
ATOM	2174	CB	CYS	227	45.567	19.841	75.570	1.00 20.00	
ATOM	2175	SG	CYS	227	47.232	19.319	76.080	1.00 20.00	
ATOM	2176	С	CYS	227	43.223	19.274	75.223	1.00 20.00	
MOTA	2177	0	CYS	227	42.833	19.255	74.056	1.00 20.00	
MOTA	2178	N	ARG	228	42.474	19.758	76.233	1.00 20.00	
MOTA	2180	CA	ARG	228	41.201	20.357	75.988	1.00 20.00	
MOTA	2181	CB	ARG	228	40.368	20.572	77.259	1.00 20.00	ı
MOTA	2182	CG	ARG	228	38.907	20.875	76.928	1.00 20.00	
MOTA	2183	CD	ARG	228	37.939	20.635	78.084	1.00 20.00	
ATOM	2184	NE	ARG	228	36.571	20.659	77.498	1.00 20.00	
MOTA	2186	CZ	ARG	228	36.083 36.848	19.543 18.415	76.880 76.804	1.00 20.00 1.00 20.00	
MOTA	2187		ARG	228 228	34.836	19.558	76.326	1.00 20.00	
ATOM	2190 2193	NH2 C	ARG ARG	228 228	41.409	21.673	75.318	1.00 20.00	
MOTA MOTA	2193	0	ARG	228	40.688	22.039	74.391	1.00 20.00	
ATOM	2195	N	LYS	229	42.443	22.406	75.766	1.00 20.00	
ATOM	2197	CA	LYS	229	42.692	23.714	75.244	1.00 20.00	
ATOM	2198	CB	LYS	229	42.841	24.767	76.353	1.00 20.00	
ATOM	2199	CG	LYS	229	41.624	24.772	77.280	1.00 20.00	
ATOM	2200	CD	LYS	229	40.295	24.908	76.533	1.00 20.00	
MOTA	2201	CE	LYS	229	39.074	24.570	77.392	1.00 20.00	
MOTA	2202	NZ	LYS	229	37.854	24.553	76.554	1.00 20.00	
ATOM	2206	С	LYS	229	43.956	23.664	74.448	1.00 20.00	
MOTA	2207	0	LYS	229	44.019	23.016	73.403	1.00 20.00	
MOTA	2208	N	PHE	230	45.000	24.379	74.908	1.00 20.00	
ATOM	2210	CA	PHE	230	46.218	24.397	74.149	1.00 20.00 1.00 20.00	
MOTA	2211	CB	PHE	230	46.761	25.815	73.900 73.039	1.00 20.00	
MOTA	2212	CG CD1	PHE	230 230	45.779 44.688	26.531 27.156	73.599	1.00 20.00	
ATOM	2213	CD1 CD2		230	44.688	26.592	73.599	1.00 20.00	
ATOM	2214 2215	CE1		230	43.786	27.829	72.809	1.00 20.00	
MOTA MOTA	2215	CE2		230	45.058	27.265	70.882	1.00 20.00	
ATOM	2217	CZ	PHE	230	43.970	27.884	71.448	1.00 20.00	
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MOTA	2218	С	PHE	230	47.283	23.651	74.882	1.00 20.00
ATOM	2219	0	PHE	230	47.373	23.717	76.105	1.00 20.00
MOTA	2220	N	ARG	231	48.130	22.916	74.135	1.00 20.00
MOT .	2222	CA	ARG	231	49.172	22.161	74.761	1.00 20.00
MO.	2223	СB	ARG	231	49.466	20.819	74.071	1.00 20.00
MOTA	2224	CG	ARG	231	50.426	19.926	74.861	1.00 20.00
MOTA	2225	CD	ARG	231	51.000	18.772	74.036	1.00 20.00
ATOM	2226	NE	ARG	231	49.855	18.058	73.407	1.00 20.00
MOTA	2228	CZ	ARG	231	50.080	17.186	72.382	1.00 20.00
MOTA	2229	NH1		231	51.359	16.908	71.991	1.00 20.00
MOTA	2232	NH2		231	49.025	16.602	71.746	1.00 20.00
MOTA	2235	С	ARG	231	50.423	22.969	74.676	1.00 20.00
MOTA	2236	0	ARG	231	50.752	23.510	73.621	1.00 20.00
MOTA	2237	N	ASP	232	51.144	23.103	75.804	1.00 20.00
MOTA	2239	CA	ASP	232	52.359	23.853	75.739	1.00 20.00
MOTA	2240	CB	ASP	232	52.188	25.331	76.136	1.00 20.00
MOTA	2241	CG	ASP	232	53.432	26.092	75.694	1.00 20.00
MOTA	2242		ASP	232	53.480	27.330	75.921	1.00 20.00
MOTA	2243		ASP	232	54.346	25.446	75.114	1.00 20.00
MOTA	2244	С	ASP	232	53.358	23.243	76.667	1.00 20.00
ATOM	2245	0	ASP	232	53.050	22.936	77.816	1.00 20.00
ATOM	2246	N	GLU	233	54.597	23.062	76.174	1.00 20.00
ATOM	2248	CA	GLU	233	55.662	22.517	76.963	1.00 20.00
MOTA	2249	СВ	GLU	233	56.221	23.517	77.989	1.00 20.00
ATOM	2250	CG	GLU	233	56.969	24.685	77.346	1.00 20.00
MOTA	2251	CD	GLU	233	58.294	24.153	76.822	1.00 20.00
ATOM	2252	OE1		233	59.095	23.647	77.652	1.00 20.00
MOTA	2253		GLU	233	58.524	24.243	75.586	1.00 20.00
MOTA	2254	C	GLU	233	55.237	21.291	77.701	1.00 20.00 1.00 20.00
ATOM	2255	0	GLU	233	55.325	21.232	78.926	
MOTA	2256	N	ALA	234	54.756	20.278	76.961	1.00 20.00
MOTA	2258	CA	ALA	234	54.388	19.025	77.554	1.00 20.00 1.00 20.00
ATOM	2259	СВ	ALA	234	55.569	18.320	78.244 78.564	1.00 20.00
ATOM	2260	С	ALA	234	53.298	19.181 18.229	79.270	1.00 20.00
MOTA	2261	0	ALA	234 235	52.972 52.681	20.374	78.663	1.00 20.00
MOTA	2262	N C2	THR THR	235	51.626	20.374	79.626	1.00 20.00
MOTA	2264 2265	CA CB	THR	235	51.897	21.482	80.717	1.00 20.00
ATOM ATOM	2266	OG1	THR	235	52.016	22.789	80.175	1.00 20.00
ATOM	2268		THR	235	53.198	21.086	81.434	1.00 20.00
ATOM	2269	C	THR	235	50.387	20.928	78.924	1.00 20.00
ATOM	2270	0	THR	235	50.447	21.651	77.930	1.00 20.00
ATOM	2271	N	CYS	236	49.216	20.483	79.421	1.00 20.00
ATOM	2273	CA	CYS	236	47.989	20.894	78.810	1.00 20.00
ATOM	2274	СВ	CYS	236	46.819	19.910	78.989	1.00 20.00
ATOM	2275	SG	CYS	236	46.939	18.467	77.899	1.00 20.00
ATOM	2276	С	CYS	236	47.599	22.168	79.473	1.00 20.00
ATOM	2277	0	CYS	236	47.313	22.189	80.669	1.00 20.00
ATOM	2278	N	LYS	237	47.579	23.269	78.694	1.00 20.00
ATOM	2280	CA	LYS	237	47.273	24.556	79.241	1.00 20.00
MOTA	2281	СВ	LYS	237	48.296	25.640	78.862	1.00 20.00
ATOM	2282	CG	LYS	237	49.668	25.442	79.509	1.00 20.00
ATOM	2283	CD	LYS	237	50.763	26.323	78.905	1.00 20.00
MOTA	2284	CE	LYS	237	52.133	26.124	79.556	1.00 20.00
MOTA	2285	NZ	LYS	237	53.141	26.973	78.882	1.00 20.00
MOTA	2289	С	LYS	237	45.937	25.018	78.754	1.00 20.00
MOTA	2290	0	LYS	237	45.538	24.748	77.623	1.00 20.00
ATOM	2291	N	ASP	238	45.193	25.697	79.650	1.00 20.00
MOTA	2293	CA	ASP	238	43.904	26.249	79.350	1.00 20.00
MOTA	2294	СВ	ASP	238	43.207	26.805	80.606	1.00 20.00
ATOM	2295	CG	ASP	238	41.761	27.127	80.258	1.00 20.00
MOTA	2296		ASP	238	41.399	27.014	79.057	1.00 20.00
ATOM	2297		ASP	238	40.999	27.492	81.194	1.00 20.00
ATOM	2298	С	ASP	238	44.080	27.378	78.383	1.00 20.00

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A .	2299	0	ASP	238	43.294	27.553	77.452	1.00 20.00			
ATOM	2300	N	THR	239	45.124	28.195	78.604	1.00 20.00			
ATOM	2302	CA	THR	239	45.395	29.288	77.721	1.00 20.00			
MC.	2303	CB	THR	239	44.901	30.613	78.222	1.00 20.00			
OM	2304	OG1	THR	239	45.004	31.594	77.201	1.00 20.00			
ATOM	2306	CG2	THR	239	45.744	31.022	79.442	1.00 20.00			
ATOM	2307	С	THR	239	46.879	29.365	77.641	1.00 20.00			
ATOM	2308	0	THR	239	47.581	28.773	78.459	1.00 20.00			
ATOM	2309	N	CYS	240	47.410	30.087	76.640	1.00 20.00			
MOTA	2311	CA	CYS	240	48.835	30.120	76.543	1.00 20.00			
MOTA	2312	CB	CYS	240	49.340	30.107	75.100	1.00 20.00			
ATOM	2313	SG	CYS	240	49.026	28.455	74.421	1.00 20.00			
MOTA	2314	С	CYS	240	49.397	31.268	77.303	1.00 20.00			
MOTA	2315	0	CYS	240	48.974	32.417	77.198	1.00 20.00			
MOTA	2316	й	PRO	241	50.343	30.894	78.119	1.00 40.00			
MOTA	2317	CD	PRO	241	50.319	29.560	78.691	1.00 40.00			
MOTA	2318	CA	PRO	241	51.014	31.831	78.973	1.00 40.00			
MOTA	2319	СВ	PRO	241	51.531	31.028	80.169	1.00 40.00			
MOTA	2320	CG	PRO	241	51.463	29.562	79.714	1.00 40.00			
MOTA	2321	C	PRO	241	52.097	32.561	78.253	1.00 40.00			
MOTA	2322	0	PRO	241	52.520	32.130	77.181	1.00 40.00		•	
MOTA	2323	N	PRO	242	52.520 51.564	33.654 34.527	78.820 79.485	1.00 60.00			
MOTA	2324	CD	PRO	242		34.327	78.227	1.00 60.00			
ATOM	2325	CA	PRO	242	53.598 53.501	35.808	78.793	1.00 60.00	•		
ATOM	2326	CB	PRO	242 242	52.014		79.154	1.00 60.00			
ATOM	2327	CG C	PRO PRO	242	54.875	33.709	78.587	1.00 60.00			
ATOM	2328 2329	0	PRO	242	54.870	32.896	79.510	1.00 60.00			
MOTA MOTA	2330	N	LEU	243	55.978	34.015	77.877	1.00 60.00			
ATOM	2332	CA	LEU	243	57.227	33.396	78.202	1.00 60.00			
ATOM	2333	CB	LEU	243	58.383	33.812	77.277	1.00 60.00			
ATOM	2334	CG	LEU	243	59.726	33.148	77.636	1.00 60.00		•	
ATOM	2335	CD1		243	59.643	31.616	77.513	1.00 60.00			
ATOM	2336		LEU	243	60.879	33.743	76.813	1.00 60.00			
ATOM	2337	С	LEU	243	57.575	33.816	79.591	1.00 60.00			
ATOM	2338	0	LEU	243	57.890	34.978	79.848	1.00 60.00			
MOTA	2339	N	MET	244	57.507	32.862	80.533	1.00 60.00			
MOTA	2341	CA	MET	244	57.791	33.161	81.903	1.00 60.00			
MOTA	2342	CB	MET	244	57.482	31.989	82.850	1.00 60.00			
ATOM	2343	CG	MET	244	55.997	31.625	82.878	1.00 60.00			
ATOM	2344	SD	MET	244	54.903	32.969	83.429	1.00 60.00			
MOTA	2345	CE	MET	244	55.431	32.907	85.165	1.00 60.00			
MOTA	2346	С	MET	244	59.235	33.503	82.057	1.00 60.00			
MOTA	2347	0	MET	244	59.576	34.511	82.673	1.00 60.00			
MOTA	2348	N	LEU	245	60.134	32.684	81.481	1.00 60.00			
MOTA	2350	CA	LEU	245	61.525	32.981	81.643	1.00 60.00 1.00 60.00			
ATOM	2351	CB	LEU	245	62.469	31.955	80.994 81.616	1.00 60.00			
ATOM	2352		LEU	245	62.377	30.548 29.579	80.947	1.00 60.00			
ATOM	2353	CD1 CD2		245 245	63.367 62.526	30.598	83.146	1.00 60.00			
ATOM	2354	CD2	LEU	245	61.771	34.296	80.992	1.00 60.00			
ATOM	2355 2356	0	LEU	245	61.191	34.605	79.952	1.00 60.00			
ATOM	2350	N	TYR	246	62.630	35.127	81.612	1.00 60.00			
ATOM ATOM	2357	CA	TYR	246	62.896	36.400	81.021	1.00 60.00			
ATOM	2360	CB	TYR	246	62.429	37.596	81.868	1.00 60.00			
ATOM	2361	CG	TYR	246	60.948	37.506	81.992	1.00 60.00			
ATOM	2362	CD1		246	60.132	37.819	80.930	1.00 60.00			
ATOM	2363		TYR	246	58.765	37.758	81.055	1.00 60.00			
MOTA	2364	CD2		246	60.374	37.171	83.196	1.00 60.00			
ATOM	2365	CE2		246	59.008	37.115	83.331	1.00 60.00			
ATOM	2366	CZ	TYR	246	58.200	37.401	82.257	1.00 60.00			
ATOM	2367	ОН	TYR	246	56.798	37.332	82.389	1.00 60.00			
ATOM	2369	С	TYR	246	64.369	36.547	80.860	1.00 60.00			
MOTA	2370	0	TYR	246	65.152	36.112	81.704	1.00 60.00			

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MOTA	2371	N	ASN	247	64.781	37.156	79.735	1.00	60.00
MOTA	2373	CA	ASN	247	66.166	37.413	79.494		60.00
ATOM	2374	CB	ASN	247	66.751	36.629	78.307		60.00
MC	2375	CG	ASN	247	66.747	35.150	78.654		60.00
A 1 OM	2376		ASN	247	66.946	34.764	79.804		60.00
MOTA	2377		ASN	247	66.512	34.291	77.626		60.00
MOTA	2380	С	ASN	247	66.194	38.845	79.091		60.00
MOTA	2381	0	ASN	247	65.156	39.427	78.784		60.00
ATOM	2382	N	PRO	248	67.343	39.452	79.108		60.00
MOTA	2383	CD	PRO	248	68.307	39.227	80.172		60.00
MOTA	2384	CA	PRO	248	67.376	40.798	78.633		60.00
ATOM	2385	СВ	PRO	248	68.694	41.391	79.120		60.00
MOTA	2386	CG	PRO	248	68.980	40.592	80.407		60.00
ATOM	2387	C	PRO	248	67.231	40.707	77.156		60.00
MOTA	2388	0	PRO	248	67.940	39.912	76.542		60.00 60.00
MOTA	2389	N	THR	249	66.324	41.498	76.561		60.00
ATOM	2391	CA	THR	249	66.157	41.376	75.148		60.00
ATOM	2392	CB	THR	249	64.766	40.988	74.743		60.00
MOTA	2393	OG1		249	63.842	41.988 39.645	75.145 75.406		60.00
MOTA	2395	CG2		249	64.419 66.445		74.528		60.00
ATOM	2396	С	THR	249		42.695 43.736	75.007		60.00
ATOM	2397	O N	THR	249 250	65.998 67.235	42.676	73.442		60.00
MOTA	2398	N CA	THR THR	250	67.522	43.894	72.758		60.00
ATOM	2400 2401	CB	THR	250	68.975	44.063	72.730		60.00
MOTA	2401	OG1	THR	250	69.407	43.023	71.556		60.00
ATOM ATOM	2402	CG2		250	69.784	44.032	73.728		60.00
MOTA	2405	C	THR	250	66.755	43.825	71.483		60.00
MOTA	2406	o	THR	250	66.991	42.953	70.648		60.00
ATOM	2407	N	TYR	251	65.783	44.738	71.313		60.00
ATOM	2409	CA	TYR	251	65.019	44.726	70.106		60.00
ATOM	2410	CB	TYR	251	63.510	44.525	70.343		60.00
ATOM	2411	CG	TYR	251	62.876	44.130	69.052	1.00	60.00
ATOM	2412		TYR	251	62.473	45.067	68.128	1.00	60.00
MOTA	2413	CE1	TYR	251	61.893	44.675	66.943	1.00	60.00
ATOM	2414	CD2	TYR	251	62.678	42.796	68.774	1.00	60.00
ATOM	2415	CE2	TYR	251	62.096	42.398	67.594		60.00
ATOM	2416	CZ	TYR	251	61.705	43.340	66.674		60.00
MOTA	2417	OH	TYR	251	61.127	42.937	65.452		60.00
MOTA	2419	С	TYR	251	65.225	46.096	69.557		60.00
MOTA	2420	0	TYR	251	65.588	47.013	70.292		60.00
MOTA	2421	N	GLN	252	65.022	46.278	68.241		60.00
MOTA	2423	CA	GLN	252	65.242	47.587	67.707		60.00
ATOM	2424	СВ	GLN	252	65.041	47.680	66.183		60.00
MOTA	2425	CG	GLN	252	63.628	47.363	65.693		60.00 60.00
MOTA	2426	CD	GLN	252	63.638	47.511	64.177		
ATOM	2427		GLN	252	62.715	47.085 48.132	63.482 63.642		60.00 60.00
ATOM	2428		GLN	252	64.724 64.296	48.522	68.381		60.00
ATOM	2431	С	GLN	252 252	64.693	49.599	68.823		60.00
ATOM	2432	O N	GLN MET	252	63.015	48.127	68.504		60.00
MOTA	2433 2435	CA	MET	253	62.094	49.001	69.160		60.00
MOTA	2435	CB	MET	253	60.612	48.669	68.906		60.00
MOTA MOTA	2437	CG	MET	253	60.179	48.955	67.466		60.00
ATOM	2437	SD	MET	253	58.436	48.593	67.098		60.00
ATOM	2439	CE	MET	253	58.658	46.796	66.971		60.00
ATOM	2440	C	MET	253	62.362	48.933	70.627		60.00
ATOM	2441	0	MET	253	63.037	48.023	71.106		60.00
ATOM	2442	N	ASP	254	61.848	49.926	71.374		60.00
ATOM	2444	CA	ASP	254	62.085	50.003	72.785		60.00
ATOM	2445	СВ	ASP	254	61.483	51.270	73.416		60.00
ATOM	2446	CG	ASP	254	62.283	52.468	72.924		60.00
ATOM	2447	OD1		254	61.662	53.540	72.691	1.00	60.00
MOTA	2448	OD2	ASP	254	63.526	52.327	72.780	1.00	60.00

A	2449	С	ASP	254	61.474	48.832	73.480	1.00	60.00
ATOM	2450	0	ASP	254	62.122	48.178	74.295		60.00
MOTA	2451	N	VAL	255	60.204	48.520	73.162		60.00
λW	2453	CA	VAL	255	59.561	47.442	73.852		60.00
A I OM	2454	СВ	VAL	255	58.158	47.754	74.280		60.00
MOTA	2455		VAL '	255	57.299	47.953	73.020		60.00
MOTA	2456	CG2		255	57.663	46.622	75.196		60.00
MOTA	2457	С	VAL	255	59.483	46.261	72.950		60.00
ATOM	2458	0	VAL	255	59.474	46.394 45.058	71.727 73.554		60.00
ATOM	2459	N	ASN	256 256	59.448 59.348	43.852	72.791		60.00
ATOM	2461	CA CB	ASN ASN	256	60.299	42.740	73.269		60.00
MOTA	2462 2463	CG	ASN	256	60.098	41.520	72.379		60.00
ATOM ATOM	2464	OD1		256	59.716	40.451	72.854		60.00
ATOM	2465	ND2		256	60.362	41.679	71.055		60.00
ATOM	2468	C	ASN	256	57.957	43.344	72.963	1.00	60.00
ATOM	2469	0	ASN	256	57.392	43.371	74.055	1.00	60.00
ATOM	2470	N	PRO	257	57.384	42.907	71.879		60.00
ATOM	2471	CD	PRO	257	57.656	43.530	70.595		60.00
ATOM	2472	CA	PRO	257	56.058	42.359	71.940		60.00
ATOM	2473	CB	PRO	257	55.447	42.551	70.550		60.00
ATOM	2474	CG	PRO	257	56.643	42.882	69.640		60.00
MOTA	2475	С	PRO	257	56.163	40.932	72.357		60.00
MOTA	2476	0	PRO	257	57.229	40.343	72.188		60.00
MOTA	2477	N	GLU	258	55.084	40.355	72.921 73.312		60.00
ATOM	2479	CA	GLU	258	55.158 56.103	38.980 38.741	74.504		60.00
ATOM	2480	CB	GLU	258 258	56.443	37.267	74.738		60.00
ATOM	2481 2482	CG CD	GLU GLU	258	57.436	36.838	73.666		60.00
ATOM ATOM	2483		GLU	258	57.797	35.632	73.640		60.00
ATOM	2484	OE2		258	57.850	37.712	72.857		60.00
ATOM	2485	C	GLU	258	53.785	38.555	73.725	1.00	60.00
ATOM	2486	0	GLU	258	52.822	39.305	73.579	1.00	60.00
ATOM	2487	N	GLY	259	53.662	37.318	74.242		60.00
ATOM	2489	CA	GLY	259	52.390	36.839	74.696		60.00
MOTA	2490	С	GLY	259	51.626	36.312	73.529		60.00
MOTA	2491	0	GLY	259	50.441	36.003	73.639		60.00
ATOM	2492	N	LYS	260	52.295	36.197	72.369		60.00
MOTA	2494	CA	LYS	260	51.630	35.712	71.199 69.917		60.00
ATOM	2495	CB	LYS	260 260	52.164 53.689	36.371 36.306	69.792		60.00
ATOM	2496	CG	LYS LYS	260	54.221	36.659	68.401		60.00
ATOM ATOM	2497 2498	CD	LYS	260	54.298	35.459	67.454		60.00
ATOM	2499	NZ	LYS	260	52.941	35.089	66.995		60.00
ATOM	2503	C	LYS	260	51.855	34.239	71.090	1.00	60.00
ATOM	2504	0	LYS	260	52.807	33.792	70.452	1.00	60.00
АТОМ	2505	N	TYR	261	50.981	33.433	71.727		40.00
ATOM	2507	CA	TYR	261	51.160	32.018	71.623		40.00
ATOM	2508	СВ	TYR	261	51.545	31.368	72.964		40.00
ATOM	2509	CG	TYR	261	52.847	31.929	73.425		40.00
MOTA	2510	CD1		261	54.032	31.338	73.054		40.00
MOTA	2511		TYR	261	55.236	31.845	73.479		40.00
MOTA	2512		TYR	261	52.884	33.038	74.239		40.00
MOTA	2513	CE2		261	54.086 55.263	33.545 32.950	74.676 74.294		40.00
MOTA	2514	CZ	TYR	261 261	56.497	33.472	74.234		40.00
MOTA	2515 2517	OH C	TYR TYR	261	49.844	31.408	71.265		40.00
ATOM	2517 2518	0	TYR	261	48.937	31.398	72.092		40.00
ATOM ATOM	2519	N	SER	262	49.703	30.888	70.027		20.00
ATOM	2521	CA	SER	262	48.521	30.173	69.622		20.00
ATOM	2522	СВ	SER	262	47.244	31.027	69.481		20.00
ATOM	2523	OG	SER	262	46.751	31.449	70.744		20.00
ATOM	2525	С	SER	262	48.809	29.661	68.248		20.00
ATOM	2526	0	SER	262	48.879	30.438	67.297	1.00	20.00

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MOTA	2527	N	PHE	263	49.007	28.337	68.103	1.00 20.00
MOTA	2529	CA	PHE	263	49.269	27.813	66.796	1.00 20.00
ATOM	2530	СВ	PHE	263	50.756	27.487	66.589	1.00 20.00
MC	2531	CG	PHE	263	51.541	28.737	66.794	1.00 20.00
MO LA	2532	CD1		263	51.722	29.238	68.063	1.00 20.00
ATOM	2533	CD2	PHE	263	52.221	29.322	65.751	1.00 20.00
MOTA	2534	CE1		263	52.514	30.340	68.283	1.00 20.00
ATOM	2535	CE2	PHE	263	53.032	30.412	65.967	1.00 20.00
ATOM	2536	CZ	PHE	263	53.171	30.932	67.232	1.00 20.00
MOTA	2537	С	PHE	263	48.550	26.503	66.726	1.00 20.00
MOTA	2538	0	PHE	263	48.960	25.536	67.364	1.00 20.00
ATOM	2539	N	GLY	264	47.473	26.411	65.928	1.00 20.00
ATOM	2541	CA	GLY	264	46.785	25.154	65.871 67.261	1.00 20.00 1.00 20.00
ATOM	2542	С	GLY	264 264	46.317 45.573	24.803 25.563	67.201	1.00 20.00
ATOM	2543	0	GLY	265	45.573	23.590	67.748	1.00 40.00
ATOM	2544	N	ALA	265	46.384	23.068	69.064	1.00 40.00
ATOM	2546 2547	CA CB	ALA ALA	265	46.496	21.535	69.117	1.00 40.00
MOTA MOTA	2548	СВ	ALA	265	47.277	23.601	70.145	1.00 40.00
ATOM	2549	0	ALA	265	46.844	23.768	71.284	1.00 40.00
ATOM	2550	N	THR	266	48.561	23.860	69.823	1.00 20.00
ATOM	2552	CA	THR	266	49.516	24.233	70.830	1.00 20.00
ATOM	2553	СВ	THR	266	50.712	23.327	70.865	1.00 20.00
ATOM	2554	OG1	THR	266	51.422	23.408	69.638	1.00 20.00
ATOM	2556	CG2	THR	266	50.227	21.887	71.101	1.00 20.00
ATOM	2557	С	THR	266	50.034	25.609	70.581	1.00 20.00
MOTA	2558	0	THR	266	49.552	26.321	69.703	1.00 20.00
MOTA	2559	N	CYS	267	51.024	26.035	71.393	1.00 20.00
MOTA	2561	CA	CYS	267	51.536	27.360	71.222	1.00 20.00
MOTA	2562	СВ	CYS	267	51.243	28.267	72.417	1.00 20.00
MOTA	2563	SG	CYS	267	49.476	28.652	72.467	1.00 20.00
ATOM	2564	С	CYS	267	53.003	27.395	70.932	1.00 20.00
MOTA	2565	0	CYS	267	53.762	26.529	71.362	1.00 20.00
MOTA	2566	N	VAL	268	53.425	28.426	70.165	1.00 20.00
MOTA	2568	CA	VAL	268	54.797	28.586	69.772	1.00 20.00 1.00 20.00
MOTA	2569	CB	VAL	268	54.998	28.615	68.284 67.997	1.00 20.00
ATOM	2570	CG1		268 268	56.489 54.457	28.857 27.305	67.684	1.00 20.00
MOTA	2571	CG2 C	VAL VAL	268	55.307	29.884	70.309	1.00 20.00
ATOM ATOM	2572 2573	0	VAL	268	54.571	30.863	70.413	1.00 20.00
ATOM	2574	N	LYS	269	56.608	29.908	70.657	1.00 20.00
MOTA	2576	CA	LYS	269	57.239	31.058	71.241	1.00 20.00
ATOM	2577	CB	LYS	269	58.729	30.813	71.532	1.00 20.00
ATOM	2578	CG	LYS	269	59.426	31.973	72.242	1.00 20.00
ATOM	2579	CD	LYS	269	60.879	31.668	72.615	1.00 20.00
ATOM	2580	CE	LYS	269	61.061	30.346	73.364	1.00 20.00
ATOM	2581	NZ	LYS	269	62.503	30.064	73.551	1.00 20.00
MOTA	2585	С	LYS	269	57.176	32.209	70.297	1.00 20.00
MOTA	2586	0	LYS	269	56.810	33.318	70.685	1.00 20.00
MOTA	2587	N	LYS	270	57.522	31.969	69.019	1.00 20.00
ATOM	2589	CA	LYS	270	57.534	33.036	68.064	1.00 20.00
MOTA	2590	СВ	LYS	270	58.948	33.382	67.571	1.00 20.00
MOTA	2591	CG	LYS	270	59.831	34.001	68.657	1.00 20.00
MOTA	2592	CD	LYS	270	61.323	33.973	68.323	1.00 20.00
MOTA	2593	CE	LYS	270	61.984	32.627	68.625	1.00 20.00
MOTA	2594	NZ	LYS	270	63.403	32.653	68.209	1.00 20.00
ATOM	2598	C	LYS	270	56.741	32.590	66.885	1.00 20.00 1.00 20.00
ATOM	2599	0	LYS	270	56.481	31.401	66.702	1.00 20.00
MOTA	2600	N CA	CYS	271 271	56.320 55.524	33.559 33.261	66.057 64.908	1.00 20.00
ATOM	2602	CA	CYS CYS	271	55.524 54.812	34.532	64.403	1.00 20.00
ATOM ATOM	2603 2604	CB SG	CYS	271	53.495	34.290	63.178	1.00 20.00
ATOM ATOM	2604	C	CYS	271	56.458	32.726	63.869	1.00 20.00
ATOM	2605	0	CYS	271	57.559	33.242	63.686	1.00 20.00
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P 1	2607	N	PRO	272	56.054	31.683	63.193	1.00 20.00			
A'I OM	2608	CD	PRO	272	55.163	30.698	63.778	1.00 20.00			
MOTA	2609	CA	PRO	272	56.883	31.103	62.177	1.00 20.00			
MΥ	2610	CB	PRO	272	56.289	29.725	61.870	1.00 20.00			
ALOM	2611	CG	PRO	272	54.955	29.688	62.639	1.00 20.00			
MOTA	2612	С	PRO	272	56.936	32.042	61.023	1.00 20.00 1.00 20.00			
ATOM	2613	0	PRO	272	56.040	32.873	60.891 60.181	1.00 20.00			
MOTA	2614	N	ARG	273	57.979 58.097	31.943 32.887	59.115	1.00 20.00			
MOTA	2616	CA	ARG	273 273	59.407	32.762	58.313	1.00 20.00			
MOTA	2617 2618	CB CG	ARG ARG	273	60.640	33.020	59.185	1.00 20.00			
ATOM	2619	CD	ARG	273	61.938	33.257	58.409	1.00 20.00			
ATOM ATOM	2620	NE	ARG	273	62.116	34.733	58.287	1.00 20.00			
ATOM	2622	CZ	ARG	273	63.314	35.307	58.603	1.00 20.00			
ATOM	2623		ARG	273	64.351	34.532	59.035	1.00 20.00			
ATOM	2626	NH2		273	63.471	36.660	58.499	1.00 20.00			
ATOM	2629	С	ARG	273	56.932	32.755	58.192	1.00 20.00			
АТОМ	2630	0	ARG	273	56.339	31.685	58.064	1.00 20.00			
ATOM	2631	N	ASN	274	56.580	33.873	57.527	1.00 20.00			
ATOM	2633	CA	ASN	274	55.465	33.937	56.628	1.00 20.00			
ATOM	2634	CB	ASN	274	55.474	32.817	55.574	1.00 20.00			
MOTA	2635	CG	ASN	274	56.592	33.129	54.587	1.00 20.00			
MOTA	2636		ASN	274	56.601	34.187	53.960	1.00 20.00			
MOTA	2637		ASN	274	57.566	32.189	54.450	1.00 20.00 1.00 20.00			
MOTA	2640	C	ASN	274	54.178 53.123	33.873 33.612	57.388 56.812	1.00 20.00			
MOTA	2641	0	ASN	274 275	54.234	34.130	58.709	1.00 20.00			
MOTA	2642 2644	N CA	TYR TYR	275 275	53.047	34.163	59.516	1.00 20.00			
ATOM ATOM	2645	CB	TYR	275	52.918	32.988	60.503	1.00 20.00			,
ATOM	2646	CG	TYR	275	52.806	31.721	59.728	1.00 20.00	•		
ATOM	2647		TYR	275	53.939	31.105	59.253	1.00 20.00			
ATOM	2648	CE1		275	53.860	29.914	58.570	1.00 20.00			
ATOM	2649		TYR	275	51.588	31.112	59.535	1.00 20.00			
ATOM	2650	CE2	TYR	275	51.502	29.919	58.855	1.00 20.00			
ATOM	2651	CZ	TYR	275	52.639	2 9 .321	58.367	1.00 20.00			
ATOM	2652	OH	TYR	275	52.555	28.099	57.668	1.00 20.00		•	
ATOM	2654	С	TYR	275	53.176	35.407	60.339	1.00 20.00 1.00 20.00		,	
MOTA	2655	0	TYR	275	54.285 52.038	35.859 36.005	60.621 60.741	1.00 20.00			
MOTA	2656		VAL	276 276	52.036	37.215	61.510	1.00 20.00			
ATOM	2658 2659	CA CB	VAL VAL	276	51.371	38.363	60.858	1.00 20.00			
MOTA MOTA	2660		VAL	276	52.076	38.692	59.532	1.00 20.00			
ATOM	2661		VAL	276	49.884	37.996	60.703	1.00 20.00			
ATOM	2662	C	VAL	276	51.393	36.980	62.815	1.00 20.00			
ATOM	2663	0	VAL	276	50.633	36.025	62.967	1.00 20.00			
MOTA	2664	N	VAL	277	51.665	37.850	63.808	1.00 20.00			
ATOM	2666	CA	VAL	277	51.031	37.704	65.084	1.00 20.00			
MOTA	2667	CB	VAL	277	51.935	38.005	66.244	1.00 20.00			
MOTA	2668		VAL	277	52.485	39.435	66.102	1.00 20.00			
MOTA	2669		VAL	277	51.138	37.780	67.538	1.00 20.00 1.00 20.00			
MOTA	2670	С	VAL	277	49.878	38.649	65.131 64.942	1.00 20.00			•
ATOM	2671	0	VAL	277 278	50.037 48.669	39.853 38.111	65.380	1.00 20.00			
ATOM	2672	N CA	THR THR	278 278	47.500	38.934	65.383	1.00 20.00			
ATOM	2674 2675	CB	THR	278	46.485	38.508	64.363	1.00 20.00			
MOTA MOTA	2675		THR	278	45.427	39.452	64.293	1.00 20.00			
ATOM	2678	CG2		278	45.941	37.126	64.761	1.00 20.00			
ATOM	2679	C	THR	278	46.832	38.866	66.713	1.00 20.00			
MOTA	2680	ō	THR	278	46.770	37.811	67.342	1.00 20.00			
ATOM	2681	N	ASP	279	46.315	40.023	67.166	1.00 20.00			
ATOM	2683	CA	ASP	279	45.606	40.114	68.405	1.00 20.00			
MOTA	2684	СВ	ASP	279	44.241	39.407	68.379	1.00 20.00			
ATOM	2685	CG	ASP	279	43.322	40.199	67.462	1.00 20.00			
MOTA	2686	OD1	ASP	279	42.154	39.763	67.277	1.00 20.00			

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ATOM	2687	OD2	ASP	279	43.775	41.249	66.933	1.00 20.00
MOTA	2688	С	ASP	279	46.411	39.511	69.499	1.00 20.00
MOTA	2689	0	ASP	279	45.855	38.829	70.358	1.00 20.00
MO	2690	N	HIS	280	47.734	39.785	69.489	1.00 20.00
_OM	2692	CA	HIS	280	48.681	39.334	70.470	1.00 20.00
MOTA	2693	СВ	HIS	280	48.754	40.258	71.699	1.00 20.00
MOTA	2694	CG	HIS	280	49.135	41.666	71.348	1.00 20.00
ATOM	2695		HIS	280	48.349	42.719	70.991	1.00 20.00
ATOM	2696		HIS	280	50.429	42.135	71.310	1.00 20.00
MOTA	2698		HIS	280	50.362	43.439	70.939	1.00 20.00
ATOM	2699		HIS	280	49.120	43.838	70.734	1.00 20.00
ATOM	2701	С	HIS	280	48.366	37.953	70.952	1.00 20.00
ATOM	2702	0	HIS	280	47.580	37.776	71.881	1.00 20.00 1.00 20.00
ATOM	2703	N	GLY	281 281	48.995 48.682	36.923 35.604	70.355 70.816	1.00 20.00
ATOM	2705	CA C	GLY GLY	281	48.423	34.647	69.699	1.00 20.00
ATOM	2706 2707	0	GLY	281	48.690	33.456	69.844	1.00 20.00
ATOM ATOM	2707	N	SER	282	47.885	35.107	68.558	1.00 20.00
ATOM	2710	CA	SER	282	47.678	34.134	67.527	1.00 20.00
ATOM	2711	СВ	SER	282	46.238	34.105	66.986	1.00 20.00
ATOM	2712	QG	SER	282	45.340	33.698	68.009	1.00 20.00
ATOM	2714	Ç	SER	282	48.580	34.438	66.380	1.00 20.00
ATOM	2715	Ō	SER	282	48.556	35.531	65.817	1.00 20.00
ATOM	2716	N	CYS	283	49.418	33.454	66.015	1.00 20.00
MOTA	2718	CA	CYS	283	50.301	33.582	64.897	1.00 20.00
ATOM	2719	CB	CYS	283	51.643	32.884	65.166	1.00 20.00
MOTA	2720	SG	CYS	283	52.649	32.524	63.700	1.00 20.00
MOTA	2721	С	CYS	283	49.600	32.877	63.794	1.00 20.00
ATOM	2722	0	CYS	283	49.413	31.660	63.829	1.00 20.00
MOTA	2723	N	VAL	284	49.168	33.651	62.786	1.00 20.00
MOTA	2725	CA	VAL	284	48.455	33.081	61.690	1.00 20.00
MOTA	2726	CB	VAL	284	47.049	33.602	61.572	1.00 20.00
MOTA	2727	CG1		284	46.360	32.936	60.368	1.00 20.00
ATOM	2728		VAL	284	46.329	33.358	62.910	1.00 20.00
ATOM	2729	С	VAL	284	49.198	33.470	60.457	1.00 20.00
ATOM	2730	0	VAL	284	49.960	34.435	60.453 59.373	1.00 20.00 1.00 20.00
ATOM ATOM	2731	N CA	ARG ARG	285 285	48.992 49.660	32.705 32.950	58.131	1.00 20.00
	2733 2734	CB	ARG	285	49.252	31.937	57.047	1.00 20.00
ATOM ATOM	2734	CG	ARG	285	49.876	32.202	55.676	1.00 20.00
ATOM	2736	CD	ARG	285	49.454	31.184	54.614	1.00 20.00
MOTA	2737	NE	ARG	285	49.985	31.653	53.304	1.00 20.00
ATOM	2739	CZ	ARG	285	50.013	30.806	52.234	1.00 20.00
ATOM	2740	NH1		285	49.586	29.517	52.373	1.00 20.00
ATOM	2743		ARG	285	50.465	31.249	51.025	1.00 20.00
ATOM	2746	C	ARG	285	49.296	34.308	57.634	1.00 20.00
MOTA	2747	0	ARG	285	50.145	35.029	57.112	1.00 20.00
MOTA	2748	N	ALA	286	48.017	34.702	57.781	1.00 20.00
ATOM	2750	CA	ALA	286	47.642	35.980	57.256	1.00 20.00
MOTA	2751	CB	ALA	286	46.727	35.885	56.023	1.00 20.00
MOTA	2752	С	ALA	286	46.913	36.796	58.272	1.00 20.00
ATOM	2753	0	ALA	286	46.410	36.290	59.274	1.00 20.00
MOTA	2754	N	CYS	287	46.855	38.113	58.006	1.00 20.00
MOTA	2756	CA	CYS	287	46.200	39.081	58.834	1.00 20.00
ATOM	2757	CB	CYS	287	46.299	40.502	58.269	1.00 20.00
ATOM	2758	SG	CYS	287	47.899	41.323	58.457	1.00 20.00
ATOM	2759	C	CYS	287	44.735	38.810	58.806	1.00 20.00 1.00 20.00
ATOM	2760 2761	O N	CYS	287	44.243	38.046 39.446	57.978 59.736	1.00 20.00
ATOM	2761 2763	N CA	GLY GLY	288 288	43.999	39.446	59.736	1.00 20.00
ATOM	2763 2764	CA	GLY	288	42.575	40.174	58.549	1.00 20.00
MOTA MOTA	2764 2765	0	GLY	288	42.177	40.174	58.028	1.00 20.00
ATOM	2766	N	ALA	289	40.906	40.066	58.126	1.00 20.00
ATOM	2768	CA	ALA	289	40.434	40.735	56.947	1.00 20.00
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A	2769	СВ	ALA	289	38.904	40.669	56.805	1.00 20.00	
ATOM	2770	С	ALA	289	40.821	42.180	56.864	1.00 20.00	
MOTA	2771	0	ALA	289	41.713	42.542	56.102	1.00 20.00	
M	2772	N	ASP	290	40.173	43.038	57.672	1.00 20.00	
MO _T A	2774	CA	ASP	290	40.355	44.462	57.620	1.00 20.00	
ATOM	2775	СВ	ASP	290	39.461	45.210	58.627 58.168	1.00 20.00 1.00 20.00	
ATOM	2776	CG	ASP	290	38.016	45.075 45.361	58.989	1.00 20.00	
ATOM	2777		ASP	290 290	37.104 37.805	44.683	56.989	1.00 20.00	
MOTA	2778		ASP ASP	290 290	41.768	44.843	57.925	1.00 20.00	
ATOM	2779	С 0	ASP	290	42.165	45.983	57.690	1.00 20.00	
MOTA MOTA	2780 2781	N	SER	291	42.566	43.912	58.480	1.00 20.00	
ATOM	2783	CA	SER	291	43.899	44.283	58.856	1.00 20.00	
ATOM	2784	СВ	SER	291	44.405	43.492	60.073	1.00 20.00	
ATOM	2785	OG	SER	291	43.597	43.771	61.208	1.00 20.00	
АТОМ	2787	С	SER	291	44.881	44.081	57.740	1.00 20.00	
ATOM	2788	0	SER	291	44.771	43.144	56.950	1.00 20.00	
MOTA	2789	N	TYR	292	45.879	44.989	57.659	1.00 20.00	
MOTA	2791	CA	TYR	292	46.897	44.937	56.647	1.00 20.00	
ATOM	2792	CB	TYR	292	46.871	46.172	55.725	1.00 20.00	
MOTA	2793	CG	TYR	29.2	47.867	45.995	54.629	1.00 20.00	
ATOM	2794		TYR	292	47.565	45.202	53.546 52.473	1.00 20.00	
ATOM	2795		TYR	292	48.422	45.115 46.728	54.606	1.00 20.00	
ATOM	2796		TYR	292 292	49.031 49.894	46.728	53.537	1.00 20.00	
ATOM	2797	CE2	TYR TYR	292 292	49.588	45.840	52.468	1.00 20.00	
MOTA MOTA	2798 2799	OH	TYR	292	50.460	45.771	51.361	1.00 20.00	
ATOM	2801	C	TYR	292	48.208	44.923	57.372	1.00 20.00	,
MOTA	2802	ō	TYR	292	48.360	45.564	58.410	1.00,20.00	
MOTA	2803	N	GLU	293	49.196	44.173	56.847	1.00 20.00	
ATOM	2805	CA	GLU	293	50.458	44.087	57.520	1.00 20.00	
MOTA	2806	СВ	GLU	293	51.435	43.108	56.848	1.00 20.00	
ATOM	2807	CG	GLU	293	50.980	41.649	56.936	1.00 20.00	
MOTA	2808	CD	GLU	293	51.942	40.809	56.112	1.00 20.00	
MOTA	2809		GLU	293	52.657	41.402	55.261 · 56.314	1.00 20.00	
MOTA	2810		GLU	293 293	51.973 51.059	39.565 45.450	57.503	1.00 20.00	
MOTA	2811 2812	С 0	GLU	293	50.902	46.201	56.544	1.00 20.00	
ATOM ATOM	2812	N	MET	294	51.769	45.811			
ATOM	2815	CA	MET	294	52.333	47.123	58.656	1.00 20.00	
ATOM	2816	CB	MET	294	53.112	47.352	59.960	1.00 20.00	
ATOM	2817	CG	MET	294	53.536	48.804	60.183	1.00 20.00	
MOTA	2818	SD	MET	294	54.296	49.118	61.805	1.00 20.00	
MOTA	2819	CE	MET	294	52.763	48.901	62.755	1.00 20.00	
ATOM	2820	С	MET	294	53.277	47.263	57.509 56.821	1.00 20.00 1.00 20.00	
MOTA	2821	0	MET	294	53.288 54.092	48.282 46.223	57.261	1.00 20.00	
MOTA	2822	N	GLU	295 295	55.006	46.271	56.159	1.00 20.00	
MOTA	2824	CA CB	GLU GLU	295	56.483	46.382	56.567	1.00 20.00	
ATOM	2825 2826	CG	GLU	295	57.405	46.649	55.377	1.00 20.00	
ATOM ATOM	2827	CD	GLU	295	57.090	48.047	54.861	1.00 20.00	
ATOM	2828		GLU	295	56.385	48.150	53.821	1.00 20.00	
MOTA	2829		GLU	295	57.540	49.030	55.507	1.00 20.00	
MOTA	2830	С	GLU	295	54.838	44.988	55.415	1.00 20.00	
ATOM	2831	0	GLU	295	54.121	44.094	55.859	1.00 20.00	
MOTA	2832	N	GLU	296	55.490	44.866	54.244	1.00 20.00	
MOTA	2834	CA	GLU	296	55.329	43.665	53.482	1.00 20.00 1.00 20.00	
MOTA	2835	CB	GLU	296	56.167	43.632	52.194	1.00 20.00	
MOTA	2836	CG	GLU	296 296	55.849	42.419	51.316 50.075	1.00 20.00	
ATOM	2837	CD	GLU GLU	296 296	56.724 57.977	42.489 42.466	50.073	1.00 20.00	
ATOM	2838 2839		GLU	296 296	56.157	42.460	48.956	1.00 20.00	
MOTA	2839 2840	C C	GLU	296	55.774	42.521	54.331	1.00 20.00	
ATOM ATOM	2841	0	GLU	296	55.066	41.525	54.468	1.00 20.00	
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ATOM	2842	N	ASP	297	56.970	42.635	54.934	1.00 40.00
MOTA	2844	CA	ASP	297	57.418	41.570	55.776	1.00 40.00
MOTA	2845	СВ	ASP	297	58.374	40.583	55.082	1.00 40.00
MC	2846	CG	ASP	297	59.628	41.336	54.661	1.00 40.00
w T.OW	2847		ASP	297	59.573	42.593	54.589	1.00 40.00
ATOM	2848		ASP	297	60.659	40.661	54.401	1.00 40.00
MOTA	2849	C	ASP	297	58.159	42.195	56.906	1.00 40.00
MOTA	2850	0	ASP	297	58.306	43.413	56.973	1.00 40.00
MOTA	2851	N	GLY	298	58.621	41.360	57.852	1.00 40.00
ATOM	2853	CA	GLY	298	59.365	41.874	58.959 59.933	1.00 40.00 1.00 40.00
ATOM	2854	C	GLY	298	58.382 58.728	42.422 42.737	61.071	1.00 40.00
MOTA	2855 2856	О И	GLY VAL	298 299	57.114	42.757	59.503	1.00 40.00
MOTA MOTA	2858	CA	VAL	299	56.137	43.068	60.407	1.00 40.00
MOTA	2859	CB	VAL	299	55.345	44.214	59.844	1.00 40.00
ATOM	2860		VAL	299	56.292	45.415	59.674	1.00 40.00
ATOM	2861		VAL	299	54.702	43.772	58.520	1.00 40.00
ATOM	2862	С	VAL	299	55.203	41.967	60.792	1.00 40.00
ATOM	2863	0	VAL	299	54.374	41.506	60.010	1.00 40.00
ATOM	2864	N	ARG	300	55.364	41.477	62.030	1.00 20.00
ATOM	2866	CA	ARG	300	54.469	40.486	62.537	1.00 20.00
ATOM	2867	СВ	ARG	300	54.946	39.864	63.859	1.00 20.00
ATOM	2868	CG	ARG	300	56.093	38.870	63.662	1.00 20.00
ATOM	2869	CD	ARG	300	57.381	39.499	63.127	1.00 20.00
MOTA	2870	NE	ARG	300	58.323	38.383	62.831	1.00 20.00
MOTA	2872	cz	ARG	300	59.632	38.640	62.541	1.00 20.00
MOTA	2873	NH1	ARG	300	60.101	39.922	62.564	1.00 20.00
MOTA	2876	NH2	ARG	300	60.473	37.612	62.228	1.00 20.00
ATOM	2879	С	ARG	300	53.169	41.175	62.776	1.00 20.00
MOTA	2880	0	ARG	300	52.100	40.597	62.589	1.00 20.00
ATOM	2881	N	LYS	301	53.247	42.451	63.196	1.00 20.00 1.00 20.00
ATOM	2883	CA	LYS	301	52.083	43.220	63.518 64.088	1.00 20.00 1.00 20.00
MOTA	2884	CB CG	LYS LYS	301 301	52.403 52.891	44.615 44.624	65.538	1.00 20.00
ATOM ATOM	2885 2886	CD	LYS	301	51.836	44.146	66.537	1.00 20.00
ATOM	2887	CE	LYS	301	52.219	44.386	68.000	1.00 20.00
ATOM	2888	NZ	LYS	301	51.988	45.804	68.357	1.00 20.00
ATOM	2892	С	LYS	301	51.244	43.447	62.312	1.00 20.00
ATOM	2893	0	LYS	301	51.740	43.586	61.194	1.00 20.00
ATOM	2894	N	CYS	302	49.917	43.473	62.525	1.00 20.00
ATOM	2896	CA	CYS	302	49.042	43.769	61.443	1.00 20.00
MOTA	2897	СВ	CYS	302	48.002	42.684	61.152	1.00 20.00
ATOM	2898	SG	CYS	302	47.330	42.959	59.499	1.00 20.00
MOTA	2899	С	CYS	302	48.314	44.990	61.905	1.00 20.00
MOTA	2900	0	CYS	302	48.036	45.132	63.095	1.00 20.00
MOTA	2901	N	LYS	303	48.003	45.922	60.983	1.00 20.00
MOTA	2903	CA	LYS	303	47.356	47.128	61.407	1.00 20.00 1.00 20.00
ATOM	2904	CB	LYS	303	48.242	48.374 48.550	61.231	1.00 20.00
ATOM	2905	CG	LYS	303 303	48.792 49.481	49.898	59.816 59.594	1.00 20.00
MOTA	2906 2907	CD CE	LYS LYS	303	50.235	49.836	58.265	1.00 20.00
ATOM ATOM	2908		LYS	303	50.255	51.323	58.116	1.00 20.00
ATOM	2912	C	LYS	303	46.078	47.329	60.654	1.00 20.00
MOTA	2913	0	LYS	303	45.879	46.778	59.574	1.00 20.00
ATOM	2914	N	LYS	304	45.169	48.129	61.247	1.00 20.00
ATOM	2916	CA	LYS	304	43.869	48.421	60.711	1.00 20.00
ATOM	2917	СВ	LYS	304	43.032	49.283	61.672	1.00 20.00
ATOM	2918	CG	LYS	304	41.630	49.631	61.174	1.00 20.00
ATOM	2919	CD	LYS	304	40.782	50.330	62.240	1.00 20.00
ATOM	2920	CE	LYS	304	39.436	50.849	61.726	1.00 20.00
ATOM	2921	NZ	LYS	304	38.423	49.771	61.774	1.00 20.00
MOTA	2925	С	LYS	304	43.997	49.190	59.438	1.00 20.00
MOTA	2926	0	LYS	304	44.899	50.012	59.285	1.00 20.00
MOTA	2927	N	CYS	305	43.095	48.927	58.472	1.00 20.00

A I	2929	CA	CYS	305	43.164	49.684	57.260		20.00
ATOM	2930	CB	CYS	305	43.302	48.823	55.985		20.00
MOTA	2931	SG	CYS	305	41.828	47.850	55.573	•	20.00
7 'YM	2932	С	CYS	305	41.923	50.512	57.184		20.00
MC	2933	0	CYS	305	40.806	49.999	57.237	1.00	
MOTA	2934	N	GLU	306	42.086	51.844	57.077 57.024	1.00	20.00
MOTA	2936	CA	GLU	306	40.918 41.217	52.669 54.178	57.024	1.00	20.00
MOTA	2937	CB	GLU	306 306	41.217	54.707	58.328		20.00
MOTA	2938 2939	CG CD	GLU GLU	306	40.654	54.677	59.357		20.00
ATOM ATOM	2939	OE1	GLU	306	39.574	54.114	59.035	1.00	20.00
ATOM	2941	OE2	GLU	306	40.861	55.214	60.478	1.00	20.00
ATOM	2942	C	GLU	306	40.199	52.336	55.763	1.00	20.00
ATOM	2943	0	GLU	306	40.732	52.501	54.667	1.00	20.00
MOTA	2944	N	GLY	307	38.949	51.857	55.896	1.00	
MOTA	2946	CA	GLY	307	38.172	51.522	54.741	1.00	
ATOM	2947	С	GLY	307	38.614	50.195	54.230		20.00
MOTA	2948	0	GLY	307	39.196	49.387	54.951		20.00
MOTA	2949	N	PRO	308	38.336	49.955	52.980		20.00
MOTA	2950	CD	PRO	308	37.118	50.454	52.364 52.409	1.00	
MOTA	2951	CA	PRO	308	38.754 38.045	48.713 48.614	51.062	1.00	
MOTA	2952	CB	PRO PRO	308 308	36.747	49.414	51.290	1.00	
ATOM	2953 2954	C	PRO	308	40.240	48.737	52.352	1.00	
ATOM ATOM	2955	0	PRO	308	40.805	49.802	52.108	1.00	
ATOM	2956	N	CYS	309	40.901	47.588	52.578	1.00	20.00
MOTA	2958	CA	CYS	309	42.329	47.631	52.587	1.00	20.00
MOTA	2959	СВ	CYS	309	43.015	46.386	53.168	1.00	20.00
ATOM	2960	SG	CYS	309	42.556	46.072	54.897	1.00	
MOTA	2961	С	CYS	309	42.789	47.801	51.182	1.00	20.00
MOTA	2962	0	CYS	309	42.104	47.406	50.240	1.00	20.00
MOTA	2963	N	ARG	310	43.972	48.421	51.015	1.00	
MOTA	2965	CA	ARG	310	44.498	48.664	49.709 49.699	1.00	
MOTA	2966	CB	ARG	310	45.726	49.594 51.064	50.032	1.00	20.00
ATOM	2967	CG	ARG ARG	310 310	45.450 44.884	51.307	51.433	1.00	20.00
ATOM ATOM	2968 2969	CD NE	ARG	310	43.403	51.169	51.346	1.00	20.00
ATOM	2971	CZ	ARG	310	42.641	52.281	51.125	1.00	20.00
MOTA	2972	NH1	ARG	310	43.236	53.506	51.036	1.00	20.00
MOTA	2975		ARG	310	41.286	52.172	50.995		20.00
MOTA	2978	С	ARG	310	44.942	47.373	49.114		20.00
MOTA	2979	0	ARG	310	45.419	46.479	49.811		20.00
MOTA	2980	N	LYS	311	44.756	47.247	47.787		20.00
MOTA	2982	CA	LYS	311	45.195	46.091	47.069		20.00
MOTA	2983	CB	LYS	311	44.107 44.629	45.021	46.887 46.300		20.00
MOTA	2984	CG	LYS	311	45.570	43.707 42.946	47.238		20.00
ATOM	2985	CD	LYS LYS	311 311	45.948	41.554	46.727		20.00
ATOM ATOM	2986 2987	CE NZ	LYS	311	46.769	41.667	45.501		20.00
ATOM	2991	C	LYS	311	45.555	46.607	45.717		20.00
ATOM	2992	ō	LYS	311	45.116	47.685	45.323	1.00	20.00
ATOM	2993	N	VAL	312	46.387	45.862	44.968		20.00
ATOM	2995	CA	VAL	312	46.732	46.345	43.667		20.00
MOTA	2996	СВ	VAL	312	47.842	45.578	43.012		20.00
MOTA	2997		VAL	312	48.059	46.152	41.602		20.00
MOTA	2998		VAL	312	49.087	45.658	43.911		20.00
ATOM	2999	С	VAL	312	45.491	46.195	42.799		20.00
MOTA	3000	0	VAL	312	44.922	47.244	42.394		20.00
ATOM	3001	UXT	VAL	312	45.095	45.029	42.529	1.00	20.00
TER									

	_			242	F4 0C2	9.046	61.837	1.00 40.00
MOTA	3	N	CYS	313	54.063			
MOTA	5	CA	CYS	313	54.050	8.871	60.363	1.00 40.00
MOTA	6	CB	CYS	313	53.300	7.570	60.029	1.00 40.00
, A	7	SG	CYS	313	54.210	6.124	60.659	1.00 40.00
ATOM	8	С	CYS	313	53.390	10.060	59.715	1.00 40.00
ATOM	9	0	CYS	313	52.565	10.713	60.344	1.00 40.00
АТОМ	10	N	ASN	314	53.749	10.398	58.452	1.00 40.00
ATOM	12	CA	ASN	314	53.183	11.550	57.785	1.00 40.00
ATOM	13	CB	ASN	314	54.130	12.176	56.746	1.00 40.00
	14	CG	ASN	314	54.433	11.136	55.678	1.00 40.00
ATOM				314	54.238	9.938	55.880	1.00 40.00
ATOM	15		ASN	314	54.937	11.606	54.505	1.00 40.00
MOTA	16	ND2	ASN		51.911	11.161	57.091	1.00 40.00
ATOM	19	C	ASN	314		9.999	57.138	1.00 40.00
MOTA	20	0	ASN	314	51.514			1.00 20.00
MOTA	21	N	GLY	315	51.235	12.143	56.442	
MOTA	23	CA	GLY	315	49.998	11.903	55.745	1.00 20.00
MOTA	24	С	GLY	315	50.241	10.746	54.839	1.00 20.00
MOTA	25	0	GLY	315	51.148	10.775	54.010	1.00 20.00
MOTA	26	N	ILE	316	49.421	9.689	54.982	1.00 20.00
MOTA	28	CA	ILE	316	49.654	8.506	54.212	1.00 20.00
ATOM	29	CB	ILE	316	49.701	7.266	55.060	1.00 20.00
MOTA	30	CG2	ILE	316	49.810	6.043	54.134	1.00 20.00
ATOM	31	CG1	ILE	316	50.840	7.372	56.089	1.00 20.00
ATOM	32	CD1	ILE	316	50.774	6.314	57.189	1.00 20.00
ATOM	33	C	ILE	316	48.554	8.324	53.222	1.00 20.00
ATOM	34	0	ILE	316	47.383	8.559	53.518	1.00 20.00
	35	N	GLY	317	48.916	7.913	51.992	1.00 20.00
ATOM				317	47.898	7.677	51.018	1.00 20.00
ATOM	37	CA	GLY		48.178	6.350	50.401	1.00 20.00
MOTA	38	С	GLY	317			49.443	1.00 20.00
MOTA	39	0	GLY	317	48.942	6.247		1.00 20.00
MOTA	40	N	ILE	318	47.543	5.290	50.933	
ATOM	42	CA	ILE	318	47.728	3.986	50.371	1.00 20.00
MOTA	43	CB	ILE	318	47.758	2.881	51.385	1.00 20.00
MOTA	44	CG2	ILE	318	49.016	3.053	52.249	1.00 20.00
MOTA	45	CG1	ILE	318	46.447	2.831	52.178	1.00 20.00
MOTA	46	CD1	ILE	318	46.354	1.602	53.078	1.00 20.00
ATOM	47	С	ILE	318	46.595	3.745	49.429	1.00 20.00
MOTA	48	0	ILE	318	45.691	4.571	49.319	1.00 20.00
ATOM	49	N	GLY	319	46.626	2.611	48.699	1.00 40.00
ATOM	51	CA	GLY	319	45.557	2.342	47.782	1.00 40.00
ATOM	52	С	GLY	319	46.137	2.189	46.416	1.00 40.00
MOTA	53	0	GLY	319	46.896	1.261	46.142	1.00 40.00
ATOM	54	N	GLU	320	45.781	3.123	45.516	1.00 40.00
ATOM	56	CA	GLU	320	46.284	3.084	44.178	1.00 40.00
АТОМ	57	СВ	GLU	320	47.797	3.351	44.098	1.00 40.00
ATOM	58	CG	GLU	320	48.335	3.435	42.670	1.00 40.00
ATOM	59	CD	GLU	320	49.826	3.732	42.752	1.00 40.00
ATOM	60		GLU	320	50.461	3.873	41.673	1.00 40.00
				320	50.350	3.829	43.894	1.00 40.00
ATOM	61 62	OE2 C	GLU GLU	320	46.002	1.771	43.534	1.00 40.00
ATOM								1.00 40.00
ATOM	63	0	GLU	320	46.780	0.825	43.637	
ATOM	64	N	PHE	321	44.840	1.688	42.861	1.00 60.00
MOTA	66	CA	PHE	321	44.481	0.492	42.166	1.00 60.00
MOTA	67	CB	PHE	321	43.051	0.531	41.598	1.00 60.00
MOTA	68	CG	PHE	321	42.809	-0.724	40.830	1.00 60.00
MOTA	69	CD1	PHE	321	43.173	-0.813	39.504	1.00 60.00
ATOM	70	CD2	PHE	321	42.188	-1.800	41.418	1.00 60.00
ATOM	71	CE1	PHE	321	42.944	-1.958	38.780	1.00 60.00
ATOM	72		PHE	321	41.947	-2.947	40.697	1.00 60.00
MOTA	73	ÇZ	PHE	321	42.326	-3.028	39.379	1.00 60.00
MOTA	74	C	PHE	321	45.414	0.351	41.014	1.00 60.00
ATOM	75	ō	PHE	321	45.223	0.969	39.967	1.00 60.00
ATOM	76	N	LYS	322	46.461	-0.474	41.190	1.00 60.00
ATOM	78	CA	LYS	322	47.379	-0.713	40.121	1.00 60.00
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Figure 7

A	79	СВ	LYS	322	48.815	-0.252	40.428	1.00 60.00	
ATOM	80	CG	LYS	322	49.803	-0.503	39.286	1.00 60.00	
ATOM	81	CD	LYS	322	49.579	0.390	38.062	1.00 60.00	
M'	82	CE	LYS	322	48.513	-0.125	37.093	1.00 60.00	
ALOM	83	NZ	LYS	322	48.375	0.808	35.950	1.00 60.00	
ATOM	87	С	LYS	322	47.420	-2.191	39.932	1.00 60.00	
ATOM	88	0	LYS	322	47.746	-2.936	40.855	1.00 60.00	
ATOM	89	N	ASP	323	47.051	-2.658	38.726	1.00 60.00	•
ATOM	91	CA	ASP	323	47.099	-4.062	38.456	1.00 60.00	
ATOM	92	CB	ASP	323	46.397	-4.458	37.143	1.00 60.00	
MOTA	93	CG	ASP	323	47.108	-3.784	35.978 34.942	1.00 60.00	
MOTA	94		ASP	323	47.322	-4.469 -2.574	36.104	1.00 60.00	
MOTA	95	OD2		323	47.433 48.538	-2.574 -4.441	38.350	1.00 60.00	
MOTA	96	С	ASP	323	48.930	-5.553	38.698	1.00 60.00	
MOTA	97	0	ASP	323 324	49.371	-3.492	37.882	1.00 60.00	
MOTA	98	N	SER SER	324	50.760	-3.756	37.658	1.00 60.00	
ATOM	100	CA CB	SER	324	51.544	-2.494	37.259	1.00 60.00	
ATOM	101 102	OG	SER	324	51.058	-1.985	36.026	1.00 60.00	
ATOM	104	C	SER	324	51.395	-4.290	38.899	1.00 60.00	
ATOM ATOM	105	0	SER	324	52.008	-5.357	38.874	1.00 60.00	
ATOM	106	N	LEU	325	51.255	-3.578	40.032	1.00 60.00	
ATOM	108	CA	LEU	325	51.896	-4.060	41.219	1.00 60.00	
ATOM	109	СВ	LEU	325	51.804	-3.116	42.430	1.00 60.00	
ATOM	110	CG	LEU	325	52.625	-1.823	42.267	1.00 60.00	
ATOM	111		LEU	325	52.077	-0.948	41.128	1.00 60.00	
ATOM	112	CD2	LEU	325	52.755	-1.070	43.601	1.00 60.00	
ATOM	113	С	LEU	325	51.288	-5.362	41.603	1.00 60.00	
MOTA	114	0	LEU	325	50.220	-5.735	41.119	1.00 60.00 1.00 60.00	
MOTA	115	N	SER	326	51.986	-6.105	42.482	1.00 60.00	
ATOM	117	CA	SER	326	51.499	-7.384	42.897 43.874	1.00 60.00	
MOTA	118	CB	SER	326 326	52.451 51.915	-8.095 -9.354	44.250	1.00 60.00	
ATOM	119	OG	SER	326 326	50.202	-7.174	43.599	1.00 60.00	
ATOM	121	C	SER SER	326	49.180	-7.743	43.219	1.00 60.00	
MOTA	122 123	O N	ILE	327	50.204	-6.324	44.644	1.00 60.00	
ATOM	125	CA	ILE	327	48.983	-6.090	45.352	1.00 60.00	
ATOM ATOM	126	CB	ILE	327	48.834	-6.950	46.573	1.00 60.00	
ATOM	127		ILE	327	49.917	-6.537	47.583	1.00 60.00	
MOTA	128		ILE	327	47.402	-6.864	47.126	1.00 60.00	
ATOM	129		ILE	327	46.352	-7.480	46.202	1.00 60.00	
ATOM	130	С	ILE	327	48.969	-4.668	45.802	1.00 60.00	
ATOM	131	0	ILE	327	50.015	-4.078	46.071	1.00 60.00	
ATOM	132	N	ASN	328	47.762	-4.072	45.865	1.00 40.00	
MOTA	134	CA	ASN	328	47.611	-2.726	46.322	1.00 40.00	
MOTA	135	СВ	ASN	328	46.295	-2.093	45.841	1.00 40.00	
ATOM	136	CG	ASN	328	46.384	-1.981	44.323	1.00 40.00	
MOTA	137		ASN	328	47.466	-1.791 -2.111	43.626	1.00 40.00	
MOTA	138		ASN	328	45.223 47.578	-2.111	47.812	1.00 40.00	
ATOM	141	C	ASN	328 328	47.893	-1.878	48.529	1.00 40.00	
MOTA	142 143	N O	ASN ALA	329	47.214	-4.025	48.301	1.00 40.00	
MOTA	145	CA	ALA	329	47.117	-4.326	49.698	1.00 40.00	
MOTA MOTA	146	CB	ALA	329	46.633	-5.761	49.967	1.00 40.00	1
ATOM	147	C	ALA	329	48.482	-4.197	50.290	1.00 40.00	
ATOM	148	Ö	ALA	329	48.636	-3.841	51.456	1.00 40.00	
ATOM	149	N	THR	330	49.518	-4.458	49.476	1.00 40.00	
ATOM	151	CA	THR	330	50.871	-4.441	49.946	1.00 40.00	
ATOM	152	СВ	THR	330	51.875	-4.612	48.845	1.00 40.00	
ATOM	153		THR	330	53.174	-4.807	49.385	1.00 40.00	
MOTA	155		THR	330	51.853	-3.347	47.972	1.00 40.00	
MOTA	156	С	THR	330	51.143	-3.117	50.583	1.00 40.00	
ATOM	157	0	THR	330	51.963	-3.021	51.493	1.00 40.00	
MOTA	158	N	ASN	331	50.459	-2.059	50.112	1.00 40.00	•

MOTA	160	CA	ASN	331	50.645	-0.728	50.616	1.00 40.00
MOTA	161	CB	ASN	331	49.784	0.317	49.883	1.00 40.00
MOTA	162	CG	ASN	331	50.411	0.592	48.522	1.00 40.00
M	163		ASN	331	50.424	-0.259	47.634	1.00 40.00
A L OM	164		ASN	331	50.947	1.831	48.353	1.00 40.00
MOTA	167	С	ASN	331	50.311	-0.634	52.079	1.00 40.00
MOTA	168	0	ASN	331	50.896	0.175	52.796	1.00 40.00
MOTA	169	N	ILE	332	49.370	-1.468	52.558	1.00 40.00 1.00 40.00
MOTA	171	CA	ILE	332	48.883	-1.467	53.915	1.00 40.00
MOTA	172	CB	ILE	332	47.753	-2.450	54.108 55.611	1.00 40.00
MOTA	173	CG2		332	47.465	-2.606 -1.984	53.324	1.00 40.00
MOTA	174	CG1		332	46.510 46.687	-1.964	51.808	1.00 40.00
ATOM	175	CD1		332 332	49.982	-1.751	54.903	1.00 40.00
ATOM	176	С	ILE	332	49.872	-1.731	56.076	1.00 40.00
ATOM	177	0	ILE	333	51.066	-2.412	54.462	1.00 40.00
ATOM	178	N CA	LYS LYS	333	52.173	-2.772	55.309	1.00 40.00
ATOM	180	CB	LYS	333	53.279	-3.515	54.544	1.00 40.00
ATOM	181 182	CG	LYS	333	52.838	-4.845	53.933	1.00 40.00
MOTA	183	CD	LYS	333	53.866	-5.413	52.953	1.00 40.00
ATOM ATOM	184	CE	LYS	333	53.457	-6.746	52.323	1.00 40.00
ATOM	185	NZ	LYS	333	54.529	-7.228	51.422	1.00 40.00
ATOM	189	C	LYS	333	52.828	-1.565	55.913	1.00 40.00
ATOM	190	0	LYS	333	53.348	-1.628	57.025	1.00 40.00
ATOM	191	N	HIS	334	52.803	-0.423	55.204	1.00 40.00
ATOM	193	CA	HIS	334	53.459	0.777	55.644	1.00 40.00
ATOM	194	СВ	HIS	334	53.101	1.980	54.753	1.00 40.00
ATOM	195	CG	HIS	334	53.623	3.291	55.265	1.00 40.00
ATOM	196		HIS	334	52.952	4.317	55.858	1.00 40.00
ATOM	197		HIS	334	54.937	3.695	55.190	1.00 40.00
MOTA	199		HIS	334	54.996	4.935	55.738	1.00 40.00
ATOM	200		HIS	334	53.816	5.355	56.157	1.00 40.00
ATOM	202	С	HIS	334	53.016	1.117	57.030	1.00 40.00
ATOM	203	0	HIS	334	53.778	1.672	57.818	1.00 40.00
ATOM	204	N	PHE	335	51.753	0.791	57.336	1.00 40.00
ATOM	206	CA	PHE	335	51.061	1.055	58.562	1.00 40.00
ATOM	207	CB	PHE	335	49.554	0.799	58.431	1.00 40.00
ATOM	208	CG	PHE	335	49.102	1.681	57.320	1.00 40.00
ATOM	209	CD1	PHE	335	48.896	1.164	56.062	1.00 40.00
MOTA	210		PHE	335	49.140	3.047	57.469	1.00 40.00
MOTA	211		PHE	335	48.627	1.983	54.990	1.00 40.00
ATOM	212		PHE	335	48.902	3.873	56.397	1.00 40.00
MOTA	213	CZ	PHE	335	48.625	3.345	55.159	1.00 40.00
MOTA	214	С	PHE	335	51.559	0.283	59.744	1.00 40.00
MOTA	215	0	PHE	335	51.268	0.647	60.879	1.00 40.00
MOTA	216	N	LYS	336	52.301	-0.815	59.536	1.00 40.00 1.00 40.00
ATOM	218	CA	LYS	336	52.650	-1.655 -2.830	60.647 60.237	1.00 40.00
ATOM	219	CB	LYS	336 336	53.554 52.800	-3.964	59.540	1.00 40.00
MOTA	220	CG	LYS	336	51.765	-4.630	60.450	1.00 40.00
ATOM	221	CD	LYS		50.988	-4.030 -5.769	59.788	1.00 40.00
ATOM	222	CE	LYS	336	50.020	-6.339	60.752	1.00 40.00
MOTA	223	NZ C	LYS LYS	336 336	53.325	-0.339	61.793	1.00 40.00
MOTA	227		LYS	336	53.026	-1.250	62.946	1.00 40.00
ATOM	228	O N	ASN	337	54.284	-0.045	61.530	1.00 40.00
ATOM	229 231	CA	ASN	337	54.284	0.629	62.589	1.00 40.00
ATOM	231	CB	ASN	337	56.335	1.211	62.109	1.00 40.00
ATOM ATOM	232	CG	ASN	337	57.267	0.038	61.842	1.00 40.00
ATOM	233		ASN	337	57.310	-0.920	62.613	1.00 40.00
MOTA	235		ASN	337	58.031	0.106	60.719	1.00 40.00
ATOM	238	C	ASN	337	54.274	1.726	63.336	1.00 40.00
ATOM	239	0	ASN	337	54.441	1.867	64.546	1.00 40.00
ATOM	240	N	CYS	338	53.450	2.529	62.634	1.00 20.00
ATOM	242	CA	CYS	338	52.859	3.733	63.159	1.00 20.00
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	0.4.0	6 5	CVC	338	52.042	4.491	62.087	1.00 20.00
A	243 244	CB SG	CYS CYS	338	52.908	4.575	60.487	1.00 20.00
MOTA MOTA	245	C	CYS	338	51.966	3.576	64.354	1.00 20.00
M	246	0	CYS	338	50.994	2.823	64.335	1.00 20.00
A·I·OM	247	N	THR	339	52.356	4.224	65.473	1.00 20.00
MOTA	249	CA	THR	339	51.526	4.354	66.634	1.00 20.00
MOTA	250	CB	THR	339	52.332	4.553	67.880	1.00 20.00
MOTA	251	OG1		339	51.470	4.672	69.000	1.00 20.00 1.00 20.00
MOTA	253	CG2		339	53.197 50.613	5.812 5.531	67.719 66.451	1.00 20.00
MOTA	254	C	THR	339 339	49.437	5.490	66.809	1.00 20.00
ATOM	255	0	THR SER	340	51.146	6.642	65.898	1.00 20.00
MOTA	256 258	N CA	SER	340	50.317	7.795	65.714	1.00 20.00
ATOM ATOM	259	CB	SER	340	50.454	8.820	66.856	1.00 20.00
ATOM	260	OG	SER	340	51.788	9.301	66.938	1.00 20.00
ATOM	262	С	SER	340	50.677	8.482	64.438	1.00 20.00
ATOM	263	0	SER	340	51.676	9.194	64.362	1.00 20.00
ATOM	264	N	ILE	341	49.850	8.318	63.390	1.00 20.00
MOTA	266	CA	ILE	341	50.200	8.984	62.177 60.942	1.00 20.00 1.00 20.00
ATOM	267	CB	ILE	341	49.518 50.047	8.470 7.067	60.638	1.00 20.00
MOTA	268	CG2		341 341	47.995	8.562	61.072	1.00 20.00
MOTA	269		ILE	341	47.273	8.284	59.755	1.00 20.00
ATOM ATOM	270 271	CDI	ILE	341	49.868	10.426	62.330	1.00 20.00
MOTA	271	0	ILE	341	48.711	10.792	62.521	1.00 20.00
MOTA	273	N	SER	342	50.901	11.287	62.273	1.00 20.00
ATOM	275	CA	SER	342	50.671	12.692	62.381	1.00 20.00
ATOM	276	CB	SER	342	51.889	13.483	62.888	1.00 20.00
MOTA	277	OG	SER	342	52.193	13.107	64.223	1.00 20.00 1.00 20.00
MOTA	279	С	SER	342	50.364	13.165	61.002 60.243	1.00 20.00
MOTA	280	0	SER	342	51.259 49.065	13.536 13.173	60.243	1.00 20.00
ATOM	281	N	GLY	343 343	49.063	13.173	59.341	1.00 20.00
MOTA	283 284	CA C	GLY GLY	343	47.366	12.873	59.096	1.00 20.00
ATOM ATOM	285	0	GLY	343	46.609	12.606	60.026	1.00 20.00
ATOM	286	N	ASP	344	47.073	12.555	57.824	1.00 20.00
ATOM	288	CA	ASP	344	45.833	11.906	57.524	1.00 20.00
ATOM	289	CB	ASP	344	44.961	12.709	56.536	1.00 20.00
MOTA	290	CG	ASP	344	45.728	12.897	55.232	1.00 20.00 1.00 20.00
ATOM	291		ASP	344	46.922	12.501 13.455	55.179 54.272	1.00 20.00
ATOM	292		ASP	344 344	45.130 46.100	10.563	56.933	1.00 20.00
ATOM	293	С О	ASP ASP	344 344	47.197	10.290	56.452	1.00 20.00
ATOM	294 295	N	LEU	345	45.098	9.664	56.999	1.00 20.00
MOTA MOTA	293 297	CA	LEU	345	45.262	8.362	56.427	1.00 20.00
ATOM	298	CB	LEU	345	45.064	7.222	57.438	1.00 20.00
ATOM	299	CG	LEU	345	45.234	5.831	56.810	1.00 20.00
MOTA	300		LEU	345	46.611	5.704	56.157	1.00 20.00
MOTA	301		LEU	345	44.967	4.716	57.834	1.00 20.00
MOTA	302	С	LEU	345	44.237	8.203	55.351	1.00 20.00 1.00 20.00
MOTA	303	0	LEU	345	43.061	8.494 7.763	55.558 54.152	1.00 20.00
ATOM	304	N	HIS	346 346	44.671 43.738	7.763	53.085	1.00 20.00
ATOM	306 307	CA CB	HIS HIS	346 346	43.738	8.395	51.827	1.00 20.00
ATOM ATOM	308	CG	HIS	346	43.667	9.851	51.988	1.00 20.00
ATOM	309		HIS	346	42.906	10.487	52.921	1.00 20.00
ATOM	310		HIS	346	44.071	10.828	51.105	1.00 20.00
ATOM	312		HIS	346	43.545	11.998	51.546	1.00 20.00
ATOM	313		HIS	346	42.830	11.841	52.645	1.00 20.00
ATOM	315	С	HIS	346	43.890	6.122	52.650	1.00 20.00
MOTA	316	0	HIS	346	44.995	5.670	52.356	1.00 20.00
MOTA	317	N	ILE	347	42.778	5.366	52.619	1.00 20.00 1.00 20.00
MOTA	319	CA	ILE	347	42.884	4.018	52.151 53.159	1.00 20.00
MOTA	320	CB	ILE	347	42.422	3.010	23.123	1.00 20.00

ATOM	321	CG2	ILE	347	42.527	1.621	52.511		20.00	
ATOM	322		ILE	347	43.253	3.143	54.449		20.00	
MOTA	323	CD1	ILE	347	42.665	2.393	55.644		20.00	
M.	324	С	ILE	347	42.000	3.938	50.952		20.00	
MOIA	325	0	ILE	347	40.795	3.715	51.052		20.00	
MOTA	326	N	LEU	348	42.607	4.094 4.138	49.766 48.533		20.00	
MOTA	328	CA	LEU	348	41.882 42.700	4.138	47.444		20.00	
MOTA	329	CB	LEU	348 348	43.043	6.285	47.877		20.00	
MOTA .	. 330	CG CD1	LEU LEU	348	43.859	7.034	46.817		20.00	
MOTA	331 332		LEU	348	41.778	7.053	48.295		20.00	
MOTA MOTA	333	CDZ	LEU	348	41.557	2.743	48.110		20.00	
MOTA	334	o	LEU	348	41.948	1.769	48.753		20.00	
ATOM	335	N	PRO	349	40.852	2.625	47.019	1.00	60.00	
ATOM	336	CD	PRO	349	40.061	3.714	46.470	1.00	60.00	
ATOM	337	CA	PRO	349	40.393	1.344	46.575	1.00	60.00	
ATOM	338	СВ	PRO	349	39.558	1.614	45.327		60.00	
ATOM	339	·CG	PRO	349	39.008	3.034	45.575		60.00	
ATOM	340	С	PRO	349	41.486	0.350	46.425		60.00	
ATOM	341	0	PRO	349	42.349	0.514	45.563		60.00	
ATOM	342	N	VAL	350	41.442	-0.704	47.259		60.00	
ATOM	344	CA	VAL	350	42.426	-1.737	47.213		60.00	
ATOM	345	CB	VAL	350	43.285	-1.798	48.441		60.00	
MOTA	346		VAL	350	42.379 44.379	-2.090	49.649 48.224		60.00	
ATOM	347		VAL	350 350	44.379	-2.856 -3.023	47.137		60.00	
MOTA	348 349	С О	VAL VAL	350	40.582	-3.149	47.684		60.00	•
MOTA MOTA	350	N	ALA	351	42.250	-4.012	46.429		60.00	
ATOM	352	CA	ALA	351	41.609	-5.287	46.311		60.00	
ATOM	353	CB	ALA	351	41.491	-5.785	44.861		60.00	
ATOM	354	C	ALA	351	42.473	-6.255	47.046	1.00	60.00	
ATOM	355	0	ALA	351	43.584	-5.918	47.450		60.00	
ATOM	356	N	PHE	352	41.974	-7.487	47.264		60.00	
ATOM	358	CA	PHE	352	42.778	-8.437	47.974		60.00	
ATOM	359	CB	PHE	352	42.087	-9.007	49.226		60.00	
ATOM	360	CG	PHE	352	43.030	-9.963	49.871		60.00	
MOTA	361		PHE	352	44.096	-9.492 -11.320	50.603 49.813		60.00	
MOTA	362		PHE	352 352		-11.320	51.235		60.00	
MOTA	363 364		PHE PHE	352		-12.192	50.452		60.00	
ATOM ATOM	365	CZ	PHE	352		-11.712	51.161		60.00	
ATOM	366	C	PHE	352		-9.582	47.065		60.00	
ATOM	367	o	PHE	352		-10.173	46.456	1.00	60.00	
ATOM	368	N	ARG	353	44.394	-9.908	46.946		60.00	
ATOM	370	CA	ARG	353		-10.999	46.123		60.00	
МОТА	371	CB	ARG	353		-10.663	44.623		60.00	
ATOM	372	CG	ARG	353		-10.313	43.988		60.00	
ATOM	373	CD	ARG	353		-10.218	42.462		60.00	
MOTA	374	NE	ARG	353	44.677	-9.228	42.122 40.869		60.00	
ATOM	376		ARG	353	44.731	-8.690 -9.023	39.946		60.00	
MOTA	377 380		ARG ARG	353 353	43.783 45.731	-7.821	40.540		60.00	•
MOTA MOTA	383	C	ARG	353		-11.284	46.553		60.00	
MOTA	384	0	ARG	353		-11.176	47.730		60.00	
ATOM	385	N	GLY	354		-11.675	45.590		60.00	
MOTA	387	CA	GLY	354		-11.908	45.900		60.00	
MOTA	388	С	GLY	354		-13.246	46.535	1.00	60.00	
MOTA	389	0	GLY	354	49.468	-13.421	47.417		60.00	
MOTA	390	N	ASP	355		-14.237	46.108		60.00	
MOTA	392	CA	ASP	355		-15.537	46.687		60.00	
MOTA	393	СВ	ASP	355		-16.153	47.215		60.00	
MOTA	394	CG	ASP	355		-16.365	46.024		60.00	
MOTA	395		ASP	355		-17.551 -15.349	45.679		60.00	
ATOM	396	OD2	ASP	355	45.289	-15.348	45.446	1.00	00.00	

A	397	С	ASP	355	48.470 -16			1.00	
ATOM	398	0	ASP	355	48.219 -16				60.00
MOTA	399	N	SER	356	49.208 -17				60.00
. М	401	CA	SER	356	49.665 -18				60.00
A. OM	402	CB	SER	356	51.181 -18				60.00 60.00
ATOM	403	OG	SER	356	51.541 -19 48.964 -19				60.00
ATOM	405	C	SER	356	48.464 -19				60.00
ATOM	406	0	SER	356 357	48.891 -20				60.00
ATOM	407	N	PHE PHE	357	48.189 -2		44.948		60.00
ATOM	409 410	CA CB	PHE	357	47.958 -22				60.00
ATOM ATOM	411	CG	PHE	357	47.190 -24			1.00	60.00
ATOM	412	CD1		357	47.831 -25		44.790	1.00	60.00
MOTA	413	CD2		357	45.832 -24	4.125	43.999	1.00	60.00
ATOM	414	CE1		357	47.123 -26				60.00
ATOM	415	CE2	PHE	357	45.118 -25				60.00
ATOM	416	CZ	PHE	357	45.766 -26				60.00
ATOM	417	С	PHE	357	49.029 -22				60.00
ATOM	418	0	PHE	357	50.005 -23		45.583		60.00 60.00
ATOM	419	N	THR	358	48.674 -23		47.236		60.00
ATOM	421	CA	THR	358	49.444 -23 50.377 -23		48.238 48.975		60.00
MOTA	422	CB	THR	358	51.242 -23		49.814		60.00
ATOM	423	OG1	THR	358 358	49.546 -2		49.809		60.00
MOTA	425 426	CG2 C	THR	358	48.515 -23		49.240		60.00
ATOM ATOM	427	0	THR	358	47.512 -2		49.627		60.00
ATOM	428	N	HIS	359	48.825 -25		49.661		60.00
ATOM	430	CA	HIS	359	48.031 -25	5.756	50.636		60.00
ATOM	431	СВ	HIS	359	48.406 -2		50.750		60.00
MOTA	432	CG	HIS	359	48.261 -2		49.456		60.00
MOTA	433	CD2		359	47.273 -28		49.019		60.00 60.00
MOTA	434	ND1		359	49.184 -2° 48.713 -2°		48.435 47.439		60.00
MOTA	436	CE1 NE2		359 359	47.556 -25		47.747		60.00
ATOM	437 439	NEZ C	HIS	359	48.286 -2		51.980		60.00
ATOM ATOM	440	0	HIS	359	47.362 -2		52.753	1.00	60.00
ATOM	441	N	THR	360	49.573 -2	4.886	52.275		60.00
ATOM	443	CA	THR	360	49.971 -2		53.563		60.00
ATOM	444	СВ	THR	360	51.419 -2		53.638		60.00
MOTA	445	OG1		360	51.804 -2		54.990		60.00
ATOM	447	CG2		360	51.624 -2		52.833 53.939		60.00 60.00
MOTA	448	C	THR	360	49.166 -2 48.683 -2		53.939		60.00
MOTA	449	O N	THR PRO	360 361	48.991 -2		55.221		60.00
ATOM ATOM	450 451	N CD	PRO	361	48.870 -2		56.090		60.00
ATOM	452	CA	PRO	361	48.265 -2		55.724	1.00	60.00
ATOM	453	СВ	PRO	361	47.721 -2		57.095		60.00
ATOM	454	CG	PRO	361	48.502 -2		57.456		60.00
MOTA	455	С	PRO	361	49.167 -2		55.759		60.00
MOTA	456	0	PRO	361	50.356 -2		56.035		60.00 60.00
MOTA	457	N	PRO	362	48.624 -1 47.213 -1		55.497 55.739		60.00
ATOM	458	CD	PRO PRO	362 362	49.387 -1		55.475		60.00
ATOM	459 460	CA CB	PRO	362	48.366 -1		55.254		60.00
MOTA MOTA	461	CG	PRO	362	47.104 -1		55.939	1.00	60.00
MOTA	462	C	PRO	362	50.049 -1		56.803		60.00
ATOM	463	0	PRO	362	49.509 -1		57.795		60.00
MOTA	464	N	LEU	363	51.229 -1		56.840		60.00
MOTA	466	CA	LEU	363	51.885 -1		58.091		60.00
ATOM	467	CB	LEU	363	53.225 -1		57.946		60.00 60.00
ATOM	468	CG	LEU	363 363	53.937 -1 54.300 -1		59.289 59.983		60.00
MOTA	469		LEU LEU	363 363	54.300 -1 55.146 -1		59.963		60.00
ATOM ATOM	470 471	CD2	LEU	363	50.973 -1		58.880		60.00
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MOTA	472	0	LEU	363	50.651	-16.791	60.030	1.00 60.00
MOTA	473	N	ASP	364		-15.401	58.255	1.00 60.00
MOTA	475	CA	ASP	364		-14.521	58.928	1.00 60.00
. М	476	СВ	ASP	364		-13.063	58.441	1.00 60.00
A.JM	477	CG	ASP	364		-12.490	58.861	1.00 60.00
MOTA	478		ASP	364		-11.302	58.532	1.00 60.00
ATOM	479		ASP	364		-13.232	59.511	1.00 60.00
MOTA	480	С	ASP	364		-15.013	58.601	1.00 60.00
ATOM	481	0	ASP	364		-16.007	57.898	1.00 60.00
ATOM	482	N	PRO	365		-14.343	59.135	1.00 60.00
MOTA	483	CD	PRO	365 365		-13.790 -14.690	60.473	1.00 60.00 1.00 60.00
ATOM	484	CA	PRO	365 365		-14.890 -14.202	58.816 59.985	1.00 60.00
ATOM	485	CB CG	PRO PRO	365		-14.202	60.784	1.00 60.00
MOTA	486 487	C	PRO	365		-14.043	57.512	1.00 60.00
MOTA MOTA	488	0	PRO	365		-13.094	57.136	1.00 60.00
MOTA	489	N	GLN	366		-14.538	56.796	1.00 60.00
ATOM	491	CA	GLN	366		-13.941	55.537	1.00 60.00
ATOM	492	СВ	GLN	366		-14.680	54.789	1.00 60.00
ATOM	493	CG	GLN	366	43.557	-16.094	54.371	1.00 60.00
ATOM	494	CD	GLN	366		-16.769	53.636	1.00 60.00
ATOM	495	OE1	GLN	366	42.506	-17.940	53.271	1.00 60.00
ATOM	496	NE2	GLN	366	41.297	-16.021	53.404	1.00 60.00
ATOM	499	C	GLN	366	43.854	-12.534	55.822	1.00 60.00
ATOM	500	0	GLN	366	44.212	-11.612	55.090	1.00 60.00
MOTA	501	N	GLU	367		-12.332	56.920	1.00 60.00
ATOM	503	CA	GLU	367		-11.010	57.300	1.00 60.00
MOTA	504	СВ	GLU	367		-11.013	58.454	1.00 60.00
MOTA	505	CG	GLU	367		-11.759	59.692	1.00 60.00
MOTA	506	CD	GLU	367		-11.857	60.693	1.00 60.00
ATOM	507		GLU	367		-10.795	61.212 60.951	1.00 60.00 1.00 60.00
ATOM	508		GLU GLU	367 367		-13.004 -10.300	57.747	1.00 60.00
ATOM	509 510	C O	GLU	367		-10.933	58.198	1.00 60.00
MOTA MOTA	511	N	LEU	368	43.971	-8.958	57.610	1.00 40.00
ATOM	513	CA	LEU	368	45.148	-8.233	57.992	1.00 40.00
ATOM	514	CB	LEU	368	45.817	-7.526	56.792	1.00 40.00
ATOM	515	CG	LEU	368	47.098	-6.716	57.097	1.00 40.00
MOTA	516		LEU	368	46.823	-5.435	57.902	1.00 40.00
MOTA	517	CD2	LEU	368	48.171	-7.612	57.734	1.00 40.00
MOTA	518	С	LEU	368	44.735	-7.199	58.981	1.00 40.00
MOTA	519	0	LEU	368	43.798	-6.437	58.752	1.00 40.00
MOTA	520	N	ASP	369	45.427	-7.161	60.132	1.00 40.00
MOTA	522	CA	ASP	369	45.144	-6.135	61.082	1.00 40.00
MOTA	523	СВ	ASP	369	45.333	-6.552	62.551	1.00 40.00
MOTA	524	CG	ASP	369	44.269	-7.568	62.932	1.00 40.00
ATOM	525		ASP	369	44.164	-7.875	64.150	1.00 40.00
MOTA	526		ASP	369 360	43.553	-8.056 -5.196	62.018 60.786	1.00 40.00 1.00 40.00
MOTA	527	C O	ASP ASP	369 369	46.245 47.393	-5.629	60.696	1.00 40.00
MOTA MOTA	528 529	N	ILE	370	45.918	-3.906	60.581	1.00 40.00
ATOM	531	CA	ILE	370	46.965	-2.968	60.332	1.00 40.00
ATOM	532	СВ	ILE	370	46.459	-1.569	60.186	1.00 40.00
ATOM	533	CG2	ILE	370	47.655	-0.605	60.196	1.00 40.00
ATOM	534	CG1	ILE	370	45.594	-1.485	58.919	1.00 40.00
ATOM	535	CD1	ILE	370	44.814	-0.183	58.792	1.00 40.00
ATOM	536	c	ILE	370	47.813	-3.082	61.542	1.00 40.00
АТОМ	537	0	ILE	370	48.973	-3.478	61.441	1.00 40.00
ATOM	538	N	LEU	371	47.230	-2.776	62.718	1.00 40.00
MOTA	540	CA	LEU	371	47.927	-3.049	63.936	1.00 40.00
MOTA	541	СВ	LEU	371	49.402	-2.609	63.988	1.00 40.00
MOTA	542	CG	LEU	371	50.110	-3.093	65.267	1.00 40.00
ATOM	543	CD1		371	50.003	-4.621	65.407	1.00 40.00
ATOM	544	CD2	LEU	371	51.575	-2.632	65.301	1.00 40.00

A	545	С	LEU	371	47.234	-2.413	65.087		40.00
AT OM	546	0	LEU	371	46.575	-1.382	64.958		40.00
MOTA	547	N	LYS	372	47.392	-3.051	66.257		20.00
. м	549	CA	LYS	372	46.865	-2.593	67.503		20.00
A.1 OM	550	СВ	LYS	372	47.005	-3.637	68.625		20.00
MOTA	551	CG	LYS	372	46.173	-4.896	68.358		20.00
MOTA	552	CD	LYS	372	46.478	-6.068	69.293		20.00
MOTA	553	CE	LYS	372	45.536	-6.144	70.496		20.00
MOTA	554	NZ	LYS	372	45.826	-7.358	71.292		20.00
MOTA	558	С	LYS	372	47.650	-1.374	67.857		20.00
MOTA	559	0	LYS	372	47.230	-0.550 -1.234	68.665 67.255		20.00
MOTA	560	N	THR	373	48.841 49.713	-0.143	67.570		20.00
MOTA	562	CA	THR	373 373	50.993	-0.161	66.790		20.00
ATOM	563	CB OG1	THR THR	373	51.913	0.773	67.334		20.00
ATOM	564	CG2	THR	373	50.677	0.195	65.327		20.00
MOTA	566 567	C	THR	373	49.078	1.188	67.308		20.00
ATOM ATOM	568	0	THR	373	49.377	2.153	68.009		20.00
ATOM	569	N	VAL	374	48.194	1.295	66.295	1.00	20.00
ATOM	571	CA	VAL	374	47.677	2.593	65.946	1.00	20.00
ATOM	572	СВ	VAL	374	47.137	2.637	64.544	1.00	20.00
MOTA	573		VAL	374	46.601	4.051	64.263		20.00
ATOM	574		VAL	374	48.245	2.177	63.578		20.00
ATOM	575	С	VAL	374	46.591	3.087	66.859		20.00
ATOM	576	0	VAL	374	45.431	2.689	66.736		20.00
ATOM	577	N	LYS	375	46.980	3.924	67.848		20.00
MOTA	579	CA	LYS	375	46.084	4.602	68.746		20.00
MOTA	580	CB	LYS	375	46.752	5.075	70.049	1.00	
ATOM	581	CG	LYS	375	47.091	3.970	71.050	1.00	20.00
MOTA	582	CD	LYS	375	47.814	4.503	72.289 73.413		20.00
MOTA	583	CE	LYS	375	47.964 48.533	3.476 4.126	74.615		20.00
ATOM	584	NZ	LYS	375 375	45.439	5.830	68.169		20.00
ATOM	588 589	С 0	LYS LYS	375	44.256	6.079	68.386		20.00
ATOM ATOM	590	N	GLU	376	46.193	6.658	67.419		20.00
ATOM	592	CA	GLÜ	376	45.613	7.918	67.049	1.00	20.00
MOTA	593	CB	GLU	376	46.103	9.051	67.971	1.00	20.00
ATOM	594	CG	GLU	376	45.540	10.438	67.665	1.00	
ATOM	595	CD	GLU	376	46.126	11.397	68.691		20.00
ATOM	596	OE1	GLU	376	45.997	11.108	69.911		20.00
ATOM	597	OE2	GLU	376	46.716	12.426	68.269		20.00
ATOM	598	С	GLU	376	45.926	8.309	65.641		20.00
ATOM	599	0	GLU	376	46.796	7.732	64.994		20.00
ATOM	600	N	ILE	377	45.148	9.283	65.121 63.833		20.00
ATOM	602	CA	ILE	377	45.362 44.403	9.865 9.370	62.791		20.00
MOTA	603	CB	ILE	377 377	44.680	10.133	61.485		20.00
ATOM	604	CG2	ILE ILE	377	44.526	7.844	62.642		20.00
ATOM	605 606	CD1	ILE	377	43.402	7.214	61.820		20.00
MOTA	607	CDI	ILE	377	45.075	11.311	64.089		20.00
MOTA MOTA	608	0	ILE	377	44.015	11.662	64.599	1.00	20.00
ATOM	609	N	THR	378	46.029	12.183	63.740	1.00	20.00
ATOM	611	CA	THR	378	45.985	13.594	63.994		20.00
ATOM	612	СВ	THR	378	47.317	14.235	63.734		20.00
ATOM	613		THR	378	48.316	13.599	64.516		20.00
MOTA	615		THR	378	47.249	15.718	64.124		20.00
ATOM	616	С	THR	378	44.965	14.303	63.159		20.00
MOTA	617	0	THR	378	44.612	15.442	63.452		20.00
MOTA	618	N	GLY	379	44.522	13.695	62.044		20.00
ATOM	620	CA	GLY	379	43.608	14.380	61.171		20.00
MOTA	621	С	GLY	379	42.325	13.631	61.001		20.00
MOTA	622	0	GLY	379	41.520	13.523	61.923		20.00
MOTA	623	N	PHE	380	42.082	13.126	59.775 59.515		20.00
ATOM	625	CA	PHE	380	40.869	12.405	و د د د د د	1.00	20.00

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MOTA	626	CB	PHE	380	39.920	13.116	58.530	1.00 20.00
MOTA	627	CG	PHE	380	40.598	13.264	57.212	1.00 20.00
ATOM	628	CD1	PHE	380	40.528	12.265	56.268	1.00 20.00
MC	629	CD2	PHE	380	41.265	14.427	56.902	1.00 20.00
A.1.OM	630	CE1	PHE	380	41.112	12.426	55.034	1.00 20.00
MOTA	631	CE2	PHE	380	41.860	14.590	55.674	1.00 20.00
MOTA	632	CZ	PHE	380	41.780	13.589	54.736	1.00 20.00
MOTA	633	С	PHE	380	41.216	11.066	58.955	1.00 20.00
MOTA	634	0	PHE	380	42.359	10.824	58.573	1.00 20.00
MOTA	635	N	LEU	381	40.231	10.141	58.942	1.00 20.00
MOTA	637	CA	LEU	381	40.454	8.822	58.422	1.00 20.00
MOTA	638	CB	LEU	381	40.156	7.725	59.462	1.00 20.00
MOTA	639	CG	LEU	381	40.369	6.281	58.972	1.00 20.00
MOTA	640		LEU	381	41.834	6.032	58.580	1.00 20.00
MOTA	641		LEU	381	39.866	5.268	60.015	1.00 20.00
MOTA	642	С	LEU	381	39.534	8.629	57.251	1.00 20.00
MOTA	643	0	LEU	381	38.318	8.782	57.368	1.00 20.00
MOTA	644	N	LEU	382	40.096	8.290	56.073	1.00 20.00
MOTA	646	CA	LEU	382	39.283	8.132	54.899	1.00 20.00
MOTA	647	СВ	LEU	382	39.642	9.158	53.808	1.00 20.00
MOTA	648	CG	LEU	382	38.818	9.062	52.511	1.00 20.00 1.00 20.00
MOTA	649		LEU	382	37.330	9.337	52.761	1.00 20.00
MOTA	650		LEU	382	39.405	9.975	51.424 54.312	1.00 20.00
ATOM	651	C	LEU	382	39.459	6.767 6.399	53.873	1.00 20.00
ATOM	652	0	LEU	382 383	40.548 38.375	5.968	54.295	1.00 20.00
ATOM	653 655	N CA	ILE ILE	383	38.451	4.677	53.681	1.00 20.00
ATOM	655 656	CB	ILE	383	38.143	3.540	54.623	1.00 20.00
ATOM ATOM	657	CG2	ILE	383	36.747	3.739	55.239	1.00 20.00
ATOM	658	CG1	ILE	383	38.351	2.191	53.916	1.00 20.00
ATOM	659	CD1	ILE	383	38.352	1.000	54.872	1.00 20.00
MOTA	660	C	ILE	383	37.471	4.676	52.553	1.00 20.00
ATOM	661	o	ILE	383	36.259	4.747	52.745	1.00 20.00
ATOM	662	N	GLN	384	37.975	4.608	51.314	1.00 20.00
MOTA	664	CA	GLN	384	37.065	4.622	50.213	1.00 20.00
ATOM	665	СВ	GLN	384	37.334	5.758	49.212	1.00 20.00
ATOM	666	CG	GLN	384	36.365	5.786	48.026	1.00 20.00
ATOM	667	CD	GLN	384	36.804	6.908	47.092	1.00 20.00
ATOM	668	OE1	GLN	384	37.864	7.503	47.279	1.00 20.00
ATOM	669	NE2	GLN	384	35.972	7.208	46.058	1.00 20.00
MOTA	672	С	GLN	384	37.241	3.340	49.472	1.00 20.00
ATOM	673	0	GLN	384	38.359	2.852	49.313	1.00 20.00
ATOM	674	N	ALA	385	36.108	2.768	49.020	1.00 20.00
MOTA	676	CA	ALA	385	36.047	1.565	48.240	1.00 20.00
MOTA	677	CB	ALA	385	36.094	1.823	46.723	1.00 20.00
MOTA	678	С	ALA	385	37.093	0.547	48.564	1.00 20.00
MOTA	679	0	ALA	385	38.095	0.433	47.860	1.00 20.00
MOTA	680	N	TRP	386	36.905	-0.206	49.665	1.00 40.00
MOTA	682	CA	TRP	386	37.807	-1.282	49.951	1.00 40.00
MOTA	683	CB	TRP	386	38.698	-1.047	51.187	1.00 40.00
MOTA	684	CG	TRP	386	39.643	-2.188	51.498	1.00 40.00
MOTA	685	CD2		386	40.808	-2.083	52.333	1.00 40.00
ATOM	686		TRP	386	41.411	-3.341	52.364	1.00 40.00
ATOM	687		TRP	386	41.335	-1.026	53.017	1.00 40.00
ATOM	688		TRP	386	39.602	-3.478	51.060	1.00 40.00
ATOM	689		TRP	386	40.658	-4.188	51.581	1.00 40.00
ATOM	691		TRP	386	42.553	-3.560	53.080	1.00 40.00
ATOM	692	CZ3		386	42.485	-1.251	53.740	1.00 40.00
MOTA	693		TRP	386	43.085	-2.492	53.768	1.00 40.00
MOTA	694	C	TRP	386 386	36.955	-2.481	50.219 51.194	1.00 40.00 1.00 40.00
MOTA	695	O N	TRP	386 387	36.205 37.010	-2.513 -3.458	49.359	1.00 40.00
ATOM	696	N CD	PRO PRO	387 387	37.010 37.070	-3.458 -3.165	49.339	1.00 40.00
ATOM	697	CA	PRO	387	36.218	-3.165 -4.629	47.936	1.00 40.00
ATOM	698	CA	FKU	307	20.210	4.027	4 2.043	1.00 40.00

	A I	699	СВ	PRO	387	35.733 -5.146	48.267	1.00 40.00	
	MOTA	700	CG	PRO	387	36.669 -4.479	47.248	1.00 40.00	
	ATOM	701	С	PRO	387	36.983 -5.651	50.398	1.00 40.00	
	. м	702	0	PRO	387	38.205 -5.705	50.273	1.00 40.00	
	A'I'OM	703	N	GLU	388	36.281 -6.468	51.211	1.00 60.00	
	MOTA	705	CA	GLU	388	36.926 -7.544	51.902	1.00 60.00	
	MOTA	706	CB	GLU	388	38.009 -7.126	52.913	1.00 60.00	
	ATOM	707	CG	GLU	388	37.503 -6.355	54.129	1.00 60.00	
	MOTA	708	CD	GLU	388	38.681 -6.251	55.088	1.00 60.00	
	MOTA	709	OE1		388	38.438 -6.226	56.323	1.00 60.00	
	MOTA	710	OE2	GLU	388	39.841 -6.199	54.597	1.00 60.00	
	ATOM	711	С	GLU	388	35.886 -8.334	52.631	1.00 60.00	
	ATOM	712	0	GLU	388	34.735 -7.917	52.752	1.00 60.00 1.00 60.00	
	ATOM	713	N	ASN	389	36.284 -9.524	53.118	1.00 60.00	
	ATOM	715	CA	ASN	389	35.397 -10.427	53.793 54.065	1.00 60.00	
	ATOM	716	CB	ASN	389	36.064 -11.789 35.053 -12.711	54.733	1.00 60.00	
	ATOM	717	CG	ASN	389	33.860 -12.668	54.438	1.00 60.00	
	ATOM	718		ASN	389 389	35.546 -13.572	55.664	1.00 60.00	
	ATOM	719		ASN	389	34.935 -9.900	55.114	1.00 60.00	
	MOTA	722	С 0	ASN ASN	389	33.736 -9.844	55.382	1.00 60.00	
	ATOM	723 724	N	ARG	390	35.880 -9.474	55.972	1.00 60.00	
ì	ATOM	724	CA	ARG	390	35.501 -9.094	57.300	1.00 60.00	
•	ATOM	727	CB	ARG	390	36.509 -9.551	58.362	1.00 60.00	
	ATOM ATOM	728	CG	ARG	390	36.820 -11.045	58.294	1.00 60.00	
	ATOM	729	CD	ARG	390	37.813 -11.498	59.364	1.00 60.00	
	ATOM	730	NE	ARG	390	38.361 -12.814	58.936	1.00 60.00	
	ATOM	732	CZ	ARG	390	37.702 -13.969	59.241	1.00 60.00	
	ATOM	733		ARG	390	38.230 -15.169	58.863	1.00 60.00	
	ATOM	736		ARG	390	36.522 -13.923	59.925	1.00 60.00	
	АТОМ	739	С	ARG	390	35.418 -7.612	57.417	1.00 60.00	
	ATOM	740	0	ARG	390	35.440 -6.887	56.423	1.00 60.00	
	ATOM	741	N	THR	391	35.301 -7.131	58.670	1.00 60.00	
	ATOM	743	CA	THR	391	35.236 -5.722	58.895	1.00 60.00	
	MOTA	744	CB	THR	391	34.997 -5.337	60.326	1.00 60.00	
	ATOM	745	OG1		391	36.067 -5.792	61.141	1.00 60.00	
	MOTA	747	CG2		391	33.669 -5.954	60.793	1.00 60.00	
	MOTA	748	С	THR	391	36.572 -5.192	58.519	1.00 60.00	
	MOTA	749	0	THR	391	37.595 -5.622		1.00 60.00 1.00 60.00	
	MOTA	750	N	ASP	392	36.586 -4.236	57.579	1.00 60.00	
•	MOTA	752	CA	ASP	392	37.814 -3.675	57.114 55.949	1.00 60.00	
	MOTA	753	CB	ASP	392	37.609 -2.694 38.951 -2.481	55.266	1.00 60.00	
	MOTA	754	CG	ASP	392		55.641	1.00 60.00	
	ATOM	755		ASP	392 392	39.929 -3.181 39.012 -1.613	54.355	1.00 60.00	
	ATOM	756		ASP	392 392	38.410 -2.927	58.259	1.00 60.00	
	MOTA	757 758	C	ASP ASP	392 392	39.629 -2.870	58.415	1.00 60.00	
	ATOM	758 759	O N	LEU	393	37.542 -2.351	59.111	1.00 40.00	
	ATOM ATOM	759 761	CA	LEU	393	37.993 -1.561	60.212	1.00 40.00	
	MOTA	762	CB	LEU	393	36.881 -0.757	60.882	1.00 40.00	
	ATOM ATOM	763	CG	LEU	393	36.203 0.250	59.929	1.00 40.00	
	ATOM	764		LEU	393	37.198 1.308	59.425	1.00 40.00	
	ATOM	765		LEU	393	35.465 -0.465	58.787	1.00 40.00	
	ATOM	766	C	LEU	393	38.699 -2.424	61.212	1.00 40.00	
	ATOM	767	o	LEU	393	39.431 -1.924	62.064	1.00 40.00	
	ATOM	768	N	HIS	394	38.494 -3.755	61.128	1.00 40.00	
	ATOM	770	CA	HIS	394	39.064 -4.696	62.056	1.00 40.00	
	ATOM	771	СВ	HIS	394	38.835 -6.171	61.670	1.00 40.00	
	MOTA	772	CG	HIS	394	39.918 -6.759	60.813	1.00 40.00	
	ATOM	773		HIS	394	40.944 -7.577	61.173	1.00 40.00	
	ATOM	774		HIS	394	40.040 -6.583	59.452	1.00 40.00	
	ATOM	776	CE1	HIS	394	41.125 -7.298	59.061	1.00 40.00	
	ATOM	777	NE2	HIS	394	41.708 -7.918	60.071	1.00 40.00	
	MOTA	779	С	HIS	394	40.542 -4.479	62.140	1.00 40.00	

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MOTA	780	0	HIS	394	41.183	-4.881	63.110	1.00 40.00
ATOM	781	N	ALA	395	41.128	-3.850	61.108	1.00 20.00
MOTA	783	CA	ALA	395	42.534	-3.591	61.111	1.00 20.00
M	784	CB	ALA	395	43.013	-2.876	59.836	1.00 20.00
MO'r.A	785	С	ALA	395	42.905	-2.722	62.278	1.00 20.00
MOTA	786	0	ALA	395	43.955	-2.932	62.885	1.00 20.00
ATOM	787	N	PHE	396	42.069	-1.717	62.626	1.00 20.00
ATOM	789	CA	PHE	396		-0.830	63.705	1.00 20.00
MOTA	790	CB	PHE	396	41.987	0.623	63.471	1.00 20.00
MOTA	791	CG	PHE	396	42.601	1.137	62.215	1.00 20.00
ATOM	792		PHE	396	41.970	0.936	61.010	1.00 20.00
ATOM	793	CD2		396	43.750	1.892	62.249	1.00 20.00
MOTA	794		PHE	396	42.471	1.484	59.854 61.097	1.00 20.00
ATOM	795	CE2	PHE	396	44.253	2.448 2.261	59.900	1.00 20.00
ATOM	796	CZ	PHE	396	43.604 41.763	-1.229	64.987	1.00 20.00
ATOM	797	С	PHE	396 396	41.763	-0.623	65.396	1.00 20.00
ATOM	798	0	PHE			-0.023	65.703	1.00 20.00
ATOM	799	N	GLU	397 397	42.341 41.757	-2.723	66.905	1.00 20.00
ATOM	801	CA	GLU	397	42.569	-3.905	67.471	1.00 20.00
ATOM	802	CB CG	GLU GLU	397	41.904	-4.650	68.632	1.00 20.00
ATOM	803	CD	GLU	397	42.496	-4.154	69.944	1.00 20.00
ATOM	804 805	OE1	GLU	397	42.450	-2.984	69.989	1.00 20.00
MOTA	806	OE2		397	42.499	-4.948	70.923	1.00 20.00
ATOM	807	C	GLU	397	41.655	-1.675	67.964	1.00 20.00
MOTA MOTA	808	0	GLU	397	40.644	-1.605	68.659	1.00 20.00
ATOM	809	N	ASN	398	42.685	-0.827	68.149	1.00 20.00
ATOM	811	CA	ASN	398	42.500	0.116	69.212	1.00 20.00
ATOM	812	СВ	ASN	398	43.278	-0.228	70.496	1.00 20.00
ATOM	813	CG	ASN	398	44.748	-0.336	70.160	1.00 20.00
ATOM	814		ASN	398	45.445	0.664	70.001	1.00 20.00
ATOM	815		ASN	398	45.231	-1.602	70.058	1.00 20.00
АТОМ	818	С	ASN	398	42.762	1.538	68.839	1.00 20.00
ATOM	819	0	ASN	398	43.417	2.273	69.576	1.00 20.00
ATOM	820	N	LEU	399	42.217	1.979	67.692	1.00 20.00
MOTA	822	CA	LEU	399	42.347	3.356	67.321	1.00 20.00
ATOM	823	CB	LEU	399	41.827	3.606	65.897	1.00 20.00
ATOM	824	CG	LEU	399	41.928	5.058	65.406	1.00 20.00
ATOM	825	CD1	LEU	399	43.391	5.505	65.279	1.00 20.00
MOTA	826		LEU	399	41.127	5.245	64.106	1.00 20.00
MOTA	827	С	LEU	399	41.471	4.100	68.289	1.00 20.00
MOTA	828	0	LEU	399	40.256	3.918	68.277	1.00 20.00
MOTA	829	N	GLU	400	42.091	4.869	69.215	1.00 20.00
ATOM	831	CA	GLU	400	41.431	5.661	70.222	1.00 20.00 1.00 20.00
ATOM	832	CB	GLU	400	42.356	6.005	71.405 72.263	1.00 20.00
ATOM	833	CG	GLU	400 400	42.782 43.606	4.812 5.354	73.425	1.00 20.00
ATOM	834	CD OF1	GLU GLU	400	44.471	6.236	73.423	1.00 20.00
MOTA	835 836		GLU	400	43.375	4.898	74.578	1.00 20.00
ATOM	837	C	GLU	400	40.825	6.981	69.817	1.00 20.00
ATOM ATOM	838	0	GLU	400	39.679	7.269	70.160	1.00 20.00
ATOM	839	N	ILE	401	41.572	7.832	69.077	1.00 20.00
ATOM	841	CA	ILE	401	41.078	9.168	68.850	1.00 20.00
ATOM	842	СВ	ILE	401	41.695	10.146	69.819	1.00 20.00
ATOM	843		ILE	401	43.157	10.343	69.395	1.00 20.00
ATOM	844		ILE	401	40.914	11.465	69.932	1.00 20.00
ATOM	845	CD1	ILE	401	39.739	11.393	70.906	1.00 20.00
ATOM	846	C	ILE	401	41.463	9.647	67.479	1.00 20.00
АТОМ	847	ō	ILE	401	42.510	9.275	66.952	1.00 20.00
ATOM	848	N	ILE	402	40.600	10.483	66.858	1.00 20.00
ATOM	850	CA	ILE	402	40.900	11.079	65.584	1.00 20.00
АТОМ	851	СВ	ILE	402	39.949	10.655	64.500	1.00 20.00
ATOM	852	CG2	ILE	402	40.278	11.455	63.230	1.00 20.00
ATOM	853	CG1	ILE	402	40.012	9.132	64.295	1.00 20.00

A	854	CD1	ILE	402		38.867	8.585	63.442		20.00
ATOM	855	C	ILE	402		40.704	12.546	65.815		20.00
ATOM	856	0	ILE	402		39.584	13.045	65.775		20.00
М	857	N	ARG	403		41.806	13.295	65.984		20.00
A'T'OM	859	CA	ARG	403		41.738	14.672	66.393		20.00
MOTA	860	СВ	ARG	403		43.121	15.317	66.557		20.00
ATOM	861	CG	ARG	403		43.868	14.804	67.785		20.00
MOTA	862	CD	ARG	403		45.126	15.607	68.111		20.00
MOTA	863	NE	ARG	403		45.666	15.072	69.390		20.00
MOTA	865	CZ	ARG	403		45.210	15.567	70.578		20.00
MOTA	866	NH1	ARG	403		45.704	15.080	71.753 70.591		20.00
MOTA	869	NH2	ARG	403		44.258	16.545 15.560	65.491		20.00
MOTA	872	C	ARG	403		40.944	16.485	65.964		20.00
ATOM	873	0	ARG	403 404		40.283	15.347	64.168		20.00
ATOM	874	N	GLY GLY	404		40.235	16.191	63.295		20.00
ATOM	876 877	CA C	GLY	404		40.869	17.541	63.176		20.00
ATOM ATOM	878	0	GLY	404		40.188	18.528	62.898		20.00
ATOM	879	N	ARG	405		42.199	17.625	63.364	1.00	20.00
ATOM	881	CA	ARG	405		42.834	18.908	63.279	1.00	20.00
ATOM	882	СВ	ARG	405		44.355	18.861	63.503		20.00
ATOM	883	CG	ARG	405		44.950	20.250	63.742		20.00
MOTA	884	CD	ARG	405		46.470	20.259	63.903		20.00
MOTA	885	NE	ARG	405		47.048	20.241	62.532		20.00
ATOM	887	CZ	ARG	405		47.194	21.412	61.846		20.00
MOTA	888	NH1	ARG	405		46.838	22.594	62.429		20.00
ATOM	891	NH2	ARG	405		47.689	21.400	60.574		20.00
ATOM	894	С	ARG	405		42.576	19.416	61.898		20.00
MOTA	895	0	ARG	405		42.315	20.602	61.697 60.902		20.00
ATOM	896	N	THR	406		42.645	18.516 18.902	59.561		20.00
MOTA	898	CA	THR	406		42.323 43.479	18.799	58.610		20.00
ATOM	899	CB	THR	406 406		43.479	17.459	58.535		20.00
ATOM	900 902	OG1 CG2	THR THR	406	•	44.604	19.723	59.109		20.00
ATOM ATOM	903	C	THR	406		41.261	17.949	59.121		20.00
MOTA	904	0	THR	406		41.354	16.748	59.368	1.00	20.00
ATOM	905	N	LYS	407		40.218	18.467	58.449		20.00
ATOM	907	CA	LYS	407		39.097	17.653	58.078		20.00
ATOM	908	СВ	LYS	407		37.788	18.227	58.638		20.00
ATOM	909	CG	LYS	407		37.577	19.672	58.180		20.00
ATOM	910	CD	LYS	407		36.235	20.287	58.571		20.00
ATOM	911	CE	LYS	407		36.072	21.725	58.076		20.00
ATOM	912	NZ	LYS	407		37.081	22.597	58.716		20.00
MOTA	916	С	LYS	407		38.962	17.595	56.591 55.878		20.00
ATOM	917	0	LYS	407		39.427 38.330	18.483 16.518	56.080		20.00
MOTA	918	N	GLN	408 408		38.139	16.441	54.663		20.00
MOTA	920	CA	GLN GLN	408		38.080	15.016	54.076		20.00
ATOM	921 922	CB CG	GLN	408		36.898	14.167	54.539		20.00
ATOM	923	CD	GLN	408		36.969	12.853	53.772		20.00
MOTA MOTA	924		GLN	408		36.014	12.455	53.107	1.00	20.00
ATOM	925			408		38.139	12.164	53.857		20.00
ATOM	928	С	GLN	408		36.847	17.130	54.381		20.00
ATOM	929	ō	GLN	408		36.081	17.408	55.301		20.00
ATOM	930	N	HIS	409		36.585	17.409	53.086		20.00
MOTA	932	CA	HIS	409		35.431	18.151	52.662		20.00
MOTA	933	СВ	HIS	409		35.166	18.082	51.145		20.00
ATOM	934	CG	HIS	409		36.230	18.712	50.294		20.00
ATOM	935		HIS	409		37.316	18.149	49.695		20.00
ATOM	936		HIS	409		36.251	20.042	49.936		20.00
MOTA	938		HIS	409		37.341	20.217	49.146		20.00
ATOM	939		HIS	409		38.018	19.097 17.607	48.972 53.323		20.00
MOTA	941	С	HIS	409		34.216	16.405	53.551		20.00
MOTA	942	0	HIS	409		34.102	10.403	10.00	2.00	_3.00

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MOTA	943	N	GLY	410	33.280	18.503	53.673	1.00 20.00
MOTA	945	CA	GLY	410	32.100	18.067	54.349	1.00 20.00
MOTA	946	С	GLY	410	32.429	18.116	55.801	1.00 20.00
)M	947	0	GLY	410	31.585	17.843	56.654	1.00 20.00
MO'r.A	948	N	GLN	411	33.681	18.501	56.113	1.00 20.00
ATOM	950	CA	GLN	411	34.103	18.580	57.477	1.00 20.00
MOTA	951	СВ	GLN	411	33.207	19.505	58.319	1.00 20.00
ATOM	952	CG	GLN	411	33.226	20.973	57.890	1.00 20.00
ATOM	953	CD	GLN	411	32.231	21.722	58.767	1.00 20.00
MOTA	954		GLN	411	31.032	21.444	58.750	1.00 20.00
	955	NE2	GLN	411	32.742	22.699	59.562	1.00 20.00
MOTA			GLN	411	34.038	17.226	58.105	1.00 20.00
MOTA	958	C		411	33.609	17.101	59.250	1.00 20.00
MOTA	959	0	GLN	412	34.488	16.174	57.393	1.00 20.00
MOTA	960	N	PHE		34.372	14.865	57.966	1.00 20.00
MOTA	962	CA	PHE	412		13.774	56.952	1.00 20.00
MOTA	963	CB	PHE	412	33.979			1.00 20.00
MOTA	964	CG	PHE	412	32.657	14.127	56.359	1.00 20.00
MOTA	965	CD1		412	32.590	14.732	55.125	
MOTA	966		PHE	412	31.494	13.933	57.068	1.00 20.00
ATOM	967	CE1	PHE	412	31.377	15.086	54.582	1.00 20.00
MOTA	968	CE2	PHE	412	30.279	14.300	56.538	1.00 20.00
MOTA	969	cz	PHE	412	30.217	14.866	55.287	1.00 20.00
MOTA	970	С	PHE	412	35.665	14.421	58.576	1.00 20.00
MOTA	971	0	PHE	412	36.735	14.549	57.986	1.00 20.00
MOTA	972	N	SER	413	35.579	13.964	59.837	1.00 20.00
ATOM	974	CA	SER	413	36.652	13.395	60.599	1.00 20.00
ATOM	975	СВ	SER	413	36.267	13.239	62.073	1.00 20.00
ATOM	976	OG	SER	413	35.611	14.412	62.523	1.00 20.00
MOTA	978	С	SER	413	36.871	12.000	60.127	1.00 20.00
MOTA	979	0	SER	413	38.002	11.534	60.023	1.00 20.00
ATOM	980	N	LEU	414	35.754	11.288	59.881	1.00 20.00
ATOM	982	CA	LEU	414	35.805	9.915	59.483	1.00 20.00
ATOM	983	CB	LEU	414	35.290	8.979	60.592	1.00 20.00
ATOM	984	CG	LEU	414	35.304	7.480	60.252	1.00 20.00
ATOM	985	CD1	LEU	414	36.732	6.966	60.018	1.00 20.00
ATOM	986	CD2	LEU	414	34.543	6.670	61.315	1.00 20.00
MOTA	987	c	LEU	414	34.909	9.756	58.304	1.00 20.00
ATOM	988	0	LEU	414	33.688	9.855	58.414	1.00 20.00
MOTA	989	N	ALA	415	35.501	9.503	57.126	1.00 20.00
ATOM	991	CA	ALA	415	34.678	9.310	55.973	1.00 20.00
ATOM	992	CB	ALA	415	35.070	10.198	54.779	1.00 20.00
	993	С	ALA	415	34.858	7.893	55.551	1.00 20.00
MOTA			ALA	415	35.981	7.453	55.314	1.00 20.00
MOTA	994	0		416	33.750	7.129	55.490	1.00 20.00
MOTA	995	N	VAL	416	33.730	5.776	55.025	1.00 20.00
MOTA	997	CA	VAL		33.376	4.767	56.042	1.00 20.00
MOTA	998	CB	VAL	416	33.451	3.368	55.405	1.00 20.00
MOTA	999		VAL	416		4.921	57.301	1.00 20.00
MOTA	1000		VAL	416	34.245	5.702	53.878	1.00 20.00
MOTA	1001	С	VAL	416	32.869			
ATOM	1002	0	VAL	416	31.655	5.739	54.068	1.00 20.00
MOTA	1003	N	VAL	417	33.392	5.581	52.645	1.00 20.00
MOTA	1005	CA	VAL	417	32.503	5.564	51.522	1.00 20.00
MOTA	1006	СВ	VAL	417	32.770	6.667	50.541	1.00 20.00
ATOM	1007	CG1	VAL	417	31.784	6.531	49.369	1.00 20.00
MOTA	1008	CG2	VAL	417	32.682	8.013	51.277	1.00 20.00
ATOM	1009	С	VAL	417	32.669	4.279	50.779	1.00 20.00
ATOM	1010	0	VAL	417	33.789	3.805	50.597	1.00 20.00
ATOM	1011	N	SER	418	31.533	3.706	50.321	1.00 40.00
ATOM	1013	CA	SER	418	31.494	2.482	49.564	1.00 40.00
ATOM	1014	СВ	SER	418	31.778	2.690	48.065	1.00 40.00
ATOM	1015	OG	SER	418	33.087	3.207	47.882	1.00 40.00
ATOM	1017	C	SER	418	32.463	1.474	50.101	1.00 40.00
ATOM	1018	o	SER	418	33.596	1.381	49.632	1.00 40.00
ATOM	1019	N	LEU	419	32.040	0.703	51.124	1.00 40.00
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A	1021	CA	LEU	419		32.930	-0.252	51.727		40.00
ATOM	1022	CB	LEU	419		33.355	0.212	53.133		40.00
ATOM	1023	CG	LEU	419		34.471	-0.608	53.800		40.00
1 1	1024	CD1	LEU	419		35.781	-0.502	53.005		40.00
MOTA	1025	CD2	LEU	419		34.654	-0.187	55.267		40.00
MOTA	1026	С	LEU	419		32.191	-1.562	51.860		40.00
MOTA	1027	0	LEU	419		30.971	-1.567	51.980		40.00
MOTA	1028	N	ASN	420		32.888	-2.724	51.824		40.00
ATOM	1030	CA	ASN	420		32.176	-3.970	51.957		40.00
MOTA	1031	CB	ASN	420		32.676	-5.083	51.022 49.636		40.00
MOTA	1032	CG	ASN	420		32.133	-4.765 -5.225	49.636		40.00
ATOM	1033	OD1		420		32.655	-3.225	49.591		40.00
MOTA	1034		ASN	420 420		31.047 32.296	-3.940 -4.436	53.366		40.00
ATOM	1037	C	ASN	420		32.230	-5.503	53.642		40.00
ATOM	1038	O N	ASN ILE	421		31.756	-3.654	54.316		40.00
ATOM	1039 1041	CA	ILE	421		31.927	-4.069	55.669		40.00
ATOM	1041	CB	ILE	421		32.813	-3.154	56.450		40.00
ATOM ATOM	1042	CG2	ILE	421		32.914	-3.688	57.888		40.00
ATOM	1043		ILE	421		34.165	-3.055	55.728	1.00	40.00
ATOM	1045	CD1		421		34.783	-4.417	55.417	1.00	40.00
ATOM	1046	C	ILE	421		30.629	-4.187	56.387	1.00	40.00
ATOM	1047	0	ILE	421		29.675	-3.461	56.115	1.00	40.00
ATOM	1048	N	THR	422		30.572	-5.185	57.289	1.00	40.00
ATOM	1050	CA	THR	422		29.453	-5.479	58.131		40.00
ATOM	1051	СВ	THR	422		29.559	-6.840	58.751	1.00	40.00
ATOM	1052	OG1	THR	422		30.720	-6.920	59.564		40.00
ATOM	1054	CG2	THR	422		29.628	-7.884	57.622		40.00
ATOM	1055	С	THR	422		29.301	-4.487	59.241		40.00
MOTA	1056	0	THR	422		28.183	-4.130	59.601		40.00
MOTA	1057	N	SER	423		30.416	-4.022	59.842		20.00
MOTA	1059	CA	SER	423		30.266	-3.123	60.951		20.00
MOTA	1060	СВ	SER	423		30.124	-3.861	62.296		20.00
MOTA	1061	OG	SER	423		29.972	-2.937	63.364		20.00
MOTA	1063	C	SER	423		31.482	-2.254	61.046 60.273		20.00
ATOM	1064	0	SER	423		32.423 31.436	-2.422 -1.238	61.938		20.00
MOTA	1065	N	LEU LEU	424 424		32.556	-0.374	62.194		20.00
ATOM	1067	CA	LEU	424		32.159	0.841	63.054		20.00
ATOM	1068 1069	CB	LEU	424		31.078	1.743	62.419		20.00
MOTA MOTA	1070		LEU	424		31.575	2.391	61.116	1.00	20.00
ATOM	1071		LEU	424		29.741	1.001	62.254	1.00	20.00
ATOM	1072	C	LEU	424		33.616	-1.131	62.947	1.00	20.00
ATOM	1073	0	LEU	424		34.764	-1.191	62.523	1.00	20.00
MOTA	1074	N	GLY	425		33.269	-1.752	64.093		20.00
MOTA	1076	CA	GLY	425		34.242	-2.537	64.818		20.00
MOTA	1077	С	GLY	425		35.328	-1.708	65.458		20.00
MOTA	1078	0	GLY	425		36.307	-2.237	65.980		20.00
ATOM	1079	N	LEU	426		35.143	-0.381	65.462		20.00
MOTA	1081	CA	LEU	426		36.012	0.656	65.963		20.00
MOTA	1082	CB	LEU	426		35.706	2.062	65.412		20.00
MOTA	1083	CG	LEU	426		36.084	2.249	63.931		20.00
MOTA	1084		LEU	426		35.790	3.681	63.458		20.00
MOTA	1085		LEU	426		37.542	1.836	63.676 67.452		20.00
MOTA	1086	C	LEU	426		35.965	0.746			20.00
MOTA	1087	0	LEU	426		36.277	1.801	67.987 68.168		20.00
ATOM	1088	N	ARG	427		35.524	-0.305 -0.216	69.568		20.00
ATOM	1090	CA	ARG	427		35.179	-0.216 -1.583	70.265		20.00
ATOM	1091	CB	ARG	427		35.061 36.373	-1.363 -2.362	70.203		20.00
MOTA	1092	CG	ARG	427 427		36.329	-2.362 -3.537	70.329		20.00
ATOM	1093	CD NE	ARG ARG	427		37.689	-3.537 -4.143	71.307		20.00
ATOM	1094 1096	CZ	ARG	427		38.665	-3.598	72.105		20.00
ATOM	1096		ARG	427		38.390	-2.515	72.890		20.00
ATOM	1091	T4117		'	•					

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ATOM 1100 NH2 ARG 427 39.924 -4.125 72.091 ATOM 1103 C ARG 427 36.081 0.609 70.444	
ATOM 1103 C ARG 427 36.081 0.609 70.444	1.00 20.00
	1.00 20.00
ATOM 1104 O ARG 427 35.606 1.179 71.423	1.00 20.00
M 1105 N SER 428 37.393 0.670 70.174	
ATOM 1107 CA SER 428 38.285 1.469 70.974	
ATOM 1108 CB SER 428 39.760 1.196 70.643	1.00 20.00
ATOM 1109 OG SER 428 40.020 1.553 69.294	1.00 20.00
ATOM 1111 C SER 428 38.056 2.952 70.818	1.00 20.00
ATOM 1112 O SER 428 38.444 3.741 71.677	1.00 20.00
ATOM 1113 N LEU 429 37.456 3.375 69.690	1.00 20.00
ATOM 1115 CA LEU 429 37.291 4.759 69.331	1.00 20.00
ATOM 1116 CB LEU 429 36.679 4.907 67.924	1.00 20.00
ATOM 1117 CG LEU 429 36.534 6.355 67.423	1.00 20.00
ATOM 1118 CD1 LEU 429 37.911 7.015 67.237	1.00 20.00
ATOM 1119 CD2 LEU 429 35.668 6.419 66.152	1.00 20.00
ATOM 1120 C LEU 429 36.441 5.523 70.302	1.00 20.00
ATOM 1121 O LEU 429 35.213 5.440 70.285	1.00 20.00
ATOM 1122 N LYS 430 37.105 6.242 71.230	1.00 20.00
ATOM 1124 CA LYS 430 36.429 7.073 72.178	1.00 20.00
ATOM 1125 CB LYS 430 37.263 7.316 73.436	1.00 20.00
ATOM 1126 CG LYS 430 37.388 6.040 74.265	1.00 20.00
ATOM 1127 CD LYS 430 38.410 6.146 75.388	1.00 20.00
ATOM 1128 CE LYS 430 38.325 4.996 76.391	1.00 20.00
ATOM 1129 NZ LYS 430 39.167 5.291 77.572	1.00 20.00
ATOM 1133 C LYS 430 35.960 8.392 71.653	1.00 20.00
ATOM 1134 O LYS 430 34.829 8.788 71.920	1.00 20.00
ATOM 1135 N GLU 431 36.797 9.134 70.896	1.00 20.00
ATOM 1137 CA GLU 431 36.277 10.402 70.477	1.00 20.00
ATOM 1138 CB GLU 431 36.374 11.497 71.552	1.00 20.00
ATOM 1139 CG GLU 431 35.636 12.776 71.151	1.00 20.00
ATOM 1140 CD GLU 431 35.614 13.725 72.339	1.00 20.00
ATOM 1141 OE1 GLU 431 36.713 14.064 72.853	1.00 20.00
ATOM 1142 OE2 GLU 431 34.491 14.125 72.749	1.00 20.00
ATOM 1143 C GLU 431 36.920 10.936 69.242	1.00 20.00
	1.00 20.00
AUCM 1144 () GDO 431 30:030 10:000 00:301	
	1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512	
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363	1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111	1.00 20.00 1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021	1.00 20.00 1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719	1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561	1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732	1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562	1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155	1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966	1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.525 17.269 69.660	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 36.637 13.880 67.732 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.525 17.269 69.660 ATOM 1160 C SER 433 37.297 16.746 67.915	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.525 17.269 69.660 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.525 17.269 69.660 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.574	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.525 17.269 69.660 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.574 ATOM 1164 CA ASP 434 36.769 17.708 65.793	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.801 14.387 68.155 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.413 16.039 68.966 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.574 ATOM 1164 CA ASP 434 36.769 17.708 65.793 ATOM 1165 CB ASP 434 37.778 18.757 65.285	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.801 14.387 68.155 ATOM 1157 CB SER 433 37.934 15.679 68.751 ATOM 1158 OG SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.525 17.269 69.660 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.574 ATOM 1164 CA ASP 434 36.769 17.708 65.793 ATOM 1165 CB ASP 434 37.778 18.757 65.285 ATOM 1165 CB ASP 434 37.778 18.757 65.285 ATOM 1166 CG ASP 434 37.778 18.757 65.285	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.525 17.269 69.660 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.574 ATOM 1164 CA ASP 434 37.373 16.661 66.574 ATOM 1165 CB ASP 434 37.778 18.757 65.285 ATOM 1166 CG ASP 434 37.778 18.757 65.285 ATOM 1166 CG ASP 434 38.367 19.559 66.437 ATOM 1167 OD1 ASP 434 39.564 19.935 66.325	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.525 17.269 69.660 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.574 ATOM 1165 CB ASP 434 37.373 16.661 66.574 ATOM 1165 CB ASP 434 37.778 18.757 65.285 ATOM 1166 CG ASP 434 37.778 18.757 65.285 ATOM 1167 OD1 ASP 434 39.564 19.935 66.325 ATOM 1168 OD2 ASP 434 39.564 19.935 66.325 ATOM 1168 OD2 ASP 434 37.636 19.820 67.428	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.413 16.039 68.966 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.574 ATOM 1165 CB ASP 434 36.769 17.708 65.793 ATOM 1166 CG ASP 434 37.778 18.757 65.285 ATOM 1166 CG ASP 434 39.564 19.935 66.325 ATOM 1167 OD1 ASP 434 39.564 19.935 66.325 ATOM 1168 OD2 ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 37.636 19.820 67.428	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.413 16.039 68.966 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 36.769 17.708 65.793 ATOM 1165 CB ASP 434 36.769 17.708 65.793 ATOM 1166 CG ASP 434 37.778 18.757 65.285 ATOM 1166 CG ASP 434 39.564 19.935 66.325 ATOM 1168 OD2 ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 36.205 17.125 64.536 ATOM 1169 C ASP 434 36.755 16.164 64.006	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.525 17.269 69.660 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.579 ATOM 1165 CB ASP 434 37.373 16.661 66.579 ATOM 1166 CG ASP 434 37.778 18.757 65.285 ATOM 1166 CG ASP 434 38.367 19.559 66.437 ATOM 1167 OD1 ASP 434 39.564 19.935 66.325 ATOM 1168 OD2 ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 36.755 16.164 64.006 ATOM 1170 O ASP 434 36.755 16.164 64.006 ATOM 1171 N GLY 435 35.099 17.712 64.023	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.525 17.269 69.660 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.574 ATOM 1165 CB ASP 434 37.373 16.661 66.574 ATOM 1166 CG ASP 434 37.778 18.757 65.285 ATOM 1166 CG ASP 434 37.778 18.757 65.285 ATOM 1167 OD1 ASP 434 39.564 19.935 66.325 ATOM 1168 OD2 ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 36.755 16.164 64.006 ATOM 1170 O ASP 434 36.755 16.164 64.006 ATOM 1171 N GLY 435 35.099 17.712 64.023 ATOM 1171 N GLY 435 35.099 17.712 64.023	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.413 16.039 68.966 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.574 ATOM 1164 CA ASP 434 37.373 16.661 66.574 ATOM 1165 CB ASP 434 37.778 18.757 65.285 ATOM 1166 CG ASP 434 37.778 18.757 65.285 ATOM 1167 OD1 ASP 434 39.564 19.935 66.437 ATOM 1168 OD2 ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 36.755 16.164 64.006 ATOM 1170 O ASP 434 36.755 16.164 64.006 ATOM 1171 N GLY 435 35.099 17.712 64.023 ATOM 1173 CA GLY 435 33.489 16.239 63.009	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1155 CB SER 433 37.934 15.679 68.751 ATOM 1158 OG SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.413 16.039 68.966 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.574 ATOM 1165 CB ASP 434 37.373 16.661 66.574 ATOM 1166 CG ASP 434 37.778 18.757 65.285 ATOM 1166 CG ASP 434 37.778 18.757 65.285 ATOM 1166 CG ASP 434 39.564 19.935 66.325 ATOM 1168 OD2 ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 37.636 19.820 67.428 ATOM 1167 OD1 ASP 434 36.205 17.125 64.536 ATOM 1168 OD2 ASP 434 36.205 17.125 64.536 ATOM 1170 O ASP 434 36.755 16.164 64.006 ATOM 1171 N GLY 435 35.099 17.712 64.023 ATOM 1173 CA GLY 435 33.489 16.239 63.009 ATOM 1174 C GLY 435 33.489 16.239 63.009 ATOM 1175 O GLY 435 33.406 15.670 64.096	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.042 10.697 65.712 ATOM 1150 CG1 ILE 432 36.042 10.697 65.713 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1155 CA SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.525 17.269 69.660 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.574 ATOM 1164 CA ASP 434 36.769 17.708 65.793 ATOM 1166 CG ASP 434 38.367 19.559 66.437 ATOM 1167 OD1 ASP 434 37.636 19.820 67.428 ATOM 1168 OD2 ASP 434 37.636 19.820 67.428 ATOM 1169 C ASP 434 36.755 16.164 64.006 ATOM 1171 N GLY 435 35.099 17.712 64.023 ATOM 1173 CA GLY 435 33.489 16.239 63.009 ATOM 1175 O GLY 435 33.489 16.239 63.009 ATOM 1175 O GLY 435 33.406 15.670 64.096	1.00 20.00 1.00 20.00
ATOM 1145 N ILE 432 36.155 11.771 68.512 ATOM 1147 CA ILE 432 36.674 12.438 67.363 ATOM 1148 CB ILE 432 35.882 12.180 66.111 ATOM 1149 CG2 ILE 432 36.343 13.160 65.021 ATOM 1150 CG1 ILE 432 36.042 10.697 65.719 ATOM 1151 CD1 ILE 432 35.157 10.240 64.561 ATOM 1152 C ILE 432 36.637 13.880 67.732 ATOM 1153 O ILE 432 35.638 14.574 67.562 ATOM 1154 N SER 433 37.801 14.387 68.155 ATOM 1156 CA SER 433 37.934 15.679 68.751 ATOM 1157 CB SER 433 39.413 16.039 68.966 ATOM 1158 OG SER 433 39.413 16.039 68.966 ATOM 1160 C SER 433 37.297 16.746 67.915 ATOM 1161 O SER 433 36.732 17.688 68.465 ATOM 1162 N ASP 434 37.373 16.661 66.574 ATOM 1165 CB ASP 434 37.373 16.661 66.574 ATOM 1166 CG ASP 434 37.778 18.757 65.285 ATOM 1166 CG ASP 434 39.564 19.935 66.325 ATOM 1168 OD2 ASP 434 39.564 19.935 66.325 ATOM 1169 C ASP 434 39.564 19.935 66.325 ATOM 1169 C ASP 434 36.765 17.125 64.536 ATOM 1169 C ASP 434 36.755 16.164 64.006 ATOM 1171 N GLY 435 35.099 17.712 64.023 ATOM 1173 CA GLY 435 33.489 16.239 63.009 ATOM 1174 C GLY 435 33.489 16.239 63.009 ATOM 1175 O GLY 435 33.406 15.670 64.096	1.00 20.00 1.00 20.00

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	7	1180	CG	ASP	436	30.254	15.669	60.138	1.00 20.00		
	ATOM	1181		ASP	436	31.256	16.260	59.658	1.00 20.00		
	ATOM	1182	OD2	ASP	436	29.252	15.318	59.459	1.00 20.00		
	I 1	1183	С	ASP	436	32.073	13.745	61.293	1.00 20.00		
	MOTA	1184	0	ASP	436	33.236	13.617	60.924	1.00 20.00		
	MOTA	1185	N	VAL	437	31.138	12.805	61.036 60.270	1.00 20.00 1.00 20.00		
	ATOM	1187	CA	VAL VAL	437 437	31.480 31.538	11.636 10.383	61.101	1.00 20.00		
	MOTA MOTA	1188 1189	CB CG1	VAL	437	31.609	9.134	60.207	1.00 20.00		
	ATOM	1190		VAL	437	32.787	10.510	61.984	1.00 20.00		
	ATOM	1191	c	VAL	437	30.518	11.447	59.139	1.00 20.00		
	ATOM	1192	0	VAL	437	29.386	11.919	59.199	1.00 20.00		
	MOTA	1193	N	ILE	438	30.965	10.802	58.037	1.00 20.00		
	ATOM	1195	CA	ILE	438	30.073	10.553	56.944	1.00 20.00		
	ATOM	1196	CB	ILE	438	30.382	11.398	55.726 55.207	1.00 20.00 1.00 20.00		
	MOTA	1197		ILE	438 438	31.787 29.259	11.046 11.328	54.670	1.00 20.00		
	ATOM ATOM	1198 1199		ILE	438	29.239	9.964	54.005	1.00 20.00		
	ATOM	1200	CDI	ILE	438	30.118	9.092	56.609	1.00 20.00		
	MOTA	1201	0	ILE	438	31.115	8.561	56.122	1.00 20.00		
	ATOM	1202	N	ILE	439	29.012	8.381	56.877	1.00 20.00		
	ATOM	1204	CA	ILE	439	29.001	6.988	56.549	1.00 20.00		
	ATOM	1205	СВ	ILE	439	28.507	6.134	57.681	1.00 20.00		
	ATOM	1206		ILE	439	28.420	4.677	57.195	1.00 20.00 1.00 20.00		
	ATOM	1207		ILE	439 439	29.412 28.821	6.316 5.723	58.910 60.188	1.00 20.00		
	ATOM ATOM	1208 1209	CDI	ILE ILE	439	28.042	6.847	55.410	1.00 20.00		
	ATOM	1210	0	ILE	439	26.831	6.784	55.614	1.00 20.00		
	ATOM	1211	N	SER	440	28.563	6.770	54.167	1.00 20.00		
	ATOM	1213	CA	SER	440	27.669	6.726	53.047	1.00 20.00		
	MOTA	1214	CB	SER	440	27.725	8.001	52.186	1.00 20.00		
	MOTA	1215	OG	SER	440	26.819	7.899	51.097	1.00 20.00		
	MOTA	1217	С	SER	440	27.936 29.056	5.571 5.070	52.133 52.032	1.00 20.00 1.00 20.00		
	MOTA	1218 1219	N O	SER GLY	440 441	26.867	5.109	51.455	1.00 20.00		
	ATOM ATOM	1221	CA	GLY	441	26.962	4.082	50.458	1.00 20.00		
	ATOM	1222		GLY	441	27.610	2.838	50.970	1.00 20.00		
	ATOM	1223	0	GLY	441	28.639	2.420	50.440	1.00 20.00		
	MOTA	1224	N	ASN	442	27.056	2.230	52.037	1.00 20.00		
	MOTA	1226	CA	ASN	442	27.610	0.991	52.508	1.00 20.00		
	MOTA	1227	CB	ASN	442	28.298	1.143	53.873 53.665	1.00 20.00 1.00 20.00		
	MOTA	1228		ASN ASN	442 442	29.495 30.454	2.061 1.711	53.665	1.00 20.00		
	ATOM ATOM	1229 1230		ASN	442	29.430	3.282	54.259	1.00 20.00		
	ATOM	1233	C	ASN	442	26.463	0.049	52.672	1.00 20.00		
	ATOM	1234	Ō	ASN	442	25.955	-0.145	53.775	1.00 20.00		
	ATOM	1235	N	LYS	443	26.091	-0.654	51.589	1.00 20.00		
	MOTA	1237	CA	LYS	443	24.876	-1.410	51.620	1.00 20.00		
	MOTA	1238	CB	LYS	443	24.582	-2.098	50.279	1.00 20.00		
	MOTA	1239	CG	LYS	443	24.381 23.303	-1.055 -0.027	49.178 49.532	1.00 20.00 1.00 20.00		
	MOTA	1240 1241	CD CE	LYS LYS	443 443	23.348	1.248	49.532	1.00 20.00		
	ATOM ATOM	1241	NZ	LYS	443	22.704	1.018	47.374	1.00 20.00		
	MOTA	1246	C	LYS	443	24.824	-2.413	52.734	1.00 20.00		
	ATOM	1247	Ō	LYS	443	23.798	-2.535	53.398	1.00 20.00		
	MOTA	1248	N	ASN	444	25.920	-3.155	52.963	1.00 20.00		
	MOTA	1250	CA	ASN	444	26.027	-4.165	53.984	1.00 20.00		
	MOTA	1251	CB	ASN	444	27.114	-5.208	53.675	1.00 20.00 1.00 20.00		
	ATOM	1252	CG	ASN	444	26.577 25.369	-6.095 -6.297	52.559 52.447	1.00 20.00		
	ATOM	1253 1254	OD1 ND2		444 444	25.369 27.490	-6.297 -6.648	52.447	1.00 20.00		
	ATOM ATOM	1254	C	ASN	444	26.247	-3.673	55.387	1.00 20.00		
	ATOM	1258	0	ASN	444	26.107	-4.446	56.333	1.00 20.00		
	ATOM	1259		LEU	445	26.670	-2.409	55.575	1.00 20.00		

ATOM	1261	CA	LEU	445	27.029	-1.962	56.894	1.00 20	.00
ATOM	1262	СВ	LEU	445	27.608	-0.533	56.890	1.00 20	.00
MOTA	1263	CG	LEU	445	28.021	-0.002	58.276	1.00 20	.00
MC	1264		LEU	445	29.207	-0.798	58.846	1.00 20	
MOLA	1265		LEU	445	28.286	1.512	58.239	1.00 20	
ATOM	1266	C	LEU	445	25.880	-2.002	57.855	1.00 20	
ATOM	1267	0	LEU	445	24.803	-1.466	57.601	1.00 20	
MOTA	1268	N	CYS	446	26.109	-2.656	59.011	1.00 20	
MOTA	1270	CA	CYS	446	25.129	-2.767	60.051	1.00 20 1.00 20	
ATOM	1271	CB SG	CYS CYS	446 446	24.604 23.521	-4.196 -4.750	60.270 58.922	1.00 20	
MOTA	1272 1273	C	CYS	446	25.815	-2.339	61.305	1.00 20	
ATOM ATOM	1274	o	CYS	446	26.913	-1.790	61.261	1.00 20	
ATOM	1275	N	TYR	447	25.170	-2.551	62.467	1.00 20	
ATOM	1277	CA	TYR	447	25.788	-2.176	63.704	1.00 20	
ATOM	1278	СВ	TYR	447	27.139	-2.860	63.933	1.00 20	.00
MOTA	1279	CG	TYR	447	26.901	-4.315	64.050	1.00 20	
ATOM	1280	CD1	TYR	447	26.684	-5.079	62.926	1.00 20	
MOTA	1281		TYR	447	26.536	-6.440	63.018	1.00 20	
ATOM	1282		TYR	447	27.005	-4.920	65.274	1.00 20	
MOTA	1283	CE2	TYR	447	26.887	-6.280	65.362	1.00 20	
MOTA	1284	CZ	TYR	447	26.639	-7.040	64.246	1.00 20	
ATOM	1285	ОН	TYR	447 447	26.509 26.099	-8.439 -0.718	64.357 63.647	1.00 20 1.00 20	
MOTA	1287 1288	C O	TYR TYR	447	27.098	-0.718	64.220	1.00 20	
ATOM ATOM	1289	N	ALA	448	25.354	0.035	62.816	1.00 20	
MOTA	1291	CA	ALA	448	25.444	1.468	62.731	1.00 20	
ATOM	1292	СВ	ALA	448	25.053	1.995	61.341	1.00 20	
ATOM	1293	С	ALA	448	24.577	2.186	63.723	1.00 20	.00
ATOM	1294	0	ALA	448	24.983	3.172	64.335	1.00 20	
ATOM	1295	N	ASN	449	23.326	1.702	63.860	1.00 20	
ATOM	1297	CA	ASN	449	22.283	2.266	64.675	1.00 20	
ATOM	1298	CB	ASN	449 449	20.909 20.560	1.646 1.977	64.371 62.927	1.00 20 1.00 20	
MOTA	1299 1300	CG OD1	ASN ASN	449	20.287	1.088	62.122	1.00 20	
ATOM ATOM	1300		ASN	449	20.574	3.293	62.586	1.00 20	
ATOM	1304	C	ASN	449	22.569	2.021	66.116	1.00 20	
ATOM	1305	0	ASN	449	22.047	2.695	67.001	1.00 20	.00
ATOM	1306	N	THR	450	23.375	0.983	66.361	1.00 20	
ATOM	1308	CA	THR	450	23.740	0.473	67.644	1.00 20	
ATOM	1309	СВ	THR	450	24.470	-0.828	67.513	1.00 20	
ATOM	1310	OG1		450	23.769	-1.689	66.632	1.00 20 1.00 20	
ATOM	1312 1313	CGZ	THR THR	450 450	24.492 24.647	-1.486 1.405	68.896 68.395	1.00 20	
ATOM ATOM	1313	0	THR	450	24.795	1.253	69.605	1.00 20	
ATOM	1315	N	ILE	451	25.329	2.350	67.707	1.00 20	
ATOM	1317	CA	ILE	451	26.316	3.163	68.373	1.00 20	.00
ATOM	1318	CB	ILE	451	27.580	3.277	67.555	1.00 20	
ATOM	1319		ILE	451	27.299	4.270	66.414	1.00 20	
MOTA	1320		ILE	451	28.815	3.653	68.399	1.00 20	
ATOM	1321		ILE	451	28.834	5.086	68.923	1.00 20	
ATOM	1322	C	ILE	451	25.818	4.546 5.166	68.693 67.913	1.00 20 1.00 20	
MOTA	1323	O N	ILE ASN	451 452	25.096 26.191	5.056	69.889	1.00 20	
ATOM ATOM	1324 1326	CA	ASN	452 452	25.793	6.369	70.309	1.00 20	
ATOM	1327	СВ	ASN	452	25.558	6.442	71.830	1.00 20	
ATOM	1328	CG	ASN	452	24.657	7.627	72.151	1.00 20	.00
ATOM	1329	OD1	ASN	452	24.663	8.643	71.460	1.00 20	
ATOM	1330		ASN	452	23.848	7.489	73.236	1.00 20	
ATOM	1333	С	ASN	452	26.916	7.303	69.951	1.00 20	
ATOM	1334	0	ASN	452	27.858	7.507	70.716	1.00 20	
MOTA	1335	N	TRP	453 453	26.809 27.799	7.922 8.801	68.762 68.207	1.00 20 1.00 20	
ATOM ATOM	1337 1338	CA CB	TRP TRP	453 453	27.799	9.218	66.759	1.00 20	
AIOM	1770	CD	**/*	200	27.400	2.210		20	-

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	A DI	1339	CG	TRP	453	27.480	8.071	65.773	1.00	
	MOTA	1340		TRP	453	28.653	7.348	65.358	1.00	
	MOTA	1341	CE2	TRP	453	28.237	6.354	64.473	1.00	
	<i>i</i> 1	1342	CE3	TRP	453	29.967	7.498	65.690	1.00	
	MO'L'A	1343		TRP	453	26.422	7.468	65.152	1.00	
	ATOM	1344		TRP	453	26.867	6.442	64.354	1.00	
	MOTA	1346		TRP	453	29.138	5.503	63.898	1.00	
	ATOM	1347		TRP	453	30.876	6.651	65.095		20.00
	MOTA	1348	CH2	TRP	453	30.468	5.670	64.215 69.043		20.00
	MOTA	1349	С	TRP	453	27.873 28.849	10.031	68.982		20.00
	MOTA	1350	0	TRP	453 454	26.814	10.771	69.823		20.00
	ATOM	1351	N CA	LYS LYS	454	26.774	11.481	70.637		20.00
	ATOM	1353 1354	CB	LYS	454	25.501	11.532	71.502		20.00
	MOTA	1354	CG	LYS	454	25.282	12.849	72.250		20.00
	MOTA MOTA	1356	CD	LYS	454	23.876	12.981	72.840	1.00	20.00
	ATOM	1357	CE	LYS	454	23.801	12.650	74.332		20.00
	ATOM	1358	NZ	LYS	454	24.177	11.237	74.560		20.00
	ATOM	1362	С	LYS	454	27.947	11.473	71.563		20.00
	ATOM	1363	0	LYS	454	28.592	12.501	71.763		20.00
	MOTA	1364	N	LYS	455	28.249	10.309	72.167		20.00
	ATOM	1366	CA	LYS	455	29.358	10.234	73.073		20.00
)	ATOM	1367	CB	LYS	455	29.457	8.875	73.785		20.00
	MOTA	1368	CG	LYS	455	30.614	8.799	74.783		20.00 20.00
	MOTA	1369	CD	LYS	455	30.517	7.613	75.745 76.748		20.00
	MOTA	1370	CE	LYS	455	31.670	7.543 6.401	77.669		20.00
	MOTA	1371	NZ	LYS	455	31.474 30.646	10.448	72.341		20.00
	MOTA	1375	С	LYS	455 455	31.520	11.181	72.801		20.00
	ATOM	1376	O N	LYS LEU	456	30.793	9.802	71.171		20.00
	MOTA	1377 1379	CA	LEU	456	32.005	9.890	70.405		20.00
	ATOM ATOM	1380	CB	LEU	456	31.950	8.928	69.195		20.00
	MOTA	1381	CG	LEU	456	33.236	8.741	68.352		20.00
	ATOM	1382	CD1		456	32.974	7.740	67.215		20.00
	ATOM	1383	CD2		456	33.819	10.056	67.809		20.00
	ATOM	1384	С	LEU	456	32.207	11.296	69.921		20.00
	MOTA	1385	0	LEU	456	33.299	11.850	70.051		20.00
	ATOM	1386	N	PHE	457	31.152	11.919	69.356		20.00
	MOTA	1388	CA	PHE	457	31.275	13.239	68.804		20.00
	MOTA	1389	CB	PHE	457	30.520	13.432 12.438	67.483 66.521		20.00
_	MOTA	1390	CG	PHE	457	31.040 32.171	12.700	65.787		20.00
,	ATOM	1391		PHE PHE	457 457	30.393	11.236	66.379		20.00
	ATOM	1392 1393		PHE	457	32.660	11.752	64.926		20.00
	ATOM ATOM	1394	CE2		457	30.882	10.287	65.522		20.00
	ATOM	1395	cz	PHE	457	32.031	10.535	64.819		20.00
	ATOM	1396	C	PHE	457	30.582	14.189	69.714		20.00
	ATOM	1397	0	PHE	457	29.355	14.198	69.791		20.00
	MOTA	1398	N	GLY	458	31.351	14.991	70.462		40.00
	ATOM	1400	CA	GLY	458	30.716	15.995	71.255		40.00
	ATOM	1401	С	GLY	458	30.329	17.121	70.356		40.00 40.00
	MOTA	1402	0	GLY	458	29.233	17.673	70.446 69.423		40.00
	MOTA	1403	N	THR	459	31.242	17.448	68.594		40.00
	ATOM	1405	CA	THR	459 459	31.117 32.178	18.607 18.671	67.530		40.00
	ATOM	1406	CB	THR	459	32.176	17.559	66.653		40.00
	ATOM	1407 1409	OG1 CG2	THR THR	459	33.557	18.683	68.213		40.00
	ATOM ATOM	1410	CGZ	THR	459	29.793	18.691	67.916		40.00
	ATOM	1411	0	THR	459	29.038	19.634	68.147		40.00
	ATOM	1412	N	SER	460	29.448	17.707	67.070		40.00
	MOTA	1414	CA	SER	460	28.205	17.880	66.388		40.00
	ATOM	1415	CB	SER	460	28.307	18.854	65.203		40.00
	ATOM	1416	OG	SER	460	27.047	18.984	64.566		40.00
	MOTA	1418	С	SER	460	27.707	16.589	65.838	1.00	40.00

ATOM	1419	0	SER	460	28.122	16.158	64.765	1.00 40.00
MOTA	1420	N	GLY	461	26.798	15.935	66.578	1.00 40.00
MOTA	1422	CA	GLY	461	26.202	14.721	66.113	1.00 40.00
. A	1423	С	GLY	461	25.299	15.063	64.973	1.00 40.00
A'I'OM	1424	0	GLY	461	25.091	14.265	64.062	1.00 40.00
ATOM	1425	N	GLN	462	24.725	16.279	65.013	1.00 40.00
MOTA	1427	CA	GLN	462	23.786	16.715	64.020	1.00 40.00
ATOM	1428	CB	GLN	462	23.223	18.115	64.315	1.00 40.00
ATOM	1429	CG	GLN	462	24.287	19.212	64.282	1.00 40.00
MOTA	1430	CD	GLN	462	23.621	20.547	64.584	1.00 40.00
ATOM	1431		GLN	462	22.443	20.753	64.300	1.00 40.00
MOTA	1432	NE2	GLN	462	24.401	21.484	65.187	1.00 40.00
ATOM	1435	C	GLN	462	24.444	16.755	62.677	1.00 40.00
ATOM	1436	0	GLN	462	23.805	16.489	61.660	1.00 40.00
MOTA	1437	N	LYS	463	25.746	17.092	62.649 61.440	1.00 40.00 1.00 40.00
MOTA	1439	CA	LYS	463 463	26.507 27.923	17.247 17.786	61.702	1.00 40.00
ATOM	1440	CB	LYS	463	28.590	18.361	60.452	1.00 40.00
ATOM	1441 1442	CG CD	LYS LYS	463	27.908	19.641	59.963	1.00 40.00
MOTA	1442	CE	LYS	463	28.550	20.258	58.720	1.00 40.00
ATOM ATOM	1444	NZ	LYS	463	27.801	21.469	58.318	1.00 40.00
ATOM	1448	C	LYS	463	26.660	15.969	60.669	1.00 40.00
ATOM	1449	0	LYS	463	26.753	15.991	59.443	1.00 40.00
ATOM	1450	N	THR	464	26.712	14.816	61.359	1.00 40.00
ATOM	1452	CA	THR	464	26.955	13.574	60.676	1.00 40.00
ATOM	1453	СВ	THR	464	26.867	12.373	61.572	1.00 40.00
MOTA	1454	OG1	THR	464	27.293	11.210	60.877	1.00 40.00
MOTA	1456	CG2	THR	464	25.409	12.209	62.037	1.00 40.00
ATOM	1457	С	THR	464	26.008	13.353	59.545	1.00 40.00
ATOM	1458	0	THR	464	24.823	13.670	59.636	1.00 40.00
MOTA	1459	N	LYS	465	26.533	12.820	58.419	1.00 40.00
MOTA	1461	CA	LYS	465	25.666	12.528	57.319	1.00 40.00
MOTA	1462	CB	LYS	465	26.015	13.230	55.998	1.00 40.00
MOTA	1463	CG	LYS	465	24.994	12.891	54.910	1.00 40.00
ATOM	1464	CD	LYS	465	25.020	13.816	53.693	1.00 40.00
ATOM	1465	CE	LYS	465	23.979	13.435	52.638	1.00 40.00
MOTA	1466	NZ	LYS	465	23.968	14.436	51.549	1.00 40.00 1.00 40.00
ATOM	1470	С	LYS	465	25.706	11.064	57.057 56.776	1.00 40.00
ATOM	1471	0	LYS	465 466	26.759 24.532	10.491 10.415	57.150	1.00 40.00
ATOM	1472 1474	N CA	ILE	466	24.500	9.007	56.923	1.00 40.00
ATOM ATOM	1474	CB	ILE	466	24.176	8.233	58.167	1.00 40.00
ATOM	1476		ILE	466	24.064	6.747	57.789	1.00 40.00
ATOM	1477		ILE	466	25.226	8.516	59.256	1.00 40.00
ATOM	1478	CD1	ILE	466	24.825	8.003	60.639	1.00 40.00
ATOM	1479	С	ILE	466	23.436	8.713	55.920	1.00 40.00
ATOM	1480	0	ILE	466	22.278	9.088	56.102	1.00 40.00
ATOM	1481	N	ILE	467	23.821	8.046	54.814	1.00 40.00
ATOM	1483	CA	ILE	467	22.874	7.661	53.810	1.00 40.00
ATOM	1484	CB	ILE	467	22.588	8.736	52.798	1.00 40.00
ATOM	1485	CG2	ILE	467	21.923	9.922	53.515	1.00 40.00
ATOM	1486	CG1	ILE	467	23.865	9.111	52.030	1.00 40.00
ATOM	1487	CD1	ILE	467	23.596	9.992	50.811	1.00 40.00
ATOM	1488	С	ILE	467	23.454	6.505	53.058	1.00 40.00
ATOM	1489	0	ILE	467	24.671	6.345	52.991	1.00 40.00
ATOM	1490	N	SER	468		5.682	52.452	1.00 40.00
ATOM	1492	CA	SER	468	22.961	4.556	51.646	1.00 40.00
ATOM	1493	СВ	SER	468	24.002	4.934	50.577	1.00 40.00
ATOM	1494	OG	SER	468	23.458	5.896	49.686	1.00 40.00
ATOM	1496	С	SER	468	23.509	3.382	52.407	1.00 40.00
ATOM	1497	0	SER	468	24.142	2.512	51.810	1.00 40.00
MOTA	1498	N	ASN	469 469	23.263	3.292	53.729 54.472	1.00 20.00 1.00 20.00
ATOM .	1500	CA	ASN	469 469	23.744 24.112	2.155 2.474	54.472 55.930	1.00 20.00
ATOM	1501	СВ	ASN	- 05	24.112	2.7/4	JJ.JJ0	2.00 20.00

M	1502	CG	ASN	469	25.381	3.315	55.913		20.00	
ATOM	1503	OD1	ASN	469	26.339	3.005	55.205		20.00	
ATOM	1504		ASN	469	25.388	4.414	56.712		20.00	
Μ′	1507	С	ASN	469	22.672	1.112	54.485		20.00	
ALOM	1508	0	ASN	469	21.660	1.240 0.022	53.800 55.254		20.00 . 20.00	
ATOM	1509	N	ARG	470 470	22.877 21.898	-1.026	55.268		20.00	
ATOM	1511 1512	CA CB	ARG ARG	470	22.443	-2.371	55.776		20.00	
MOTA MOTA	1512	CG	ARG	470	21.540	-3.550	55.415		20.00	
ATOM	1514	CD	ARG	470	22.221	-4.913	55.539	1.00	20.00	
ATOM	1515	NE	ARG	470	21.220	-5.939	55.132	1.00	20.00	
ATOM	1517	CZ	ARG	470	21.018	-6.201	53.807		20.00	
MOTA	1518		ARG	470	20.128	-7.165	53.429		20.00	
MOTA	1521		ARG	470	21.699	-5.492	52.859		20.00	
MOTA	1524	C	ARG	470	20.742	-0.619	56.128 57.048		20.00	
MOTA	1525	0	ARG	470 471	20.889 19.546	0.183 -1.171	55.835		20.00	
MOTA	1526 1528	N CA	GLY GLY	471	18.369	-0.820	56.575		20.00	
ATOM ATOM	1529	C	GLY	471	18.410	-1.520	57.892		20.00	
ATOM	1530	ō	GLY	471	18.635	-2.726	57.968	1.00	20.00	
ATOM	1531	N	GLU	472	18.110	-0.768	58.964	1.00	20.00	
ATOM	1533	CA	GLU	472	18.175	-1.258	60.308		20.00	
MOTA	1534	CB	GLU	472	17.700	-0.191	61.312		20.00	
MOTA	1535	CG	GLU	472	17.766	-0.618	62.778		20.00	
ATOM	1536	CD	GLU	472	17.265	0.550	63.621		20.00 20.00	
MOTA	1537		GLU	472	17.843 16.297	1.662 0.348	63.488 64.401		20.00	
ATOM	1538	CE2	GLU	472 472	17.281	-2.449	60.428		20.00	
ATOM ATOM	1539 1540	0	GLU	472	17.601	-3.408	61.131		20.00	
ATOM	1541	N	ASN	473	16.126	-2.412	59.741	1.00	20.00	
ATOM	1543	CA	ASN	473	15.193	-3.499	59.794		20.00	
MOTA	1544	CB	ASN	473	13.928	-3.214	58.965		20.00	
MOTA	1545	CG	ASN	473	13.138	-2.118	59.669		20.00	
ATOM	1546		ASN	473	12.431	-2.374	60.643		20.00 20.00	
MOTA	1547		ASN	473 473	13.264 15.837	-0.859 -4.727	59.169 59.232		20.00	
MOTA	1550 1551	С 0	ASN ASN	473	15.707	-5.817	59.788		20.00	
ATOM ATOM	1551	N	SER	474	16.555	-4.573	58.103		20.00	
ATOM	1554	CA	SER	474	17.194	-5.681	57.451		20.00	
ATOM	1555	СВ	SER	474	17.843	-5.283	56.113		20.00	
MOTA	1556	OG	SER	474	18.457	-6.413	55.510		20.00	
MOTA	1558	С	SER	474	18.276	-6.232	58.324		20.00	
MOTA	1559	0	SER	474	18.449	-7.445	58.429		20.00	
MOTA	1560	N	CYS	475	19.036 20.125	-5.344 -5.779	58.987 59.808		20.00	
ATOM	1562	CA CB	CYS CYS	475 475	20.125	-4.613	60.438		20.00	
MOTA ATOM	1563 1564	SG	CYS	475	21.836	-3.652	59.208		20.00	
ATOM	1565	Ç	CYS	475	19.582	-6.621	60.912	1.00	20.00	
ATOM	1566	0	CYS	475	20.186	-7.628	61.278		20.00	
ATOM	1567	N	LYS	476	18.409	-6.242	61.459		60.00	
ATOM	1569	CA	LYS	476	17.874	-6.990	62.558		60.00	
ATOM	1570	СВ	LYS	476	17.613	-8.468	62.216		60.00 60.00	
MOTA	1571	CG	LYS	476	16.317	-8.703	61.436 62.266		60.00	
ATOM	1572	CE	LYS LYS	476 476	15.048 14.947	-8.476 -7.089	62.200		60.00	
ATOM ATOM	1573 1574	NZ	LYS	476	13.748	-7.033	63.770		60.00	
ATOM ATOM	1574	C	LYS	476	18.921	-6.920	63.604		60.00	
ATOM	1579	ō	LYS	476	19.139	-7.855	64.372	1.00	60.00	
ATOM	1580	N	ALA	477	19.596	-5.764	63.640		60.00	
ATOM	1582	CA	ALA	477	20.675	-5.551	64.538		60.00	
ATOM	1583	СВ	ALA	477	21.779	-4.658	63.931		60.00	
MOTA	1584	C	ALA	477	20.208	-4.882	65.785		60.00	
ATOM	1585	0	ALA	477	19.038	-4.543 -4.797	65.960 66.700		60.00 60.00	
ATOM	1586	N	THR	478	21.182	-4.797	00.700	1.00	55.00	

MOTA	1588	CA	THR	478	21.298	-4.164	67.976	1.00 60.00
MOTA	1589	CB	THR	478	20.348	-4.676	69.025	1.00 60.00
MOTA	1590	OG1	THR	478	20.460	-6.086	69.145	1.00 60.00
. <u>M</u>	1592	CG2	THR	478	18.907	-4.266	68.681	1.00 60.00
MOTA	1593	С	THR	478	22.621	-4.786	68.220	1.00 60.00
ATOM	1594	0	THR	478	22.914	-5.304	69.294	1.00 60.00
MOTA	1595	N	GLY	479	23.468	-4.695	67.178	1.00 60.00
ATOM	1597	CA	GLY	479	24.658	-5.480	67.102	1.00 60.00
ATOM	1598	С	GLY	479	24.076	-6.585	66.277	1.00 60.00
ATOM	1599	0	GLY	479	23.056	-6.365	65.632	1.00 60.00
ATOM	1600	N	GLN	480	24.678	-7.792	66.239	1.00 60.00
ATOM	1602	CA	GLN	480	23.982	-8.847	65.552	1.00 60.00
MOTA	1603	CB	GLN	480	24.733	-10.188	65.586	1.00 60.00
MOTA	1604	CG	GLN	480	24.025	-11.318	64.839	1.00 60.00
ATOM	1605	CD	GLN	480		-12.541	64.896	1.00 60.00
	1606		GLN	480		-13.330	63.955	1.00 60.00
ATOM			GLN	480	25.659	-12.704	66.032	1.00 60.00
ATOM	1607	NE2	GLN	480	22.824	-8.945	66.475	1.00 60.00
ATOM	1610			480	21.664	-9.097	66.095	1.00 60.00
MOTA	1611	0	GLN	481	23.201	-8.820	67.750	1.00 60.00
MOTA	1612	N	VAL	481	22.411	-8.694	68.923	1.00 60.00
ATOM	1614	CA	VAL			-10.002	69.518	1.00 60.00
MOTA	1615	CB	VAL	481	21.982		69.947	1.00 60.00
ATOM	1616		VAL	481		-10.779		
MOTA	1617		VAL	481	21.013	-9.716	70.677	1.00 60.00
MOTA	1618	С	VAL	481	23.529	-8.182	69.755	1.00 60.00
MOTA	1619	0	VAL	481	24.685	-8.456	69.436	1.00 60.00
MOTA	1620	N	CYS	482	23.285	-7.401	70.814	1.00 20.00
MOTA	1622	CA	CYS	482	24.503	-7.039	71.462	1.00 20.00
MOTA	1623	CB	CYS	482	24.576	-5.617	72.037	1.00 20.00
MOTA	1624	SG	CYS	482	26.326	-5.221	72.294	1.00 20.00
ATOM	1625	С	CYS	482	24.696	-8.015	72.582	1.00 20.00
MOTA	1626	0	CYS	482	23.907	-8.945	72.738	1.00 20.00
MOTA	1627	N	HIS	483	25.765	-7.848	73.388	1.00 20.00
ATOM	1629	CA	HIS	483	25.982	-8.790	74.444	1.00 20.00
MOTA	1630	СВ	HIS	483	27.387	-8.739	75.065	1.00 20.00
ATOM	1631	CG	HIS	483		-10.003	75.804	1.00 20.00
ATOM	1632		HIS	483		-11.158	75.361	1.00 20.00
MOTA	1633		HIS	483		-10.228	77.118	1.00 20.00
ATOM	1635		HIS	483		-11.494	77.410	1.00 20.00
ATOM	1636		HIS	483		-12.098	76.375	1.00 20.00
MOTA	1638	С	HIS	483	24.956	-8.511	75.490	1.00 20.00
ATOM	1639	0	HIS	483	24.359	-7.436	75.521	1.00 20.00
ATOM	1640	N	ALA	484	24.706	-9.497	76.368	1.00 20.00
ATOM	1642	CA	ALA	484	23.706	-9.332	77.379	1.00 20.00
MOTA	1643	CB	ALA	484	23.553	-10.571	78.276	1.00 20.00
ATOM	1644	С	ALA	484	24.123	-8.198	78.258	1.00 20.00
ATOM	1645	0	ALA	484	23.301	-7.383	78.673	1.00 20.00
MOTA	1646	N	LEU	485	25.432	-8.123	78.554	1.00 20.00
MOTA	1648	CA	LEU	485	25.971	-7.130	79.435	1.00 20.00
MOTA	1649	CB	LEU	485	27.458	-7.364	79.760	1.00 20.00
ATOM	1650	CG	LEU	485	27.723	-8.604	80.636	1.00 20.00
ATOM	1651	CD1	LEU	485	27.110	-8.438	82.033	1.00 20.00
MOTA	1652	CD2	LEU	485	27.254	-9.899	79.959	1.00 20.00
ATOM	1653	С	LEU	485	25.859	-5.731	78.922	1.00 20.00
ATOM	1654	0	LEU	485	25.609	-4.816	79.705	1.00 20.00
ATOM	1655	N	CYS	486	26.059	-5.521	77.605	1.00 20.00
ATOM	1657	CA	CYS	486	26.024	-4.183	77.088	1.00 20.00
MOTA	1658	СВ	CYS	486	26.159	-4.089	75.561	1.00 20.00
MOTA	1659	SG	CYS	486	27.793	-4.607	74.972	1.00 20.00
ATOM	1660	C	CYS	486	24.710	-3.584	77.445	1.00 20.00
ATOM	1661	o	CYS	486	23.680	-4.253	77.418	1.00 20.00
ATOM	1662	N	SER	487	24.725	-2.298	77.834	1.00 40.00
ATOM	1664	CA	SER	487	23.489	-1.683	78.191	1.00 40.00
ATOM	1665	CB	SER	487	23.641	-0.401	79.021	1.00 40.00
AION	1000	C15	~~					

A	1666	OG	SER	487	24.221	0.618	78.222	1.00 40.00		
ATOM	1668	С	SER	487	22.857	-1.321	76.902	1.00 40.00		
MOTA	1669	0	SER	487	23.476	-1.424	75.845	1.00 40.00		
i M	1670	N	PRO	488	21.639	-0.873	76.994	1.00 40.00		
MOTA	1671	CD	PRO	488	20.819	-1.107	78.169	1.00 40.00		
MOTA	1672	CA	PRO	488	20.856	-0.523	75.848	1.00 40.00		
ATOM	1673	CB	PRO	488	19.425	-0.323	76.356	1.00 40.00		
MOTA	1674	CG	PRO	488	19.548	-0.293	77.891 75.183	1.00 40.00 1.00 40.00		
MOTA	1675	C	PRO	488 488	21.442 20.909	0.669 1.090	74.158	1.00 40.00		
ATOM	1676	0	PRO GLU	489	22.526	1.231	75.750	1.00 40.00		
ATOM	1677 1679	N CA	GLU	489	23.141	2.350	75.730	1.00 40.00		
ATOM ATOM	1680	CB	GLU	489	24.424	2.824	75.815	1.00 40.00		
MOTA	1681	CG	GLU	489	24.146	3.512	77.152	1.00 40.00		
MOTA	1682	CD	GLU	489	23.356	4.780	76.856	1.00 40.00		
ATOM	1683		GLU	489	22.242	4.929	77.426	1.00 40.00		
ATOM	1684		GLU	489	23.854	5.615	76.055	1.00 40.00		
ATOM	1685	С	GLU	489	23.486	1.912	73.726	1.00 40.00		
ATOM	1686	0	GLU	489	23.147	2.591	72.758	1.00 40.00		
ATOM	1687	N	GLY	490	24.148	0.746	73.581	1.00 40.00		
ATOM	1689	CA	GLY	490	24.436	0.300	72.246	1.00 40.00		
ATOM	1690	С	GLY	490	25.782	-0.344	72.202	1.00 40.00		
MOTA	1691	0	GLY	490	26.427	-0.520	73.233	1.00 40.00		
ATOM	1692	N	CYS	491	26.229	-0.748	70.993	1.00 20.00		
MOTA	1694	CA	CYS	491	27.534	-1.322	70.876	1.00 20.00		
MOTA	1695	CB	CYS	491	27.666	-2.693	71.547	1.00 20.00		
MOTA	1696	SG	CYS	491	26.822	-4.060	70.710	1.00 20.00		
MOTA	1697	C	CYS	491	27.974	-1.427	69.448	1.00 20.00 1.00 20.00		
MOTA	1698	0	CYS	491	27.191	-1.256	68.516 69.249	1.00 20.00		
ATOM	1699	N	TRP	492 492	29.286 29.852	-1.658 -1.751	67.932	1.00 20.00		
MOTA	1701 1702	CA CB	TRP TRP	492	31.383	-1.624	67.949	1.00 20.00		
ATOM ATOM	1702	CG	TRP	492	31.841	-0.264	68.422	1.00 20.00		
ATOM	1703		TRP	492	31.829	0.923	67.613	1.00 20.00		
ATOM	1705		TRP	492	32.262	1.975	68.421	1.00 20.00		
ATOM	1706		TRP	492	31.478	1.122	66.309	1.00 20.00		
ATOM	1707		TRP	492	32.250	0.120	69.665	1.00 20.00		
ATOM	1708	NE1	TRP	492	32.522	1.466	69.675	1.00 20.00		
ATOM	1710	CZ2	TRP	492	32.349	3.248	67.934	1.00 20.00		
ATOM	1711	CZ3	TRP	492	31.572	2.407	65.820	1.00 20.00		
ATOM	1712	CH2	TRP	492	31,998	3.449	66.617	1.00 20.00		
ATOM	1713	С	TRP	492	29.484	-3.013	67.207	1.00 20.00		
MOTA	1714	0	TRP	492	29.238	-2.994	66.001	1.00 20.00		
MOTA	1715	N	GLY	493	29.448	-4.151 -5.416	67.926	1.00 20.00 1.00 20.00		
ATOM	1717	CA	GLY	493	29.135 28.919	-5.416 -6.347	67.316 68.463	1.00 20.00		
ATOM	1718	C	GLY	493 493	28.919	-5.883	69.565	1.00 20.00		
ATOM	1719 1720	O N	GLY PRO	493 494	28.961	-7.638	68.284	1.00 40.00		
MOTA MOTA	1721	CD	PRO	494	28.323	-8.259	67.136	1.00 40.00		
ATOM	1721	CA	PRO	494	28.822	-8.443	69.463	1.00 40.00		
ATOM	1723	CB	PRO	494	28.300	-9.802	69.006	1.00 40.00		
ATOM	1724	CG	PRO	494	27.573	-9.482	67.689	1.00 40.00		
ATOM	1725	c	PRO	494	30.128	-8.514	70.185	1.00 40.00		
ATOM	1726	0	PRO	494	31.072	-9.053	69.613	1.00 40.00		
ATOM	1727	N	GLU	495	30.195	-8.014	71.436	1.00 40.00		
ATOM	1729	CA	GLU	495	31.375	-8.089	72.256	1.00 40.00		
MOTA	1730	CB	GLU	495	32.593	-7.287	71.749	1.00 40.00		
ATOM	1731	CG	GLU	495	33.353	-7.900	70.573	1.00 40.00		
MOTA	1732	CD	GLU	495	34.454	-6.930	70.171	1.00 40.00		
ATOM	1733		GLU	495	35.343	-7.337	69.376	1.00 40.00		
ATOM	1734		GLU	495	34.417	-5.764	70.646	1.00 40.00		
MOTA	1735	C	GLU	495	31.004	-7.432	73.546	1.00 40.00 1.00 40.00		
ATOM	1736	0	GLU	495 496	30.221	-6.486 -7.915	73.553	1.00 40.00		
MOTA	1737	N	PRO	496	31.509	-7.915	74.645	1.00 20.00		

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ATOM	1738	CD	PRO	496	31.711	-9.341	74.819	1.00 20.00
ATOM	1739	CA	PRO	496	31.264	-7.251	75.897	1.00 20.00
MOTA	1740	CB	PRO	496	31.515	-8.293	76.991	1.00 20.00
i 1	1741	CG	PRO	496	32.200	-9.467	76.268	1.00 20.00
MOTA	1742	С	PRO	496	32.127	-6.031	76.014	1.00 20.00
MOTA	1743	0	PRO	496	31.852	-5.174	76.853	1.00 20.00
ATOM	1744	N	ARG	497	33.221	-5.983	75.231	1.00 20.00
MOTA	1746	CA	ARG	497	34.147	-4.887	75.215	1.00 20.00
ATOM	1747	CB	ARG	497	35.506	-5.301	74.623	1.00 20.00
ATOM	1748	CG	ARG	497	35.420	-5.828	73.193	1.00 20.00
MOTA	1749	CD	ARG	497	36.661	-6.603	72.744	1.00 20.00
ATOM	1750	NE	ARG	497	36.424	-8.046	73.041	1.00 20.00
ATOM	1752	CZ	ARG	497	36.759	-8.573	74.256	1.00 20.00
ATOM	1753	NH1	ARG	497	37.298	-7.778	75.225	1.00 20.00
MOTA	1756	NH2	ARG	497	36.552	-9.900	74.501	1.00 20.00
ATOM	1759	C	ARG	497	33.629	-3.696	74.461	1.00 20.00
ATOM	1760	0	ARG	497	33.927	-2.551	74.796	1.00 20.00
ATOM	1761	N	ASP	498	32.856	-3.946	73.391	1.00 20.00
ATOM	1763	CA	ASP	498	32.360	-2.918	72.516	1.00 20.00
MOTA	1764	СВ	ASP	498	31.966	-3.444	71.128	1.00 20.00
ATOM	1765	CG	ASP	498	30.893	-4.496	71.291	1.00 20.00
ATOM	1766	OD1	ASP	498	30.029	-4.348	72.195	1.00 20.00
ATOM	1767		ASP	498	30.949	-5.482	70.511	1.00 20.00
ATOM	1768	C	ASP	498	31.265	-2.044	73.055	1.00 20.00
ATOM	1769	0	ASP	498	31.035	-0.965	72.509	1.00 20.00
ATOM	1770	N	CYS	499	30.544	-2.499	74.102	1.00 20.00
ATOM	1772	CA	CYS	499	29.422	-1.807	74.694	1.00 20.00
ATOM	1773	СВ	CYS	499	29.165	-2.202	76.162	1.00 20.00
ATOM	1774	SG	CYS	499	29.015	-3.986	76.458	1.00 20.00
ATOM	1775	C	CYS	499	29.589	-0.312	74.732	1.00 20.00
MOTA	1776	o	CYS	499	30.701	0.208	74.795	1.00 20.00
MOTA	1777	N	VAL	500	28.468	0.426	74.575	1.00 20.00
MOTA	1779	CA	VAL	500	28.473	1.851	74.753	1.00 20.00
ATOM	1780	СВ	VAL	500	27.278	2.529	74.157	1.00 20.00
ATOM	1781	CG1	VAL	500	27.349	4.028	74.498	1.00 20.00
ATOM	1782	CG2	VAL	500	27.267	2.235	72.648	1.00 20.00
ATOM	1783	С	VAL	500	28.452	2.106	76.226	1.00 20.00
ATOM	1784	Ō	VAL	500	29.131	3.004	76.723	1.00 20.00
АТОМ	1785	N	SER	501	27.643	1.306	76.956	1.00 20.00
АТОМ	1787	CA	SER	501	27.519	1.440	78.381	1.00 20.00
АТОМ	1788	СВ	SER	501	26.337	2.321	78.819	1.00 20.00
АТОМ	1789	OG	SER	501	26.279	2.402	80.235	1.00 20.00
ATOM	1791	С	SER	501	27.309	0.062	78.932	1.00 20.00
ATOM	1792	0	SER	501	27.178	-0.900	78.175	1.00 20.00
MOTA	1793	N	CYS	502	27.269	-0.068	80.277	1.00 20.00
ATOM	1795	CA	CYS	502	27.190	-1.365	80.887	1.00 20.00
MOTA	1796	СВ	CYS	502	28.384	-1.609	81.830	1.00 20.00
ATOM	1797	SG	CYS	502	28.554	-3.311	82.433	1.00 20.00
MOTA	1798	С	CYS	502	25.908	-1.495	81.653	1.00 20.00
ATOM	1799	0	CYS	502	25.412	-0.529	82.231	1.00 20.00
ATOM	1800	N	ARG	503	25.307	-2.704	81.621	1.00 20.00
ATOM	1802	CA	ARG	503	24.084	-2.958	82.327	1.00 20.00
MOTA	1803	СВ	ARG	503	23.441	-4.308	81.965	1.00 20.00
ATOM	1804	CG	ARG	503	22.036	-4.476	82.549	1.00 20.00
ATOM	1805	CD	ARG	503	21.326	-5.747	82.079	1.00 20.00
ATOM	1806	NE	ARG	503	21.250	-5.684	80.591	1.00 20.00
ATOM	1808	CZ	ARG	503	20.221	-5.027	79.980	1.00 20.00
ATOM	1809	NH1	ARG	503	19.253	-4.425	80.731	1.00 20.00
ATOM	1812	NH2		503	20.160	-4.971	78.618	1.00 20.00
ATOM	1815	С	ARG	503	24.343	-2.949	83.798	1.00 20.00
АТОМ	1816	0	ARG	503	23.570	-2.388	84.573	1.00 20.00
АТОМ	1817	N	ASN	504	25.466	-3.564	84.211	1.00 20.00
ATOM	1819	CA	ASN	504	25.811	-3.647	85.600	1.00 20.00
ATOM	1820	СВ	ASN	504	26.210	-5.061	86.059	1.00 20.00

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F 1	1821	CG	ASN	504	24.945	-5.909	86.120		20.00
ATOM	1822		ASN	504	24.548	-6.522	85.131		20.00
MOTA	1823		ASN	504	24.293	-5.950	87.313		20.00
. М	1826	С	ASN	504	26.980 26.865	-2.740 -1.522	85.824 85.689		20.00
MOTA	1827	О	ASN VAL	504 505	28.139	-3.314	86.200		20.00
ATOM ATOM	1828 1830	CA	VAL	505	29.288	-2.505	86.489		20.00
ATOM	1831	СВ	VAL	505	29.963	-2.869	87.780		20.00
ATOM	1832	CG1	VAL	505	28.979	-2.620	88.935	1.00	20.00
ATOM	1833	CG2	VAL	505	30.445	-4.325	87.684		20.00
MOTA	1834	С	VAL	505	30.314	-2.635	85.410		20.00
MOTA	1835	0	VAL	505	30.472	-3.695	84.808		20.00
ATOM	1836	N	SER	506	31.038	-1.534	85.132		20.00
ATOM	1838	CA	SER	506 506	32.047 32.071	-1.574 -0.323	84.117 83.220		20.00
ATOM	1839	CB OG	SER SER	506 506	33.101	-0.437	82.250		20.00
ATOM ATOM	1840 1842	C	SER	506	33.370	-1.667	84.795		20.00
ATOM	1843	o	SER	506	33.630	-0.956	85.765		20.00
ATOM	1844	N	ARG	507	34.236	-2.583	84.319	1.00	20.00
ATOM	1846	CA	ARG	507	35.518	-2.700	84.940		20.00
ATOM	1847	СВ	ARG	507	35.551	-3.770	86.044		20.00
ATOM	1848	CG	ARG	507	36.846	-3.786	86.857		20.00
ATOM	1849	CD	ARG	507	38.033	-4.429	86.137		20.00
ATOM	1850	NÉ	ARG ARG	507 507	39.153 40.019	-4.497 -3.451	87.119 87.258		20.00
ATOM	1852 1853	CZ NH1	ARG	507	41.011	-3.511	88.194		20.00
ATOM ATOM	1856	NH2	ARG	507	39.896	-2.347	86.465		20.00
ATOM	1859	С	ARG	507	36.547	-3.076	83.922	1.00	20.00
ATOM	1860	0	ARG	507	36.361	-4.008	83.140		20.00
MOTA	1861	N	GLY	508	37.671	-2.337	83.903		20.00
MOTA	1863	CA	GLY	508	38.761	-2.667	83.032		20.00
ATOM	1864	C	GLY	508	38.308	-2.741	81.610		20.00
MOTA	1865	0	GLY ARG	508 509	38.630 37.533	-3.693 -1.743	80.902 81.151		20.00
ATOM ATOM	1866 1868	N CA	ARG	509	37.133	-1.717	79.773		20.00
ATOM	1869	СВ	ARG	509	38.342	-1.804	78.826		20.00
ATOM	1870	CG	ARG	509	39.300	-0.620	78.975		20.00
MOTA	1871	CD	ARG	509	40.611	-0.784	78.205		20.00
MOTA	1872	NE	ARG	509	40.319	-0.592	76.758		20.00
MOTA	1874	CZ	ARG	509	41.257	-0.011	75.954		20.00
ATOM	1875	NH1 NH2		509 509	41.009 42.441	0.154 0.412	74.622 76.486		20.00
ATOM ATOM	1878 1881	NH2 C	ARG	509	36.214	-2.859	79.461		20.00
ATOM	1882	0	ARG	509	35.901	-3.104	78.297		20.00
ATOM	1883	N	GLU	510	35.726	-3.579	80.491	1.00	20.00
ATOM	1885	CA	GLU	510	34.853	-4.686	80.217		20.00
ATOM	1886	СВ	GLU	510	35.456	-6.027	80.669		20.00
MOTA	1887	CG	GLU	510	36.723	-6.393	79.890		20.00
ATOM	1888	CD CD1	GLU	510 510	37.447 37.664	-7.508 -8.583	80.630 80.009		20.00
ATOM	1889	OE1 OE2		510	37.801	-7.298	81.821		20.00
ATOM ATOM	1890 1891	C	GLU	510	33.589	-4.481	80.984		20.00
ATOM	1892	0	GLU	510	33.600	-3.976	82.105		20.00
ATOM	1893	N	CYS	511	32.451	-4.875	80.385		20.00
ATOM	1895	CA	CYS	511	31.191	-4.703	81.042		20.00
MOTA	1896	СВ	CYS	511	30.037	-4.512	80.039		20.00
MOTA	1897	SG	CYS	511	28.372	-4.452	80.762		20.00
ATOM	1898	С	CYS	511	30.961	-5.930 -7.003	81.858 81.320		20.00
ATOM ATOM	1899 1900	O N	CYS VAL	511 512	30.691 31.079	-7.003 -5.786	83.195		20.00
ATOM ATOM	1900	CA	VAL	512	30.909	-6.884	84.104		20.00
ATOM ATOM	1903	CB	VAL	512	31.969	-6.991	85.164		20.00
ATOM	1904			512	33.231	-7.611	84.562		20.00
ATOM	1905	CG2	VAL	512	32.239	-5.583	85.710	1.00	20.00

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ATOM	1906	С	VAL	512	29.591	-6.838	84.803	1.00 20.00
MOTA	1907	0	VAL	512	29.045	-5.775	85.096	1.00 20.00
ATOM	1908	N	ASP	513	29.025	-8.039	85.028	1.00 20.00
i 1	1910	CA	ASP	513	27.799	-8.215	85.747	1.00 20.00
MOTA	1911	СВ	ASP	513	27.233	-9.641	85.627	1.00 20.00
MOTA	1912	CG	ASP	513		-10.614	86.169	1.00 20.00
MOTA	1913	OD1	ASP	513		-11.193	87.262	1.00 20.00
MOTA	1914	OD2	ASP	513	29.313	-10.800	85.487	1.00 20.00
MOTA	1915	С	ASP	513	28.029	-7.927	87.193	1.00 20.00
MOTA	1916	0	ASP	513	27.143	-7.429	87.887	1.00 20.00
ATOM	1917	N	LYS	514	29.224	-8.282	87.700	1.00 20.00
MOTA	1919	CA	LYS	514	29.519	-8.023	89.077	1.00 20.00
MOTA	1920	CB	LYS	514	29.130	-9.178	90.019	1.00 20.00
MOTA	1921	CG	LYS	514		-10.535	89.641	1.00 20.00
MOTA	1922	CD	LYS	514		-10.640	89.842	1.00 20.00
ATOM	1923	CE	LYS	514		-12.028	89.510	1.00 20.00
ATOM	1924	NZ	LYS	514		-13.034	90.424	1.00 20.00
MOTA	1928	С	LYS	514	30.987	-7.772	89.197	1.00 20.00
MOTA	1929	0	LYS	514	31.771	-8.128	88.318	1.00 20.00
MOTA	1930	N	CYS	515	31.388	-7.130	90.309	1.00 20.00
MOTA	1932	CA	CYS	515	32.760	-6.793	90.544	1.00 20.00
MOTA	1933	CB	CYS	515	32.987	-6.056	91.874	1.00 20.00
MOTA	1934	SG	CYS	515	32.657	-4.275	91.855	1.00 20.00
MOTA	1935	С	CYS	515	33.608	-8.019	90.651	1.00 20.00
MOTA	1936	0	CYS	515	33.193	-9.045	91.187	1.00 20.00
MOTA	1937	N	LYS	516	34.854	-7.916	90.148	1.00 20.00
ATOM	1939	CA	LYS	516	35.779	-9.006	90.231	1.00 20.00
MOTA	1940	СВ	LYS	516	36.980	-8.859	89.281	1.00 20.00 1.00 20.00
MOTA	1941	CG	LYS	516	36.574	-8.714	87.813	1.00 20.00 1.00 20.00
MOTA	1942	CD	LYS	516	35.721	-9.868	87.279 86.944	1.00 20.00
ATOM	1943	CE	LYS	516		-11.130 -12.169	86.398	1.00 20.00
ATOM	1944	NZ	LYS	516 516	36.308	-8.986	91.632	1.00 20.00
ATOM	1948	С	LYS	516	36.045	-8.054	92.389	1.00 20.00
MOTA	1949	O N	LYS LEU	517		-10.024	92.024	1.00 20.00
MOTA	1950 1952	CA	LEU	517		-10.086	93.364	1.00 20.00
ATOM	1953	CB	LEU	517		-11.391	93.662	1.00 20.00
ATOM ATOM	1954	CG	LEU	517		-12.646	93.499	1.00 20.00
ATOM	1955		LEU	517		-13.929	93.807	1.00 20.00
ATOM	1956		LEU	517		-12.536	94.320	1.00 20.00
ATOM	1957	C	LEU	517	38.532	-8.949	93.545	1.00 20.00
ATOM	1958	0	LEU	517	39.091	-8.440	92.575	1.00 20.00
ATOM	1959	N	LEU	518	38.719	-8.513	94.809	1.00 20.00
ATOM	1961	CA	LEU	518	39.625	-7.448	95.142	1.00 20.00
MOTA	1962	СВ	LEU	518	40.947	-7.494	94.355	1.00 20.00
ATOM	1963	CG	LEU	518	41.918	-6.351	94.714	1.00 20.00
MOTA	1964	CD1	LEU	518	42.433	-6.480	96.156	1.00 20.00
MOTA	1965	CD2	LEU	518	43.044	-6.226	93.676	1.00 20.00
MOTA	1966	С	LEU	518	38.997	-6.114	94.879	1.00 20.00
ATOM	1967	0	LEU	518	39.208	-5.171	95.640	1.00 20.00
ATOM	1968	N	GLU	519	38.191	-5.992	93.804	1.00 20.00
ATOM	1970	CA	GLU	519	37.604	-4.713	93.517	1.00 20.00
ATOM	1971	CB	GLU	519	37.515	-4.360	92.020	1.00 20.00
ATOM	1972	CG	GLU	519	38.842	-3.943	91.381	1.00 20.00
MOTA	1973	CD	GLU	519	39.585	-5.191	90.933	1.00 20.00
ATOM	1974		GLU	519	38.935	-6.078	90.320	1.00 20.00
MOTA	1975		GLU	519	40.814	-5.272	91.196	1.00 20.00
MOTA	1976	С	GLU	519	36.208	-4.674	94.044	1.00 20.00
MOTA	1977	0	GLU	519	35.528	-5.696	94.136	1.00 20.00
ATOM	1978	N	GLY	520	35.758	-3.463	94.422	1.00 20.00
ATOM	1980	CA	GLY	520	34.439	-3.272	94.938	1.00 20.00
ATOM	1981	C	GLY	520	33.813	-2.189	94.136	1.00 20.00
MOTA	1982	0	GLY	520	34.491	-1.278	93.667	1.00 20.00
ATOM	1983	N	GLU	521	32.483	-2.262	93.968	1.00 40.00

M	1985	CA	GLU	521	31.802	-1.288	93.176	1.00	40.00
ALOM	1986	CB	GLU	521	30.416	-1.771	92.716		40.00
MOTA	1987	CG	GLU	521	29.514	-2.180	93.882		40.00
. M	1988	CD	GLU	521	28.220	-2.746	93.314		40.00
A.¹ ∩W	1989	OE1		521	27.535	-3.502	94.053		40.00
ATOM	1990	OE2		521	27.901	-2.435	92.135 93.973		40.00
ATOM	1991	C	GLU	521 521	31.612 31.258	-0.046 -0.082	95.150		40.00
ATOM	1992	O N	GLU PRO	521	31.238	1.066	93.130		40.00
ATOM ATOM	1993 1994	CD	PRO	522	33.036	1.177	92.484		40.00
ATOM	1995	CA	PRO	522	31.617	2.298	94.026		40.00
ATOM	1996	СВ	PRO	522	32.447	3.373	93.318	1.00	40.00
ATOM	1997	CG	PRO	522	33.044	2.661	92.089	1.00	40.00
ATOM	1998	С	PRO	522	30.143	2.511	94.004	1.00	40.00
MOTA	1999	0	PRO	522	29.528	2.289	92.962		40.00
MOTA	2000	N	ARG	523	29.558	2.927	95.142		60.00
MOTA	2002	CA	ARG	523	28.138	3.104	95.212		60.00
MOTA	2003	CB	ARG	523	27.632	3.334	96.647		60.00
MOTA	2004	CG	ARG	523	27.668	2.065	97.500		60.00
MOTA	2005	CD	ARG	523	26.622	1.037 -0.152	97.064 97.951		60.00
ATOM	2006	NE	ARG	523 523	26.744 25.823	-0.152	97.856		60.00
ATOM	2008	CZ	ARG	523 523	24.792	-1.133	96.968		60.00
ATOM	2009	NH1 NH2	ARG ARG	523	25.934	-2.264	98.645		60.00
ATOM ATOM	2012 2015	C	ARG	523	27.691	4.256	94.375		60.00
ATOM	2016	0	ARG	523	26.770	4.121	93.570		60.00
ATOM	2017	N	GLU	524	28.341	5.425	94.525		60.00
ATOM	2019	CA	GLU	524	27.889	6.552	93.767	1.00	60.00
ATOM	2020	СВ	GLU	524	28.307	7.917	94.338	1.00	60.00
ATOM ·	2021	CG	GLU	524	29.821	8.130	94.358		60.00
MOTA	2022	CD	GLU	524	30.077	9.592	94.694		60.00
MOTA	2023	OE1	GLU	524	29.169	10.425	94.430		60.00
MOTA	2024	OE2	GLU	524	31.183	9.896	95.214		60.00
MOTA	2025	С	GLU	524	28.463	6.463	92.398		60.00
MOTA	2026	0	GLU	524 525	29.462	5.782	92.170 91.438		60.00
MOTA	2027	N	PHE	525 525	27.807 28.296	7.140 7.136	90.096		60.00
MOTA	2029	CA CB	PHE PHE	525	27.511	6.173	89.180		60.00
ATOM	2030 2031	CG	PHE	525	26.062	6.520	89.262		60.00
ATOM ATOM	2031		PHE	525	25.327	6.139	90.361		60.00
ATOM	2033		PHE	525	25.421	7.158	88.224	1.00	60.00
ATOM	2034	CE1		525	23.986	6.428	90.447		60.00
ATOM	2035	CE2		525	24.079	7.449	88.302		60.00
ATOM	2036	CZ	PHE	525	23.361	7.094	89.419		60.00
MOTA	2037	С	PHE	525	28.221	8.522	89.541		60.00
MOTA	2038	0	PHE	525	27.144	9.036	89.244		60.00
ATOM	2039	N	VAL	526	29.385	9.185	89.416		60.00
MOTA	2041	CA	VAL	526	29.371	10.481	88.812 88.964		60.00
MOTA	2042	CB	VAL	526 526	30.667	11.230 10.425	88.324		60.00
MOTA	2043	CG1		526 526	31.810 30.481	12.633	88.360		60.00
ATOM	2044	CG2 C	VAL	526	29.111	10.214	87.369		60.00
ATOM ATOM	2045 2046	0	VAL	526	28.324	10.904	86.722		60.00
ATOM	2047	N	GLU	527	29.766	9.165	86.840		60.00
ATOM	2049	CA	GLU	527	29.567	8.755	85.486	1.00	60.00
ATOM	2050	СВ	GLU	527	30.877	8.509	84.718	1.00	60.00
ATOM	2051	CG	GLU	527	31.745	7.401	85.318	1.00	60.00
ATOM	2052	CD	GLU	527	32.996	7.277	84.460		60.00
ATOM	2053	OE1	GLU	527	33.118	8.051	83.473		60.00
ATOM	2054	OE2		527	33.850	6.407	84.782		60.00
MOTA	2055	С	GLU	527	28.852	7.454	85.613		60.00
MOTA	2056	0	GLU	527	28.059	7.264	86.534		60.00
MOTA	2057	N	ASN	528	29.098	6.517	84.682		60.00
MOTA	2059	CA	ASN	528	28.438	5.254	84.795	T.00	60.00

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ATOM	2060	CB	ASN	528	28.583	4.372	83.545	1.00 60.00
ATOM	2061	CG	ASN	528	27.745	5.007	82.446	1.00 60.00
MOTA	2062	OD1	ASN	528	28.080	6.064	81.915	1.00 60.00
; A	2063	ND2	ASN	528	26.613	4.339	82.093	1.00 60.00
ATOM	2066	С	ASN	528	29.058	4.542	85.951	1.00 60.00
ATOM	2067	0	ASN	528	30.106	4.946	86.451	1.00 60.00
ATOM	2068	N	SER	529	28.404	3.462	86.420	1.00 60.00
ATOM	2070	CA	SER	529	28.932	2.745	87.541	1.00 60.00
MOTA	2071	СВ	SER	529	27.912	1.823	88.230	1.00 60.00
ATOM	2072	OG	SER	529	26.889	2.597	88.837	1.00 60.00
MOTA	2074	С	SER	529	30.065	1.899	87.074	1.00 60.00
MOTA	2075	0	SER	529	30.100	1.453	85.928	1.00 60.00
ATOM	2076	N	GLU	530	31.040	1.679	87.972	1.00 40.00
АТОМ	2078	CA	GLU	530	32.187	0.891	87.648	1.00 40.00
АТОМ	2079	СВ	GLU	530	33.402	1.722	87.198	1.00 40.00
ATOM	2080	CG	GLU	530	33.230	2.428	85.852	1.00 40.00
АТОМ	2081	CD	GLU	530	34.477	3.269	85.618	1.00 40.00
ATOM	2082		GLU	530	34.663	3.755	84.470	1.00 40.00
MOTA	2083	OE2	GLU	530	35.262	3.437	86.590	1.00 40.00
ATOM	2084	С	GLU	530	32.595	0.225	88.914	1.00 40.00
ATOM	2085	ō	GLU	530	31.996	0.441	89.966	1.00 40.00
ATOM	2086	N	CYS	531	33.630	-0.629	88.833	1.00 20.00
ATOM	2088	CA	CYS	531	34.103	-1.267	90.016	1.00 20.00
MOTA	2089	СВ	CYS	531	34.350	-2.774	89.869	1.00 20.00
ATOM	2090	SG	CYS	531	34.511	-3.530	91.504	1.00 20.00
ATOM	2091	C	CYS	531	35.424	-0.624	90.264	1.00 20.00
ATOM	2092	ō	CYS	531	36.142	-0.277	89.328	1.00 20.00
ATOM	2093	N	ILE	532	35.769	-0.436	91.548	1.00 20.00
ATOM	2095	CA	ILE	532	36.989	0.225	91.890	1.00 20.00
MOTA	2096	CB	ILE	532	36.762	1.494	92.659	1.00 20.00
ATOM	2097	CG2	ILE	532	36.068	1.136	93.983	1.00 20.00
ATOM	2098	CG1	ILE	532	38.073	2.277	92.821	1.00 20.00
ATOM	2099	CD1	ILE	532	37.862	3.702	93.330	1.00 20.00
ATOM	2100	C	ILE	532	37.797	-0.698	92.746	1.00 20.00
ATOM	2101	ō	ILE	532	37.286	-1.694	93.251	1.00 20.00
ATOM	2102	N	GLN	533	39.099	-0.398	92.911	1.00 20.00
ATOM	2104	CA	GLN	533	39.970	-1.243	93.677	1.00 20.00
ATOM	2105	СВ	GLN	533	41.456	-1.010	93.368	1.00 20.00
ATOM	2106	CG	GLN	533	41.913	0.404	93.730	1.00 20.00
ATOM	2107	CD	GLN	533	43.389	0.531	93.386	1.00 20.00
ATOM	2108		GLN	533	44.031	-0.438	92.983	1.00 20.00
ATOM	2109		GLN	533	43.948	1.759	93.553	1.00 20.00
ATOM	2112	C	GLN	533	39.798	-0.994	95.138	1.00 20.00
ATOM	2113	0	GLN	533	39.414	0.096	95.558	1.00 20.00
ATOM	2114	N	CYS	534	40.071	-2.031	95.955	1.00 20.00
MOTA	2116	CA	CYS	534	40.010	-1.852	97.371	1.00 20.00
ATOM	2117	СВ	CYS	534	39.102	-2.844	98.131	1.00 20.00
MOTA	2118	SG	CYS	534	37.326	-2.688	97.744	1.00 20.00
ATOM	2119	C	CYS	534	41.410	-2.018	97.894	1.00 20.00
ATOM	2120	0	CYS	534	42.283	-2.538	97.200	1.00 20.00
ATOM	2121	N	HIS	535	41.663	-1.554	99.138	1.00 20.00
ATOM	2123	CA	HIS	535	42.975	-1.624	99.726	1.00 20.00
ATOM	2124	СВ	HIS	535	43.142		100.943	1.00 20.00
ATOM	2125	CG	HIS	535	44.548		101.466	1.00 20.00
ATOM	2126		HIS	535	45.604		101.031	1.00 20.00
ATOM	2127		HIS	535	45.030		102.507	1.00 20.00
ATOM	2129		HIS	535	46.342		102.649	1.00 20.00
ATOM	2130		HIS	535	46.737		101.775	1.00 20.00
ATOM	2132	C	HIS	535	43.233		100.155	1.00 20.00
ATOM	2133	ō	HIS	535	42.305		100.356	1.00 20.00
MOTA	2134	N	PRO	536	44.486		100.264	1.00 20.00
ATOM	2135	CD	PRO	536	45.537	-2.747	99.494	1.00 20.00
ATOM	2136	CA	PRO	536	44.852		100.662	1.00 20.00
ATOM	2137	CB	PRO	536	46.357		100.391	1.00 20.00
VION	211	CD	1		,			

M	2138	CG	PRO	536	46.816	-3.419	100.015	1.00 20.00
ATOM	2139	С	PRO	536	44.427		102.064	1.00 20.00
АТОМ	2140	0	PRO	536	44.167	-6.187		1.00 20.00
: 1	2141	N	GLU	537	44.390	-4.005	102.944	1.00 20.00 1.00 20.00
MOTA	2143	CA	GLU	537	43.977 44.378	-4.177 -2.999	104.307 105.211	1.00 20.00
ATOM	2144	CB	GLU GLU	537 537	45.885		105.478	1.00 20.00
ATOM	2145 2146	CG CD	GLU	537	46.253		106.397	1.00 20.00
ATOM ATOM	2140	OE1	GLU	537	45.370		107.186	1.00 20.00
ATOM	2148	OE2	GLÜ	537	47.420		106.324	1.00 20.00
ATOM	2149	С	GLU	537	42.503	-4.368	104.422	1.00 20.00
ATOM	2150	0	GLU	537	42.021	-5.109	105.278	1.00 20.00
ATOM	2151	N	CYS	538	41.750		103.557	1.00 20.00
ATOM	2153	CA	CYS	538	40.321		103.554	1.00 20.00
MOTA	2154	СВ	CYS	538	39.797		102.292	1.00 20.00
ATOM	2155	SG	CYS	538	37.999		102.127	1.00 20.00 1.00 20.00
ATOM	2156	C	CYS	538	39.911		103.539 102.854	1.00 20.00
MOTA	2157	0	CYS	538 539	40.518 38.889		102.834	1.00 60.00
ATOM	2158	N CA	LEU LEU	539	38.409		104.428	1.00 60.00
ATOM ATOM	2160 2161	CB	LEU	539	38.406	-7.409	105.860	1.00 60.00
ATOM	2162	CG	LEU	539	37.889	-8.855	105.959	1.00 60.00
ATOM	2163	CD1		539	38.825	-9.831	105.231	1.00 60.00
ATOM	2164	CD2		539	37.635	-9.253	107.421	1.00 60.00
ATOM	2165	С	LEU	539	36.994		103.954	1.00 60.00
ATOM	2166	0	LEU	539	36.240		104.147	1.00 60.00
MOTA	2167	N	PRO	540	36.662		103.289	1.00 60.00
ATOM	2168	CD	PRO	540	37.663		102.484	1.00 60.00 1.00 60.00
MOTA	2169	CA	PRO	540	35.343		102.736 101.512	1.00 60.00
ATOM	2170	CB	PRO	540 540	35.489 36.865		101.512	1.00 60.00
ATOM	2171 2172	CG C	PRO PRO	540	34.342		103.690	1.00 60.00
ATOM ATOM	2172	0	PRO	540	34.718		104.661	1.00 60.00
MOTA	2174	N	GLN	541	33.050		103.404	1.00 60.00
ATOM	2176	CA	GLN	541	31.990	-8.912	104.186	1.00 60.00
ATOM	2177	CB	GLN	541	30.807		104.410	1.00 60.00
ATOM	2178	CG	GLN	541	31.077		105.446	1.00 60.00
ATOM	2179	CD	GLN	541	31.039	-7.529	106.816	1.00 60.00
ATOM	2180	OE1		541	31.871	-8.379 -7.140	107.132	1.00 60.00 1.00 60.00
MOTA	2181		GLN	541		-7.140		1.00 60.00
MOTA	2184	С	GLN	541 541		-10.030		1.00 60.00
MOTA	2185 2186	O N	GLN ALA	542		-10.148		1.00 60.00
ATOM ATOM	2188	CA	ALA	542		-11.216		1.00 60.00
ATOM	2189	СВ	ALA	542		-11.108		1.00 60.00
ATOM	2190	С	ALA	542	30.081	-11.120	101.144	1.00 60.00
ATOM	2191	0	ALA	542		-12.127		1.00 60.00
MOTA	2192	N	MET	543	30.177			1.00 60.00
MOTA	2194	CA	MET	543	30.686	-9.713	99.290	1.00 60.00
MOTA	2195	CB	MET	543	30.785	-8.239	98.861	1.00 60.00 1.00 60.00
ATOM	2196	CG	MET	543	31.247 30.011	-8.054 -8.524	97.416 96.170	1.00 60.00
ATOM	2197	SD CE	MET MET	543 543	28.880	-7.154		1.00 60.00
MOTA ATOM	2198 2199	CE	MET	543		-10.297	99.248	1.00 60.00
ATOM	2200	0	MET	543		-10.610		1.00 60.00
ATOM	2201	N	ASN	544		-10.480	98.026	1.00 60.00
ATOM	2203	CA	ASN	544	33.905	-11.044	97.865	1.00 60.00
ATOM	2204	СВ	ASN	544		-11.292	96.389	1.00 60.00
ATOM	2205	CG	ASN	544	34.181	-9.971	95.639	1.00 60.00
MOTA	2206		ASN	544	35.191	-9.411	95.218	1.00 60.00
MOTA	2207		ASN	544	32.934	-9.453	95.470	1.00 60.00
MOTA	2210	C.	ASN	544		-10.129	98.468	1.00 60.00 1.00 60.00
ATOM	2211	0 N	ASN ILE	544 545		-10.570 -8.826	99.231 98.131	1.00 60.00
MOTA	2212	N	TUE	747	74.031	0.020	JU. 1J1	2.00 00.00

ATOM	2214	CA	ILE	545	35.738	-7.858	98.706	1.00 60.00	
MOTA	2215	СВ	ILE	545	36.858	-7.450	97.791	1.00 60.00	
АТОМ	2216	CG2	ILE	545	36.259	-6.690	96.596	1.00 60.00	
<i>i</i> 4	2217	CG1		545	37.926	-6.670	98.574	1.00 60.00	
ATOM	2218	CD1		545	38.669	-7.527	99.599	1.00 60.00	
MOTA	2219	С	ILE	545	34.872	-6.670	98.974	1.00 60.00	
MOTA	2220	0	ILE	545	34.027	-6.327	98.149	1.00 60.00	
MOTA	2221	N	THR	546	35.013		100.138	1.00 60.00	
MOTA	2223	CA	THR	546	34.063		100.276	1.00 60.00	
MOTA	2224	CB	THR	546	32.913		101.162	1.00 60.00	
MOTA	2225		THR	546	32.278 31.908		100.657 101.168	1.00 60.00	
MOTA	2227		THR THR	546 546	34.655		100.798	1.00 60.00	
MOTA	2228 2229	С 0	THR	546	35.273		101.862	1.00 60.00	
ATOM ATOM	2230	N	CYS	547	34.478		100.028	1.00 20.00	
ATOM	2232	CA	CYS	547	34.910		100.451	1.00 20.00	
ATOM	2233	CB	CYS	547	36.397		100.138	1.00 20.00	
ATOM	2234	SG	CYS	547	36.804	-0.821	98.370	1.00 20.00	
ATOM	2235	C	CYS	547	34.054	-0.301	99.741	1.00 20.00	
АТОМ	2236	0	CYS	547	33.714	-0.488	98.574	1.00 20.00	
ATOM	2237	N	THR	548	33.658	0.777	100.443	1.00 20.00	
ATOM	2239	CA	THR	548	32.823	1.753	99.812	1.00 20.00	
MOTA	2240	СВ	THR	548	32.286		100.761	1.00 20.00	
ATOM	2241	OG1	THR	548	31.326	3.597		1.00 20.00	
ATOM	2243	CG2	THR	548	33.444		101.295	1.00 20.00	
ATOM	2244	С	THR	548	33.588	2.446	98.731	1.00 20.00	
ATOM	2245	0	THR	548	33.071	2.659	97.635	1.00 20.00	
ATOM	2246	N	GLY	549	34.860	2.795	99.006	1.00 20.00	
ATOM	2248	CA	GLY	549	35.646	3.490	98.029 98.301	1.00 20.00 1.00 20.00	
ATOM	2249	С	GLY	549	37.075 37.389	3.158 2.474	99.273	1.00 20.00	
ATOM	2250	O N	GLY ARG	549 550	37.987	3.642	97.439	1.00 40.00	
ATOM ATOM	2251 2253	CA	ARG	550	39.369	3.329	97.635	1.00 40.00	
ATOM	2254	CB	ARG	550	40.252	3.660	96.418	1.00 40.00	
ATOM	2255	CG	ARG	550	40.302	5.146	96.055	1.00 40.00	
ATOM	2256	CD	ARG	550	40.796	5.399	94.628	1.00 40.00	
MOTA	2257	NE	ARG	550	41.174	6.836	94.522	1.00 40.00	
MOTA	2259	CZ	ARG	550	42.474	7.204	94.715	1.00 40.00	
ATOM	2260	NH1	ARG	550	43.427	6.249	94.930	1.00 40.00	
MOTA	2263	NH2		550	42.824	8.522	94.685	1.00 40.00	
MOTA	2266	С	ARG	550	39.863	4.106	98.812	1.00 40.00	
ATOM	2267	0	ARG	550	39.578	5.294	98.953	1.00 40.00	
АТОМ	2268	N	GLY	551	40.613	3.430	99.704 100.872	1.00 40.00 1.00 40.00	
ATOM	2270	CA	GLY	551 551	41.142 40.981		100.872	1.00 40.00	
MOTA	2271	C 0	GLY GLY	551	40.981		102.054	1.00 40.00	
ATOM ATOM	2272 2273	N	PRO	552	41.932		102.888	1.00 20.00	
MOTA	2274	CD	PRO	552	43.306		102.469	1.00 20.00	
ATOM	2275	CA	PRO	552	41.863		104.002	1.00 20.00	
ATOM	2276	СВ	PRO	552	43.276		104.570	1.00 20.00	
ATOM	2277	CG	PRO	552	44.168	2.400	103.355	1.00 20.00	
ATOM	2278	С	PRO	552	40.827		105.015	1.00 20.00	
ATOM	2279	0	PRO	552	40.513		105.877	1.00 20.00	
ATOM	2280	N	ASP	553	40.354		104.987	1.00 20.00	
MOTA	2282	CA	ASP	553	39.319		105.875	1.00 20.00	
MOTA	2283	СВ	ASP	553	39.206		105.947	1.00 20.00	
ATOM	2284	CG	ASP	553	38.294		107.117	1.00 20.00	
MOTA	2285		ASP	553	37.963		107.264	1.00 20.00	
MOTA	2286	OD2		553	37.920		107.883	1.00 20.00 1.00 20.00	
ATOM	2287	C	ASP	553 553	37.996 37.059		105.403 106.176	1.00 20.00	
ATOM	2288	O N	ASP ASN	55 <i>3</i>	37.059		104.081	1.00 20.00	
ATOM ATOM	2289 2291	N CA	ASN	554	36.688		103.405	1.00 20.00	
ATOM	2291	CB	ASN ASN	554	36.819		101.872	1.00 20.00	
WI OLI	2276	Ų.							

H A	2293	CG	ASN	554	36.906		101.440		20.00
ATOM	2294	OD1	ASN	554	36.433		100.361		20.00
M O π A	2295	ND2		554	37.526		102.283		20.00
i 4	2298	С	ASN	554	36.198		103.736		20.00
ATOM	2299	0	ASN	554	35.006		103.612 104.155		20.00
MOTA	2300	N	CYS	555 555	37.096 36.709		104.133		20.00
MOTA	2302	CA	CYS CYS	555	37.838		104.693		20.00
ATOM	2303 2304	CB SG	CYS	555	37.418		104.055		20.00
ATOM ATOM	2304	C	CYS	555	35.503		105.127	1.00	20.00
ATOM	2306	o	CYS	555	35.108		105.987	1.00	20.00
ATOM	2307	N	ILE	556	34.806	-1.877	104.783		20.00
MOTA	2309	CA	ILE	556	33.694		105.529		20.00
MOTA	2310	СВ	ILE	556	32.844		104.721		20.00
ATOM	2311	CG2	ILE	556	31.910		105.694		20.00
MOTA	2312	CG1		556	32.088		103.635		20.00
MOTA	2313	CD1		556	32.991		102.621		20.00
MOTA	2314	C	ILE	556	34.192 33.569		106.749 107.807		20.00
MOTA	2315	0	ILE	556 557	35.331		106.620		20.00
ATOM	2316	N CA	GLN GLN	557	35.888		107.717		20.00
ATOM	2318 2319	CB	GLN	557	35.398		107.749		20.00
MOTA MOTA	2320	CG	GLN	557	35.950		108.917	1.00	20.00
ATOM	2321	CD	GLN	557	35.315		110.194		20.00
ATOM	2322	OE1		557	35.729		110.735		20.00
АТОМ	2323	NE2	GLN	557	34.271		110.688		20.00
MOTA	2326	С	GLN	557	37.382		107.564		20.00
ATOM	2327	0	GLN	557	37.912		106.540		20.00
MOTA	2328	N	CYS	558	38.134		108.568		20.00
MOTA	2330	CA	CYS	558	39.559		108.413 109.577		20.00
ATOM	2331	CB	CYS	558 558	40.210 41.972		109.377		20.00
MOTA	2332	SG C	CYS CYS	558	40.134		108.333		20.00
ATOM ATOM	2333 2334	0	CYS	558	39.608		108.930		20.00
MOTA	2335	N	ALA	559	41.202		107.523		20.00
ATOM	2337	CA	ALA	559	41.859		107.368		20.00
MOTA	2338	CB	ALA	559	42.906		106.242		20.00
MOTA	2339	С	ALA	559	42.574		108.632		20.00
MOTA		0	ALA	559	42.555		109.090		20.00
MOTA	2341	N	HIS	560	43.214		109.234 110.413		20.00
MOTA	2343	CA	HIS	560 560	44.004 45.392		110.313		20.00
MOTA	2344 2345	CB CG	HIS HIS	560	46.258		109.265		20.00
ATOM ATOM	2345		HIS	560	47.279		109.413		20.00
ATOM	2347		HIS	560	46.127		107.907	1.00	20.00
MOTA	2349		HIS	560	47.068		107.307		20.00
ATOM	2350	NE2	HIS	560	47.792		108.180		20.00
ATOM	2352	С	HIS	560	43.278		111.530		20.00
MOTA	2353	0	HIS	560	42.187		111.915		20.00
ATOM	2354	N	TYR	561	43.886 43.280		112.101 113.218		20.00
MOTA	2356	CA	TYR	561 561	44.253		114.387		20.00
ATOM	2357	CB CG	TYR TYR	561	44.768		114.759		20.00
ATOM	2358 2359		TYR	561	45.838		114.078		20.00
MOTA MOTA	2360		TYR	561	46.328		114.398	1.00	20.00
ATOM	2361		TYR	561	44.182	-6.812	115.764		20.00
ATOM	2362	CE2		561	44.670		116.091		20.00
ATOM	2363	CZ	TYR	561	45.744		115.408		20.00
ATOM	2364	ОН	TYR	561	46.253		115.746		20.00
MOTA	2366	С	TYR	561	42.788		112.823		20.00
ATOM	2367	0	TYR	561	43.405		112.019		20.00
MOTA	2368	N	ILE	562	41.644		113.406		20.00
MOTA	2370	CA	ILE	562 562	41.077		113.085 113.043		20.00
MOTA	2371	CB	ILE	562	39.577	-1.318	113.043	1.00	

ATOM 2372 CC2 ILE 562 39.067 -0.478 112.787 1.00 20.00 ATOM 2373 CC1 ILE 562 39.067 -2.929 112.004 1.00 20.00 20.00 ATOM 2374 CD1 ILE 562 37.575 -3.238 112.135 1.00 20.00 20.00 ATOM 2375 C ILE 562 41.455 -0.963 114.180 1.00 20.00 ATOM 2377 N ASP 563 42.010 -0.207 113.817 1.00 20.00 ATOM 2379 CA ASP 563 42.010 -0.207 113.817 1.00 20.00 ATOM 2380 CB ASP 563 42.010 -0.207 113.817 1.00 20.00 ATOM 2380 CB ASP 563 42.010 -0.207 113.817 1.00 20.00 ATOM 2381 CG ASP 563 42.010 1.009 115.205 1.00 20.00 ATOM 2380 CB ASP 563 44.724 1.403 113.991 1.00 20.00 ATOM 2380 CD ASP 563 44.724 1.403 113.991 1.00 20.00 ATOM 2385 C ASP 563 44.203 1.239 112.847 1.00 20.00 ATOM 2385 C ASP 563 42.036 2.940 113.269 1.00 20.00 ATOM 2386 N GLY 564 41.419 3.312 115.279 1.00 20.00 ATOM 2388 C A GLY 564 41.419 3.312 115.279 1.00 20.00 ATOM 2388 C A GLY 564 40.994 4.620 114.891 1.00 20.00 ATOM 2389 C GLY 564 40.994 4.620 114.891 1.00 20.00 ATOM 2389 C GLY 564 40.994 4.620 114.891 1.00 20.00 ATOM 2390 C GLY 564 40.994 4.620 114.891 1.00 20.00 ATOM 2390 C GLY 564 40.994 4.620 114.891 1.00 20.00 ATOM 2391 N PRO 565 39.999 6.582 113.101 1.00 20.00 ATOM 2392 CD PRO 565 39.999 6.582 113.101 1.00 20.00 ATOM 2393 C G PRO 565 39.999 6.582 113.101 1.00 20.00 ATOM 2395 C PRO 565 39.999 6.582 113.101 1.00 20.00 ATOM 2395 C PRO 565 39.999 6.582 113.101 1.00 20.00 20.00 ATOM 2395 C PRO 565 39.999 A 4.835 111.684 1.00 20.00 ATOM 2397 C PRO 565 39.999 A 4.835 111.684 1.00 20.00 ATOM 2397 C PRO 565 39.999 A 4.835 111.684 1.00 20.00 ATOM 2397 C PRO 565 39.999 A 4.835 111.684 1.00 20.00 ATOM 2397 C PRO 565 39.999 A 4.835 111.694 1.00 20.00 ATOM 2397 C PRO 565 39.999 A 4.835 111.694 1.00 20.00 ATOM 2400 C PRO 565 39.999 A 4.835 111.694 1.00 20.00 ATOM 2400 C PRO 565 39.999 A 4.835 111.694 1.00 20.00 ATOM 2401 C PRO 565 39.999 A 4.835 111.694 1.00 20.00 ATOM 2401 C PRO 565 39.999 A 4.835 111.694 1.00 20.00 ATOM 2402 C PRO 565 39.999 A 4.835 111.694 1.00 20.00 ATOM 2402 C PRO 565 39.999 A 4.835 111.694 1.00 20.00 ATOM 2402 C PRO 565 39.999 A 4.835 111.694 1.00 20.00									
ATOM	MOTA	2372	CG2	ILE					
ATOM 2376 O ILE 562 41.281 -1.264 115.360 1.00 20.00 ATOM 2377 N ASP 563 42.010 0.207 113.817 1.00 20.00 ATOM 2380 CB ASP 563 42.010 0.207 113.817 1.00 20.00 ATOM 2381 CG ASP 563 44.724 1.003 113.981 1.00 20.00 ATOM 2382 ODI ASP 563 44.724 1.003 113.981 1.00 20.00 ATOM 2383 ODZ ASP 563 44.724 1.003 113.981 1.00 20.00 ATOM 2383 ODZ ASP 563 44.724 1.003 113.981 1.00 20.00 ATOM 2385 0 ASP 563 45.905 1.802 114.161 1.00 20.00 ATOM 2385 0 ASP 563 42.380 2.940 113.269 1.00 20.00 ATOM 2386 N GLY 564 40.994 4.620 114.891 1.00 20.00 ATOM 2389 C GLY 564 40.094 4.620 114.891 1.00 20.00 ATOM 2389 C GLY 564 40.094 4.620 114.891 1.00 20.00 ATOM 2389 C GLY 564 40.094 4.620 114.891 1.00 20.00 ATOM 2393 N RD 565 40.053 5.164 112.786 1.00 20.00 ATOM 2393 C RD FO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2393 C RD FO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2393 C RD FO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2395 CG PRO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2395 CG PRO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2395 CG PRO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2395 CG PRO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2395 CG PRO 565 39.993 4.835 111.684 1.00 20.00 ATOM 2397 C RD FO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2397 C RD FO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2397 C RD FO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2404 ND HIS 566 41.815 3.590 110.938 1.00 20.00 ATOM 2407 C RD HIS 566 41.815 3.591 110.684 1.00 20.00 ATOM 2407 C RD HIS 566 41.815 3.591 110.694 1.00 20.00 ATOM 2407 CR HIS 566 41.815 3.591 110.898 1.00 20.00 ATOM 2407 CR HIS 566 41.815 3.591 110.898 1.00 20.00 ATOM 2407 CR HIS 566 41.815 3.591 110.898 1.00 20.00 ATOM 2407 CR HIS 566 41.815 3.591 110.898 1.00 20.00 ATOM 2401 CR HIS 566 41.815 3.591 110.898 1.00 20.00 ATOM 2401 CR HIS 566 41.815 3.591 110.898 1.00 20.00 ATOM 2402 CR HIS 566 41.815 3.591 110.896 1.00 20.00 ATOM 2403 CR HIS 566 41.815 3.591 110.896 1.00 20.00 ATOM 2401 CR HIS 566 41.815 3.591 110.896 1.00 20.00 ATOM 2402 CR HIS 566 41.815 3.591 110.896 1.00 20.00 ATOM 2402 CR HIS 566 41.815						_			
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ATOM 2386 N							2.940	113.269	1.00 20.00
ATOM 2388 CA GLY 564 40.994 4.620 114.891 1.00 20.00 ATOM 2390 C GLY 564 40.076 4.323 131.755 1.00 20.00 ATOM 2391 N PRO 565 40.053 5.164 112.786 1.00 20.00 ATOM 2392 CD PRO 565 39.999 6.582 113.111 1.00 20.00 ATOM 2393 CA PRO 565 39.193 4.835 111.684 1.00 20.00 ATOM 2395 CG PRO 565 38.720 6.167 111.103 1.00 20.00 ATOM 2395 CG PRO 565 38.849 7.155 112.272 1.00 20.00 ATOM 2395 CG PRO 565 39.914 4.021 110.669 1.00 20.00 ATOM 2395 CG PRO 565 39.914 4.021 110.669 1.00 20.00 ATOM 2397 CG PRO 565 39.914 4.021 110.669 1.00 20.00 ATOM 2398 N HIS 566 41.161 3.590 110.938 1.00 20.00 ATOM 2400 CA HIS 566 41.161 3.590 110.938 1.00 20.00 ATOM 2402 CG HIS 566 41.857 2.923 109.880 1.00 20.00 ATOM 2402 CG HIS 566 43.183 4.857 108.927 1.00 20.00 ATOM 2404 NDI HIS 566 43.183 4.857 108.927 1.00 20.00 ATOM 2404 NDI HIS 566 43.183 4.857 108.927 1.00 20.00 ATOM 2406 CEI HIS 566 43.183 4.857 108.927 1.00 20.00 ATOM 2407 NEE HIS 566 42.052 1.463 110.093 1.00 20.00 ATOM 2410 N HIS 566 42.052 1.463 110.093 1.00 20.00 ATOM 2411 N CYS 567 42.132 0.741 108.961 1.00 20.00 ATOM 2411 N CYS 567 42.132 0.741 108.961 1.00 20.00 ATOM 2412 CA CYS 567 42.132 0.741 108.961 1.00 20.00 ATOM 2413 CA CYS 567 42.132 0.741 108.961 1.00 20.00 ATOM 2414 CB CYS 567 42.132 0.741 108.961 1.00 20.00 ATOM 2415 SG CYS 567 42.066 -3.090 107.483 1.00 20.00 ATOM 2416 N VAL 568 46.459 -0.634 111.294 1.00 20.00 ATOM 2423 CG VAL 568 46.189 -0.634 111.294 1.00 20.00 ATOM 2422 CG VAL 568 46.189 -0.634 111.294 1.00 20.00			N		564	41.419	3.312	115.279	1.00 20.00
ATOM 2391 N PRO 565 40.053 5.164 112.786 1.00 20.00 ATOM 2392 CD PRO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2393 CA PRO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2393 CA PRO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2395 CG PRO 565 38.720 6.167 111.103 1.00 20.00 ATOM 2396 C PRO 565 38.849 7.155 112.272 1.00 20.00 ATOM 2396 C PRO 565 38.849 7.155 112.272 1.00 20.00 ATOM 2397 O PRO 565 39.914 4.021 110.669 1.00 20.00 ATOM 2398 N HIS 566 41.161 3.590 110.938 1.00 20.00 ATOM 2398 N HIS 566 41.161 3.590 110.938 1.00 20.00 ATOM 2400 CA HIS 566 41.857 2.923 109.880 1.00 20.00 ATOM 2401 CB HIS 566 43.183 4.857 108.927 1.00 20.00 ATOM 2402 CG HIS 566 43.183 4.857 108.927 1.00 20.00 ATOM 2403 CD2 HIS 566 43.183 4.857 108.927 1.00 20.00 ATOM 2404 ND1 HIS 566 43.342 6.056 109.584 1.00 20.00 ATOM 2406 CE1 HIS 566 43.183 7.00 8.056 109.584 1.00 20.00 ATOM 2409 C HIS 566 42.955 6.547 107.494 1.00 20.00 ATOM 2409 C HIS 566 42.955 6.547 107.494 1.00 20.00 ATOM 2409 C HIS 566 42.955 6.547 107.494 1.00 20.00 ATOM 2409 C HIS 566 42.955 6.547 107.499 1.00 20.00 ATOM 2401 ND HIS 566 42.131 0.968 111.216 1.00 20.00 ATOM 2401 ND HIS 566 42.131 0.968 111.216 1.00 20.00 ATOM 2410 ND HIS 566 42.131 0.968 111.216 1.00 20.00 ATOM 2411 N CYS 567 42.132 0.741 108.965 1.00 20.00 ATOM 2411 N CYS 567 42.132 0.741 108.965 1.00 20.00 ATOM 2418 N CYS 567 42.132 0.741 108.965 1.00 20.00 ATOM 2418 N VAL 568 44.384 -1.275 10.017 1.00 20.00 ATOM 2418 N VAL 568 45.807 -1.419 110.192 1.00 20.00 ATOM 2418 N VAL 568 46.188 0.853 111.019 1.00 20.00 ATOM 2418 N VAL 568 46.188 0.853 111.019 1.00 20.00 ATOM 2422 CG1 VAL 568 46.188 0.853 111.019 1.00 20.00 ATOM 2423 CG2 VAL 568 46.188 0.853 111.019 1.00 20.00 ATOM 2424 C VAL 568 46.188 0.853 111.019 1.00 20.00 ATOM 2428 CA VAL 568 46.188 0.853 111.019 1.00 20.00 ATOM 2428 CA VAL 569 47.951 -4.488 109.640 1.00 20.00 ATOM 2428 CA VAL 569 569 51.739 -4.059 108.741 1.00 20.00 0.00 ATOM 2428 CA LYS 569 51.739 -4.059 108.741 1.00 20.00 0.00 ATOM 2428 CA LYS 569 51.739 -4.059 108.741 1.00 20.00 0.00 ATOM 2431 CD LYS		2388	CA	GLY	564	40.994	4.620	114.891	1.00 20.00
ATOM 2391 N PRO 565	MOTA	2389	С	GLY	564	40.076			
ATOM 2392 CD PRO 565 39.999 6.582 113.110 1.00 20.00 ATOM 2393 CA PRO 565 39.193 4.835 111.684 1.00 20.00 ATOM 2394 CB PRO 565 38.720 6.167 111.103 1.00 20.00 ATOM 2395 CG PRO 565 38.720 6.167 111.103 1.00 20.00 ATOM 2396 C PRO 565 39.914 4.021 110.669 1.00 20.00 ATOM 2397 O PRO 565 39.330 3.776 109.616 1.00 20.00 ATOM 2398 N HIS 566 41.161 3.590 110.938 1.00 20.00 ATOM 2400 CA HIS 566 41.857 2.923 109.880 1.00 20.00 ATOM 2402 CG HIS 566 43.245 3.513 109.586 1.00 20.00 ATOM 2402 CG HIS 566 43.245 3.513 109.586 1.00 20.00 ATOM 2402 CG HIS 566 43.183 4.857 108.927 1.00 20.00 ATOM 2404 ND1 HIS 566 43.183 4.857 108.927 1.00 20.00 ATOM 2404 ND1 HIS 566 43.183 4.857 108.927 1.00 20.00 ATOM 2406 CE1 HIS 566 43.189 7.033 108.654 1.00 20.00 ATOM 2407 NE2 HIS 566 42.946 5.175 107.625 1.00 20.00 ATOM 2407 NE2 HIS 566 42.955 6.547 107.449 1.00 20.00 ATOM 2401 O HIS 566 42.052 1.463 110.093 1.00 20.00 ATOM 2411 N CYS 567 42.132 0.741 108.961 1.00 20.00 ATOM 2411 N CYS 567 42.132 0.741 108.965 1.00 20.00 ATOM 2411 N CYS 567 42.132 0.741 108.965 1.00 20.00 ATOM 2411 N CYS 567 42.132 0.741 108.965 1.00 20.00 ATOM 2415 NG CYS 567 42.335 -0.671 108.965 1.00 20.00 ATOM 2416 C CYS 567 42.335 -0.671 108.965 1.00 20.00 ATOM 2416 C CYS 567 42.335 -0.671 108.965 1.00 20.00 ATOM 2416 C CYS 567 42.335 -0.671 108.965 1.00 20.00 ATOM 2416 C CYS 567 42.335 -0.671 108.965 1.00 20.00 ATOM 2416 C CYS 567 42.348 -0.684 108.966 1.00 20.00 ATOM 2416 C CYS 567 43.819 -0.844 108.966 1.00 20.00 ATOM 2416 C CYS 567 43.819 -0.844 108.966 1.00 20.00 ATOM 2416 C CYS 567 44.481 -0.582 107.963 1.00 20.00 ATOM 2420 CA VAL 568 45.807 -1.419 110.192 1.00 20.00 ATOM 2421 CB VAL 568 45.807 -1.419 110.192 1.00 20.00 ATOM 2422 CG VAL 568 45.432 -3.715 110.728 1.00 20.00 ATOM 2423 CG2 VAL 568 45.432 -3.715 110.728 1.00 20.00 ATOM 2428 CA VAL 568 45.432 -3.715 110.728 1.00 20.00 ATOM 2428 CA VAL 568 45.432 -3.715 110.728 1.00 20.00 ATOM 2428 CA VAL 568 45.432 -3.715 110.728 1.00 20.00 ATOM 2428 CA VAL 568 45.432 -3.715 110.728 1.00 20.00 ATOM 2428 CA LYS 569 51.9	ATOM	2390	0	GLY					
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ATOM 2416 C CYS 567						42.066	-3.090	107.483	1.00 20.00
ATOM 2417 O CYS 567 44.481 -0.582 107.963 1.00 20.00 ATOM 2418 N VAL 568 44.384 -1.275 110.117 1.00 20.00 ATOM 2420 CA VAL 568 45.807 -1.419 110.192 1.00 20.00 ATOM 2421 CB VAL 568 46.459 -0.634 111.294 1.00 20.00 ATOM 2422 CG1 VAL 568 47.967 -0.920 111.276 1.00 20.00 ATOM 2423 CG2 VAL 568 46.188 0.853 111.019 1.00 20.00 ATOM 2424 C VAL 568 46.188 0.853 111.019 1.00 20.00 ATOM 2425 O VAL 568 46.191 -2.866 110.262 1.00 20.00 ATOM 2426 N LYS 569 47.374 -3.176 109.694 1.00 20.00 ATOM 2428 CA LYS 569 47.374 -3.176 109.694 1.00 20.00 ATOM 2429 CB LYS 569 49.216 -4.537 108.767 1.00 20.00 ATOM 2430 CG LYS 569 50.380 -3.748 109.372 1.00 20.00 ATOM 2431 CD LYS 569 51.739 -4.059 108.741 1.00 20.00 ATOM 2432 CE LYS 569 51.739 -4.059 108.741 1.00 20.00 ATOM 2433 NZ LYS 569 51.739 -4.059 108.741 1.00 20.00 ATOM 2433 NZ LYS 569 51.942 -3.094 106.869 1.00 20.00 ATOM 2433 NZ LYS 569 53.302 -3.698 106.869 1.00 20.00 ATOM 2437 C LYS 569 48.373 -4.943 111.002 1.00 20.00 ATOM 2438 O LYS 569 48.373 -4.943 111.002 1.00 20.00 ATOM 2438 O LYS 569 48.373 -4.943 111.002 1.00 20.00 ATOM 2439 N THR 570 48.869 -4.007 111.834 1.00 20.00 ATOM 2441 CA THR 570 48.869 -4.007 111.834 1.00 20.00 ATOM 2441 CA THR 570 48.869 -4.007 111.834 1.00 20.00 ATOM 2442 CB THR 570 51.085 -5.522 114.500 1.00 20.00 ATOM 2443 OG1 THR 570 51.085 -5.522 114.500 1.00 20.00 ATOM 2445 CG2 THR 570 51.560 -3.385 113.022 1.00 20.00 ATOM 2445 CG2 THR 570 51.560 -3.385 113.022 1.00 20.00 ATOM 2445 CG2 THR 570 51.560 -3.385 113.022 1.00 20.00 ATOM 2446 C THR 570 51.560 -3.385 113.022 1.00 20.00 ATOM 2446 C THR 570 51.560 -3.385 113.022 1.00 20.00 ATOM 2447 O THR 570 49.043 -3.196 114.041 1.00 20.00			С	CYS	567	43.819			
ATOM 2420 CA VAL 568 45.807 -1.419 110.192 1.00 20.00 ATOM 2421 CB VAL 568 46.459 -0.634 111.294 1.00 20.00 ATOM 2422 CG1 VAL 568 47.967 -0.920 111.276 1.00 20.00 ATOM 2423 CG2 VAL 568 46.188 0.853 111.019 1.00 20.00 ATOM 2424 C VAL 568 46.188 0.853 111.019 1.00 20.00 ATOM 2425 O VAL 568 46.191 -2.866 110.262 1.00 20.00 ATOM 2426 N LYS 569 47.374 -3.176 109.694 1.00 20.00 ATOM 2428 CA LYS 569 47.951 -4.488 109.640 1.00 20.00 ATOM 2429 CB LYS 569 49.216 -4.537 108.767 1.00 20.00 ATOM 2430 CG LYS 569 50.380 -3.748 109.372 1.00 20.00 ATOM 2431 CD LYS 569 51.739 -4.059 108.741 1.00 20.00 ATOM 2432 CE LYS 569 51.739 -4.059 108.741 1.00 20.00 ATOM 2433 NZ LYS 569 51.942 -3.404 107.375 1.00 20.00 ATOM 2433 NZ LYS 569 53.302 -3.698 106.869 1.00 20.00 ATOM 2437 C LYS 569 48.373 -4.943 111.002 1.00 20.00 ATOM 2438 O LYS 569 48.373 -4.943 111.002 1.00 20.00 ATOM 2438 O LYS 569 48.373 -4.943 111.002 1.00 20.00 ATOM 2438 O LYS 569 48.373 -4.943 111.002 1.00 20.00 ATOM 2439 N THR 570 48.869 -4.007 111.834 1.00 20.00 ATOM 2431 CA THR 570 49.301 -4.370 113.153 1.00 20.00 ATOM 2441 CA THR 570 49.301 -4.370 113.153 1.00 20.00 ATOM 2442 CB THR 570 50.768 -4.685 113.237 1.00 20.00 ATOM 2445 CG2 THR 570 51.085 -5.252 114.500 1.00 20.00 ATOM 2445 CG2 THR 570 51.560 -3.385 113.022 1.00 20.00 ATOM 2445 CG2 THR 570 51.560 -3.385 113.022 1.00 20.00 ATOM 2446 C THR 570 49.043 -3.196 114.041 1.00 20.00 ATOM 2447 O THR 570 48.887 -2.073 113.571 1.00 20.00	MOTA	2417	0	CYS					
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ATOM 2429 CB LYS 569									1.00 20.00
ATOM 2431 CD LYS 569 51.739 -4.059 108.741 1.00 20.00 ATOM 2432 CE LYS 569 51.942 -3.404 107.375 1.00 20.00 ATOM 2433 NZ LYS 569 53.302 -3.698 106.869 1.00 20.00 ATOM 2438 O LYS 569 48.373 -4.943 111.002 1.00 20.00 ATOM 2439 N THR 570 48.869 -4.007 111.834 1.00 20.00 ATOM 2441 CA THR 570 49.301 -4.370 113.153 1.00 20.00 ATOM 2442 CB THR 570 50.768 -4.685 113.237 1.00 20.00 ATOM 2443 OG1 THR 570 50.768 -4.685 113.237 1.00 20.00 ATOM 2445 CG2 THR 570 51.085 -5.252 114.500 1.00 20.00 ATOM 2446 C THR 570 49.043 -3.196 114.041 1.00 20.00 ATOM 2447 O THR 570 48.887 -2.073 113.571 1.00 20.00						49.216	-4.537	108.767	1.00 20.00
ATOM 2432 CE LYS 569 51.942 -3.404 107.375 1.00 20.00 ATOM 2433 NZ LYS 569 53.302 -3.698 106.869 1.00 20.00 ATOM 2437 C LYS 569 48.373 -4.943 111.002 1.00 20.00 ATOM 2438 O LYS 569 48.320 -6.133 111.312 1.00 20.00 ATOM 2439 N THR 570 48.869 -4.007 111.834 1.00 20.00 ATOM 2441 CA THR 570 49.301 -4.370 113.153 1.00 20.00 ATOM 2442 CB THR 570 50.768 -4.685 113.237 1.00 20.00 ATOM 2443 OG1 THR 570 51.085 -5.252 114.500 1.00 20.00 ATOM 2445 CG2 THR 570 51.560 -3.385 113.022 1.00 20.00 ATOM 2446 C THR 570 49.043 -3.196 114.041 1.00 20.00 ATOM 2447 O THR 570 48.887 -2.073 113.571 1.00 20.00	MOTA	2430	CG	LYS	569	50.380			
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ATOM 2448 N CYS 571 49.001 -3.415 115.365 1.00 20.00			0						
	MOTA	2448	N	CYS	571	49.001	-3.415	115.365	1.00 20.00

M	2450	CA	CYS	571	48.677	-2.326	116.236		20.00	
ALOM	2451	CB	CYS	571	48.297		117.655		20.00	
MOTA	2452	SG	CYS	571	46.798		117.635		20.00	
i 1	2453	С	CYS	571	49.804		116.339		20.00	
MO'LY	2454	0	CYS	571	50.985		116.291		20.00	
MOTA	2455	N	PRO	572	49.410		116.467		20.00	
MOTA	2456	CD	PRO	572	48.187		115.816		20.00	
MOTA	2457	CA	PRO	572	50.361		116.601		20.00	
ATOM	2458	CB	PRO	572	49.585		116.339		20.00	
ATOM	2459	CG	PRO	572	48.435		115.422		20.00	
MOTA	2460	C	PRO	572	50.958		117.971 118.840		20.00	
ATOM	2461	0	PRO	572 573	50.380 52.112		118.188		20.00	
ATOM	2462	N	ALA	573 573	52.753		119.469		20.00	
ATOM	2464	CA CB	ALA ALA	573	54.133		119.501		20.00	
MOTA	2465 2466	СВ	ALA	573			120.503		20.00	
ATOM ATOM	2467	0	ALA	573	51.194		120.229		20.00	
ATOM	2468	N	GLY	574	51.916		121.729		20.00	
ATOM	2470	CA	GLY	574	51.186		122.834	1.00	20.00	
ATOM	2471	C	GLY	574	49.808		122.845	1.00	20.00	
ATOM	2472	0	GLY	574	49.070	1.709	123.817	1.00	20.00	
ATOM	2473	N	VAL	575	49.425	0.868	121.753	1.00	20.00	
MOTA	2475	CA	VAL	575	48.121		121.693		20.00	
MOTA	2476	CB	VAL	575	47.314		120.509		20.00	
ATOM	2477	CG1	VAL	575	46.002		120.470		20.00	
MOTA	2478	CG2	VAL	575	47.105		120.612		20.00	
ATOM	2479	С	VAL	575	48.343		121.542		20.00	
MOTA	2480	0	VAL	575	49.335		120.954		20.00	
MOTA	2481	N	MET	576	47.427		122.094		20.00	
ATOM	2483	CA	MET	576		-3.428			20.00	
ATOM	2484	CB	MET	576	47.818 48.045		123.311 123.110		20.00	
ATOM	2485	CG	MET MET	576 576	49.614		122.282		20.00	
ATOM	2486	SD CE	MET	576	49.204		121.961		20.00	
ATOM ATOM	2487 2488	CE	MET	576	46.416		121.335		20.00	
ATOM	2489	0	MET	576	45.309		121.390		20.00	
ATOM	2490	N	GLY	577	46.635		120.684		20.00	
ATOM	2492	CA	GLY	577	45.556		120.037	1.00	20.00	
ATOM	2493		GLY	577	44.786		121.098	1.00	20.00	
MOTA	2494	0	GLY	577	45.342		121.898		20.00	
MOTA	2495	N	GLU	578	43.466		121.130		40.00	
ATOM	2497	CA	GLU	578	42.669		122.105		40.00	
MOTA	2498	CB	GLU	578	41.196		122.069		40.00	
MOTA	2499	CG	GLU	578	40.554		120.691		40.00	
MOTA	2500	CD	GLU	578	39.200		120.734 121.862		40.00	
MOTA	2501	OE1		578	38.692		119.638		40.00	
ATOM	2502	OE2		578 570	38.658 42.767		121.768		40.00	
ATOM	2503	С	GLU GLU	578 578	42.470		120.643		40.00	
ATOM	2504 2505	O N	ASN	579	43.221	-9.250			40.00	
ATOM ATOM	2507	CA	ASN	579		-10.652			40.00	
ATOM	2508	CB	ASN	579		-11.428			40.00	
ATOM	2509	CG	ASN	579		-11.027			40.00	
ATOM	2510	OD1		579		-11.102		1.00	40.00	
ATOM	2511	ND2		579		-10.587			40.00	
ATOM	2514	С	ASN	579		-11.186			40.00	
ATOM	2515	0	ASN	579	41.839	-11.805	121.113		40.00	
ATOM	2516	N	ASN	580	41.051	-10.939	123.042		60.00	
ATOM	2518	CA	ASN	580		-11.401			60.00	
MOTA	2519	СВ	ASN	580		-12.684			60.00	
MOTA	2520	CG	ASN	580		-13.837			60.00	
ATOM	2521	OD1		580		-14.129			60.00	
MOTA	2522	ND2		580		-14.516			60.00	
ATOM	2525	С	ASN	580	38.812	-10.328	123.263	1.00	60.00	

to go

ATOM	2526	0	ASN	580	39.232	-9.411	123.968	1.00 60.00
ATOM	2527	N	THR	581	37.530	-10,406	122.869	1.00 60.00
ATOM	2529	CA	THR	581	36.598	-9.428	123.333	1.00 60.00
i 4	2530	СВ	THR	581	35.565	-9.040	122.316	1.00 60.00
ATOM	2531	OG1	THR	581	36.188	-8.483	121.168	1.00 60.00
ATOM	2533	CG2	THR	581	34.606	-8.019	122.953	1.00 60.00
ATOM	2534	С	THR	581	35.871	-10.061	124.467	1.00 60.00
ATOM	2535	Ō	THR	581	35.253	-11.113	124.311	1.00 60.00
ATOM	2536	N	LEU	582	35.949		125.656	1.00 60.00
ATOM	2538	CA	LEU	582	35.234	-9.983	126.768	1.00 60.00
ATOM	2539	CB	LEU	582	35.778		128.134	1.00 60.00
ATOM	2540	CG	LEU	582	35.012	-10.111		1.00 60.00
ATOM	2541		LEU	582	35.132	-11.644	129.400	1.00 60.00
ATOM	2542		LEU	582	35.449	-9.427	130.643	1.00 60.00
ATOM	2543	C	LEU	582	33.850	-9.457	126.615	1.00 60.00
ATOM	2544	0	LEU	582	33.652		126.247	1.00 60.00
	2545	N	VAL	583		-10.305		1.00 60.00
ATOM	2545 2547	CA	VAL	583	31.499		126.695	1.00 60.00
MOTA		CB	VAL	583	30.462	-10.907		1.00 60.00
MOTA	2548 ⁻	CG1	VAL	583	29.073	-10.265	126.789	1.00 60.00
ATOM	2549	CG1	VAL	583	30.715	-12.079	125.980	1.00 60.00
MOTA	2550		VAL	583	31.241	-8.720	127.629	1.00 60.00
ATOM	2551	C		583	31.685		128.776	1.00 60.00
ATOM	2552	0	VAL	584	30.519		127.128	1.00 60.00
MOTA	2553	N	TRP	584	30.185		127.120	1.00 60.00
ATOM	2555	CA	TRP		31.011	-5.309		1.00 60.00
MOTA	2556	CB	TRP	584	30.852		128.493	1.00 60.00
MOTA	2557	CG	TRP	584		-2.948	128.430	1.00 60.00
MOTA	2558	CD2	TRP	584	31.646	-2.340		1.00 60.00
MOTA	2559	CE2	TRP	584	31.259		127.561	1.00 60.00
MOTA	2560	CE3	TRP	584	32.627		127.501	1.00 60.00
ATOM	2561	CD1		584	30.038	-4.008 -2.799	130.191	1.00 60.00
MOTA	2562	NE1		584	30.266		129.710	1.00 60.00
MOTA	2564	CZ2	TRP	. 584	31.844	-0.923 -1.337	127.780	1.00 60.00
MOTA	2565	CZ3	TRP	584	33.218	-0.533	128.833	1.00 60.00
MOTA	2566	CH2	TRP	584	32.833			1.00 60.00
MOTA	2567	C	TRP	584	28.765		127.534 127.193	1.00 60.00
MOTA	2568	0	TRP	584	28.044	-7.238	127.193	1.00 60.00
MOTA	2569	N	LYS	585	28.305		127.002	1.00 60.00
MOTA	2571	CA	LYS	585	26.959			1.00 60.00
MOTA	2572	CB	LYS	585	26.533		127.263 128.696	1.00 60.00
ATOM	2573	CG	LYS	585	26.441		128.778	1.00 60.00
ATOM	2574	CD	LYS	585	26.260		127.914	1.00 60.00
MOTA	2575	CE	LYS	585	27.256			1.00 60.00
ATOM	2576	ΝZ	LYS	585	28.639		128.280 125.739	1.00 60.00
MOTA	2580	C	LYS	585	26.950		125.287	1.00 60.00
MOTA	2581	0	LYS	585 506	26.086		124.988	1.00 60.00
ATOM	2582	N	TYR	586	27.950		123.609	1.00 60.00
ATOM	2584	CA	TYR	586	28.085		122.638	1.00 60.00
MOTA	2585	CB	TYR	586	27.690		122.030	1.00 60.00
MOTA	2586	CG	TYR	586	28.454		122.545	1.00 60.00
ATOM	2587		TYR	586	29.742		122.848	1.00 60.00
MOTA	2588	CE1		586	30.421			1.00 60.00
MOTA	2589	CD2		586	27.853		123.734	1.00 60.00
MOTA	2590	CE2		586	28.527		124.039	
MOTA	2591	CZ	TYR	586	29.814		123.594	1.00 60.00
ATOM	2592	OH	TYR	586	30.511		123.910	1.00 60.00
MOTA	2594	С	TYR	586	29.514		123.390	1.00 60.00
MOTA	2595	0	TYR	586	30.384		124.192	1.00 60.00
MOTA	2596	N	ALA	587	29.789		122.299	1.00 60.00
MOTA	2598	CA	ALA	587	31.126		122.057	1.00 60.00
MOTA	2599	СВ	ALA	587	31.191		121.539	1.00 60.00
MOTA	2600	С	ALA	587	31.792		121.035	1.00 60.00
ATOM	2601	0	ALA	587	31.219		120.541	1.00 60.00
ATOM	2602	N	ASP	588	33.053	-6.109	120.713	1.00 60.00

No. 2604 C.A. ASP 588 33.809 -5.378 119.742 1.00 60.00											
ATOM	M	2604	CA	ASP					•		
1	A.JM	2605	CB	ASP							
ATOM 2608 ODZ ASP 588 36.148 -4.754 122.286 1.00 60.00 ATOM 2610 O ASP 588 33.720 -6.146 118.473 1.00 60.00 ATOM 2611 N ALIA 589 33.720 -6.146 118.473 1.00 60.00 ATOM 2613 CA ALIA 589 33.704 -6.126 116.067 1.00 60.00 ATOM 2613 CA ALIA 589 33.704 -6.126 116.067 1.00 60.00 ATOM 2615 C ALIA 589 33.704 -6.126 116.067 1.00 60.00 ATOM 2616 C ALIA 589 33.708 -5.442 117.305 1.00 60.00 ATOM 2617 N GLY 590 35.061 -6.195 115.455 1.00 60.00 ATOM 2617 N GLY 590 35.829 -7.298 114.730 1.00 60.00 ATOM 2610 O ALIA 589 35.084 -5.296 115.622 1.00 60.00 ATOM 2610 O ALIA 589 35.884 -5.296 115.622 1.00 60.00 ATOM 2610 O GLY 590 36.583 -7.458 114.088 1.00 60.00 ATOM 2620 C GLY 590 37.680 -7.372 115.064 1.00 60.00 ATOM 2621 O GLY 590 37.680 -7.372 115.064 1.00 60.00 ATOM 2620 C GLY 590 37.499 -7.336 116.299 1.00 60.00 ATOM 2621 N HIS 591 40.055 -7.246 115.456 1.00 60.00 ATOM 2625 C B HIS 591 40.055 -7.246 115.456 1.00 60.00 ATOM 2626 C G HIS 591 40.055 -7.246 115.456 1.00 60.00 ATOM 2627 C D2 HIS 591 40.894 -9.768 113.16 1.00 60.00 ATOM 2628 NDI HIS 591 40.894 -9.768 113.16 1.00 60.00 ATOM 2620 C GLY 590 37.499 -7.336 114.491 1.00 60.00 ATOM 2630 C HIS 591 40.895 -7.246 115.456 1.00 60.00 ATOM 2631 N EZ HIS 591 40.895 -7.246 115.456 1.00 60.00 ATOM 2631 N EZ HIS 591 40.895 -9.768 113.16 1.00 60.00 ATOM 2632 C HIS 591 40.895 -9.768 113.196 1.00 60.00 ATOM 2631 N EZ HIS 591 40.895 -9.768 113.196 1.00 60.00 ATOM 2631 C HIS 591 40.895 -9.768 113.197 1.00 60.00 ATOM 2631 N EZ HIS 591 40.895 -9.768 113.197 1.00 60.00 ATOM 2631 N EZ HIS 591 40.895 -9.768 113.197 1.00 60.00 ATOM 2631 N EZ HIS 591 40.895 -9.399 115.240 1.00 60.00 ATOM 2631 N EZ HIS 591 40.895 -9.768 113.197 1.00 60.00 ATOM 2631 N EZ HIS 591 40.895 -9.399 115.20 1.00 60.00 ATOM 2630 C HIS 591 40.295 -9.292 114.411 1.00 60.00 ATOM 2641 C VAL 592 39.887 -1.741 11.771 11.40 14.00 60.00 ATOM 2650 N HIS 591 40.295 -9.292 114.41 11.00 60.00 ATOM 2650 N EX HIS 594 40.755 -9.289 114.699 1.00 00.00 ATOM 2650 C VAL 592 39.887 -1.741 117.881 10.00 00.00 ATOM 2650 C R HIS 594 40.756 -9.393	ATOM	2606									
Archine											
ATOM 2610 0 ASP 588 33.563 -7.366 118.473 1.00 60.00 60.00 ATOM 2611 N ALA 589 33.802 -7.366 118.473 1.00 60.00 60.00 ATOM 2611 N ALA 589 33.802 -5.442 117.320 1.00 60.00 60.00 ATOM 2615 C ALA 589 33.802 -7.26 116.067 1.00 60.00 60.00 ATOM 2615 C ALA 589 35.061 -6.195 115.453 1.00 60.00 60.00 ATOM 2616 O ALA 589 35.804 -6.226 115.453 1.00 60.00 60.00 ATOM 2617 N GLY 590 35.804 -7.298 114.730 1.00 60.00 60.00 ATOM 2617 N GLY 590 35.804 -7.298 114.730 1.00 60.00 60.00 ATOM 2619 CA GLY 590 37.680 -7.372 115.652 1.00 60.00 60.00 ATOM 2620 C GLY 590 37.680 -7.372 115.641 1.00 60.00 ATOM 2621 O GLY 590 37.680 -7.372 115.641 1.00 60.00 ATOM 2622 N HIS 591 38.932 -7.335 114.574 1.00 60.00 ATOM 2622 N HIS 591 40.055 -7.246 115.454 1.00 60.00 ATOM 2625 CB HIS 591 41.328 -7.299 114.471 1.00 60.00 ATOM 2626 CG HIS 591 41.328 -7.299 114.471 1.00 60.00 ATOM 2626 CG HIS 591 41.328 -7.299 114.411 1.00 60.00 ATOM 2630 CEL HIS 591 40.884 -9.768 113.156 1.00 60.00 ATOM 2630 CEL HIS 591 40.885 -9.768 113.156 1.00 60.00 ATOM 2630 CEL HIS 591 40.885 -9.768 113.471 11.449 1.00 60.00 ATOM 2631 NEZ HIS 591 40.885 -11.471 11.444 1.00 60.00 ATOM 2631 NEZ HIS 591 40.885 -11.471 11.444 1.00 60.00 ATOM 2631 NEZ HIS 591 40.885 -11.471 11.444 1.00 60.00 ATOM 2631 NEZ HIS 591 40.885 -11.471 11.444 1.00 60.00 ATOM 2631 NEZ HIS 591 40.885 -11.471 11.449 1.00 60.00 ATOM 2631 NEZ HIS 591 40.885 -11.471 11.449 1.00 60.00 ATOM 2631 NEZ HIS 591 40.885 -13.471 11.449 1.00 60.00 ATOM 2631 NEZ HIS 591 40.885 -13.471 11.449 1.00 60.00 ATOM 2631 NEZ HIS 591 40.885 -13.471 11.449 1.00 60.00 ATOM 2631 NEZ HIS 591 40.895 -9.399 11.6859 1.00 40.00 ATOM 2636 NEX HIS 591 40.311 -5.785 115.616 1.00 60.00 ATOM 2636 NEX HIS 591 40.311 -5.785 115.616 1.00 60.00 ATOM 2640 NEX HIS 591 40.311 -5.785 115.616 1.00 60.00 ATOM 2640 NEX HIS 591 40.311 -5.785 115.616 1.00 60.00 ATOM 2650 NEX HIS 591 40.311 -5.785 115.616 1.00 60.00 ATOM 2650 NEX HIS 591 40.311 -5.785 115.616 1.00 60.00 ATOM 2650 NEX HIS 591 40.311 -5.785 115.616 1.00 60.00 ATOM 2650 NEX HIS 591 40.311 -5.78											
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ATOM 2645 CA CYS 593							-4.696	118.769	1.00 40.00		
ATOM 2645 CA CYS 593						42.565	-2.597	117.989	1.00 20.00		
ATOM 2646 CB CYS 593			CA	CYS	593	43.667					
ATOM 2648 C CYS 593		2646	CB	CYS	593	44.810					
ATOM 2649 O CYS 593	MOTA	2647	SG								
ATOM 2650 N HIS 594 43.460 -1.661 121.173 1.00 20.00 ATOM 2652 CA HIS 594 42.998 -0.809 122.227 1.00 20.00 ATOM 2653 CB HIS 594 42.101 -1.511 123.263 1.00 20.00 ATOM 2654 CG HIS 594 40.743 -1.878 122.739 1.00 20.00 ATOM 2655 CD2 HIS 594 40.743 -1.878 122.739 1.00 20.00 ATOM 2656 ND1 HIS 594 39.677 -1.007 122.698 1.00 20.00 ATOM 2658 CE1 HIS 594 38.622 -1.700 122.200 1.00 20.00 ATOM 2659 NE2 HIS 594 38.935 -2.953 121.920 1.00 20.00 ATOM 2661 C HIS 594 44.178 -0.267 122.972 1.00 20.00 ATOM 2663 N LEU 595 43.994 0.898 123.625 1.00 20.00 ATOM 2665 CA LEU 595 45.068 1.563 124.306 1.00 20.00 ATOM 2666 CB LEU 595 44.724 3.014 124.684 1.00 20.00 ATOM 2666 CB LEU 595 45.878 3.792 125.340 1.00 20.00 ATOM 2666 CD1 LEU 595 45.878 3.792 125.340 1.00 20.00 ATOM 2667 C LEU 595 45.878 3.792 125.340 1.00 20.00 ATOM 2667 C LEU 595 45.894 0.813 125.533 1.00 20.00 ATOM 2667 C LEU 595 45.890 5.145 125.882 1.00 20.00 ATOM 2667 C LEU 595 45.454 0.813 125.533 1.00 20.00 ATOM 2670 C LEU 595 45.454 0.813 125.533 1.00 20.00 ATOM 2671 O LEU 595 45.454 0.813 125.533 1.00 20.00 ATOM 2670 C C CYS 596 46.758 0.870 125.863 1.00 20.00 ATOM 2670 C C CYS 596 46.758 0.870 125.863 1.00 20.00 ATOM 2677 C CYS 596 47.264 0.207 127.023 1.00 20.00 ATOM 2676 CG CYS 596 48.515 -0.637 126.706 1.00 20.00 ATOM 2677 C CYS 596 47.623 1.323 127.945 1.00 20.00 ATOM 2677 C CYS 596 47.623 1.323 127.945 1.00 20.00 ATOM 2677 C CYS 596 47.623 1.323 127.945 1.00 20.00	MOTA		С								
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				CYS	596	48.193					
		2679	N	HIS	597	47.271	1.201	129.238	1.00 20.00		

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MOTA	2681	CA	HIS	597	47.588		130.103	1.00 20.00
MOTA	2682	CB	HIS	597	47.048	2.169	131.538	1.00 20.00
ATOM	2683	CG	HIS	5 97	47.173	3.456	132.300	1.00 20.00
i 4	2684	CD2	HIS	597	46.290	4.484	132.432	1.00 20.00
ATOM	2685	ND1	HIS	597	48.302	3.843	132.988	1.00 20.00
ATOM	2687	CE1	HIS	597	48.046	5.072	133.502	1.00 20.00
ATOM	2688	NE2	HIS	597	46.837	5.503	133.190	1.00 20.00
MOTA	2690	С	HIS	597	49.072	2.360	130.162	1.00 20.00
MOTA	2691	0	HIS	597	49.764	1.360	129.977	1.00 20.00
MOTA	2692	N	PRO	598	49.579	3.531	130.393	1.00 20.00
ATOM	2693	CD	PRO	598	48.912	4.745	129.963	1.00 20.00
ATOM	2694	CA	PRO	598	51.001	3.693	130.432	1.00 20.00
MOTA	2695	CB	PRO	598	51.263	5.199	130.329	1.00 20.00
MOTA	2696	CG	PRO	598	49.870	5.853	130.423	1.00 20.00
MOTA	2697	С	PRO	598	51.602	3.024	131.623	1.00 20.00
ATOM	2698	0	PRO	598	52.811	2.794	131.617	1.00 20.00
MOTA	2699	N	ASN	599	50.801	2.740	132.668	1.00 20.00
MOTA	2701	CA	ASN	599	51.344	2.085	133.822	1.00 20.00
MOTA	2702	СB	ASN	599	50.402		135.045	1.00 20.00
MOTA	2703	CG	ASN	599	49.235	1.134	134.789	1.00 20.00
MOTA	2704	OD1	ASN	599	48.184	1.517		1.00 20.00
MOTA	2705	ND2	ASN	599	49.442		135.149	1.00 20.00
ATOM	2708	С	ASN	599	51.666	0.659		1.00 20.00
MOTA	2709	0	ASN	599	52.704		133.906	1.00 20.00
MOTA	2710	N	CYS	600	50.788		132.731	1.00 20.00
MOTA	2712	CA	CYS	600	50.992		132.501	1.00 20.00
MOTA	2713	CB	CYS	600	49.842	-2.099		1.00 20.00
MOTA	2714	SG	CYS	600	50.052	-3.899	131.760	1.00 20.00
MOTA	2715	С	CYS	600	52.221	-1.614		1.00 20.00
MOTA	2716	0	CYS	600	52.686		130.998	1.00 20.00
MOTA	2717	N	THR	601	52.793	-2.827		1.00 20.00
MOTA	2719	CA	THR	601	53.970		131.063	1.00 20.00
MOTA	2720	СВ	THR	601	55.171		131.927	1.00 20.00
MOTA	2721	OG1	THR	601	56.342		131.129	1.00 20.00
MOTA	2723	CG2	THR	601	54.952		132.700	1.00 20.00
MOTA	2724	С	THR	601	53.703	-4.418	130.327	1.00 20.00
ATOM	2725	0	THR	601	52.841	-5.208	130.709	1.00 20.00 1.00 20.00
MOTA	2726	N	TYR	602	54.441		129.223	1.00 20.00
ATOM	2728	CA	TYR	602 602	54.362 54.867		128.443 129.202	1.00 20.00
ATOM	2729	CB	TYR	602	56.329		129.202	1.00 20.00
MOTA	2730	CG CD1	TYR TYR	602	56.796		130.515	1.00 20.00
MOTA	2731 2732		TYR	602	58.142		130.676	1.00 20.00
ATOM	2732		TYR	602	57.227		128.452	1.00 20.00
ATOM ATOM	2734	CE2	TYR	602	58.573		128.605	1.00 20.00
MOTA	2735	CZ	TYR	602	59.034		129.720	1.00 20.00
MOTA	2736	OH	TYR	602	60.414		129.872	1.00 20.00
ATOM	2738	c	TYR	602	53.006		127.884	1.00 20.00
ATOM	2739	o	TYR	602	52.663		127.710	1.00 20.00
ATOM	2740	N	GLY	603	52.193		127.573	1.00 20.00
ATOM	2742	CA	GLY	603	50.950		126.904	1.00 20.00
ATOM	2743	C	GLY	603	49.741		127.771	1.00 20.00
ATOM	2744	Ō	GLY	603	49.831		128.996	1.00 20.00
ATOM	2745	N	CYS	604	48.564		127.110	1.00 20.00
ATOM	2747	CA	CYS	604	47.299		127.778	1.00 20.00
ATOM	2748	СВ	CYS	604	46.694		127.763	1.00 20.00
ATOM	2749	SG	CYS	604	47.402		128.930	1.00 20.00
ATOM	2750	C	CYS	604	46.311		127.031	1.00 20.00
ATOM	2751	0	CYS	604	46.297		125.800	1.00 20.00
ATOM	2752	N	THR	605	45.467		127.765	1.00 20.00
ATOM	2754	CA	THR	605	44.432		127.116	1.00 20.00
ATOM	2755	СВ	THR	605	43.712		128.033	1.00 20.00
ATOM	2756	OG1	THR	605	42.795	-9.093	127.292	1.00 20.00
ATOM	2758	CG2		605	42.979	-7.508	129.129	1.00 20.00

M	2759	С	THR	605	43.453 -6.350 126.590 1.00 20.00
AroM	2760	0	THR	605	42.937 -6.487 125.482 1.00 20.00
M \cap T A	2761	N	GLY	606	43.191 -5.295 127.388 1.00 20.00
<i>1</i> ,1	2763	CA	GLY	606	42.260 -4.280 126.998 1.00 20.00
MOTA	2764	С	GLY	606	42.606 -3.041 127.757 1.00 20.00
MOTA	2765	0	GLY	606	43.364 -3.061 128.725 1.00 20.00
MOTA	2766	N	PRO	607	42.027 -1.958 127.325 1.00 40.00
MOTA	2767	CD	PRO	607	40.706 -2.007 126.719 1.00 40.00 42.301 -0.674 127.908 1.00 40.00
MOTA	2768	CA	PRO	607	
MOTA	2769	CB	PRO	607 607	41.315 0.279 127.244 1.00 40.00 40.092 -0.622 126.987 1.00 40.00
ATOM	2770	CG	PRO PRO	607	42.024 -0.743 129.374 1.00 40.00
ATOM	2771	С 0	PRO	607	41.162 -1.522 129.776 1.00 40.00
ATOM	2772 2773	N	GLY	608	42.749 0.046 130.191 1.00 40.00
ATOM ATOM	2775	CA	GLY	608	42.462 0.063 131.595 1.00 40.00
ATOM	2776	C	GLY	608	43.620 -0.455 132.383 1.00 40.00
ATOM	2777	ō	GLY	608	44.459 -1.200 131.881 1.00 40.00
MOTA	2778	N	LEU	609	43.675 -0.047 133.666 1.00 20.00
ATOM	2780	CA	LEU	609	44.685 -0.468 134.593 1.00 20.00
ATOM	2781	CB	LEU	609	44.536 0.218 135.962 1.00 20.00
ATOM	2782	CG	LEU	609	45.581 -0.222 137.005 1.00 20.00
ATOM	2783	CD1	LEU	609	47.002 0.209 136.609 1.00 20.00
ATOM	2784		LEU	609	45.180 0.238 138.415 1.00 20.00
ATOM	2785	С	LEU	609	44.529 -1.936 134.820 1.00 20.00
ATOM	2786	0	LEU	609	45.510 -2.671 134.926 1.00 20.00 43.268 -2.394 134.896 1.00 20.00
ATOM	2787	N	GLU	610	
MOTA	2789	CA	GLU	610	42.951 -3.768 135.153 1.00 20.00 41.439 -4.034 135.267 1.00 20.00
ATOM	2790	CB	GLU	610 610	40.784 -3.454 136.522 1.00 20.00
ATOM	2791	CG CD	GLU GLU	610	40.474 -1.986 136.274 1.00 20.00
MOTA	2792 2793	OE1		610	40.013 -1.657 135.149 1.00 20.00
ATOM ATOM	2794	OE2		610	40.693 -1.174 137.212 1.00 20.00
MOTA	2795	C	GLU	610	43.449 -4.617 134.033 1.00 20.00
ATOM	2796	ō	GLU	610	43.861 -5.757 134.241 1.00 20.00
ATOM	2797	N	GLY	611	43.438 -4.066 132.809 1.00 20.00
MOTA	2799	CA	GLY	611	43.816 -4.811 131.648 1.00 20.00
MOTA	2800	С	GLY	611	45.192 -5.340 131.856 1.00 20.00
MOTA	2801	0	GLY	611	45.560 -6.368 131.291 1.00 20.00
ATOM	2802	N	CYS	612	46.004 -4.617 132.648 1.00 20.00 47.344 -5.054 132.897 1.00 20.00
ATOM	2804	CA	CYS	612	
ATOM		CB	CYS	612	48.076 -4.190 133.927 1.00 20.00 49.864 -4.351 133.729 1.00 20.00
MOTA	2806	SG	CYS CYS	612 612	47.272 -6.451 133.421 1.00 20.00
MOTA	2807 2808	C -	CYS	612	46.224 -6.915 133.873 1.00 20.00
ATOM ATOM	2809	N	PRO	613	48.373 -7.149 133.341 1.00 60.00
ATOM	2810	CD	PRO	613	49.228 -6.991 132.183 1.00 60.00
ATOM	2811	CA	PRO	613	48.378 -8.500 133.834 1.00 60.00
ATOM	2812	СВ	PRO	613	49.563 -9.188 133.157 1.00 60.00
ATOM	2813	CG	PRO	613	49.734 -8.405 131.846 1.00 60.00
ATOM	2814	С	PRO	613	48.448 -8.547 135.319 1.00 60.00
ATOM	2815	0	PRO	613	48.851 -7.567 135.934 1.00 60.00
MOTA	2816	N	THR	614	48.042 -9.690 135.912 1.00 60.00
ATOM	2818	CA	THR	614	48.080 -9.856 137.334 1.00 60.00 46.716 -9.892 137.960 1.00 60.00
MOTA	2819	CB	THR	614	
MOTA	2820	OG1		614 614	46.814 -9.809 139.377 1.00 60.00 46.026 -11.203 137.550 1.00 60.00
MOTA	2822	CG2	THR	614 614	48.711 -11.188 137.572 1.00 60.00
MOTA	2823	C	THR THR	614	49.329 -11.761 136.676 1.00 60.00
MOTA	2824 2825	O N	ASN	615	48.591 -11.704 138.810 1.00 60.00
MOTA MOTA	2827	CA	ASN	615	49.141 -12.989 139.110 1.00 60.00
ATOM	2828	CB	ASN	615	48.878 -13.439 140.557 1.00 60.00
ATOM	2829	CG	ASN	615	49.650 -12.521 141.491 1.00 60.00
ATOM	2830		ASN	615	49.126 -12.068 142.508 1.00 60.00
ATOM	2831		ASN	615	50.933 -12.237 141.141 1.00 60.00

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MOTA	2834	C	ASN	615		-13.952			60.00
MOTA	2835	0	ASN	615		-14.838			
ΜĊΨΑ	2836	N	GLY	616		-13.780			60.00
. 04	2838	CA	GLY	616		-14.672			60.00
MOTA	2839	С	GLY	616		-15.544	•		60.00
MOTA	2840	0	GLY	616		-15.467			60.00
MOTA	2841	N	PRO	617		-16.368			60.00
MOTA	2842	CD	PRO	617		-15.954			60.00
MOTA	2843	CA	PRO	617		-17.246			60.00
ATOM	2844	CB	PRO	617		-17.730			60.00
MOTA	2845	CG	PRO	617		-16.582			60.00
MOTA	2846	С	PRO	617		-18.336			60.00
MOTA	2847	0	PRO	617		-18.646			60.00
ATOM	2848	N	LYS	618	44.622	-18.921	140.257		60.00
MOTA	2850	CA	LYS	618	45.463	-19.964	140.754		60.00
ATOM	2851	СВ	LYS	618	44.979	-20.535	142.097	1.00	60.00
ATOM	2852	CG	LYS	618	44.979	-19.536	143.255		60.00
MOTA	2853	CD	LYS	618	44.189	-20.044	144.463	1.00	60.00
MOTA	2854	CE	LYS	618	42.726	-20.355	144.136	1.00	60.00
ATOM	2855	NZ	LYS	618	42.066	-20.995	145.296	1.00	60.00
ATOM	2859	С	LYS	618	45.382	-21.073	139.764	1.00	60.00
АТОМ	2860	0	LYS	618	46.397	-21.621	139.338	1.00	60.00
ATOM	2861	N	ILE	619		-21.416		1.00	60.00
ATOM	2863	CA	ILE	619	43.985	-22.494	138.432	1.00	60.00
ATOM	2864	СВ	ILE	619		-23.256	138.630	1.00	60.00
ATOM	2865	CG2	ILE	619		-24.284			60.00
ATOM	2866	CG1		619	42.667	-23.878		1.00	60.00
ATOM	2867	CD1		619		-24.870		1.00	60.00
ATOM	2868	C	ILE	619		-21.931		1.00	60.00
ATOM	2869	ō	ILE	619		-21.468		1.00	60.00
ATOM	2870	N	PRO	620		-21.962	136.408	1.00	60.00
ATOM	2871	CD	PRO	620		-22.886	136.747	1.00	60.00
ATOM	2872	CA	PRO	620		-21.499		1.00	60.00
ATOM	2873	СВ	PRO	620	46.580	-21.807	134.621	1.00	60.00
ATOM	2874	CG	PRO	620	46.929	-23.064	135.443	1.00	60.00
ATOM	2875	C	PRO	620		-22.326			60.00
ATOM	2876	ō	PRO	620		-23.448		1.00	60.00
ATOM	2877	N	SER	621		-21.796	133.195	1.00	60.00
	2879	CA	SER	621		-22.575			60.00
ATOM ATOM	2880	CB	SER	621		-21.723	131.609		60.00
ATOM	2881	OG	SER	621		-20.982	132.473		60.00
	2883	C	SER	621		-23.423	131.466		60.00
ATOM	2884	0	SER	621		-22.836	130.715		60.00
MOTA		OXT	SER	621		-24.669	131.461	1.00	60.00
ATOM	2885	OXT	SEK	021	47.63 3	24.003	201.401		,,,,,,
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F	240	N	LEU	25	50.889	2.127	50.184		40.00
A'TOM	242	CA	LEU	25	52.244	2.155	50.646		40.00
ATOM	243	CB	LEU	25	53.260	1.846	49.534		40.00
MC	244	CG	LEU	25	53.122	0.432	48.944		40.00
MOLA	245	CD1		25	51.761	0.244	48.255		40.00
MOTA	246	CD2		25	54.305	0.103	48.021		40.00
MOTA	247	C	LEU	25	52.535	3.540	51.127		40.00
ATOM	248	0	LEU	25 26	53.309 51.919	3.726 4.552	52.063 50.489		40.00
ATOM	249	N	SER	26 26	52.128	5.925	50.853		40.00
ATOM	251 252	CA CB	SER SER	26	51.479	6.924	49.885		40.00
ATOM ATOM	253	OG	SER	26	52.186	6.916	48.654		40.00
ATOM	255	C	SER	26	51.646	6.179	52.249		40.00
ATOM	256	0	SER	26	52.061	7.144	52.888		40.00
ATOM	257	N	LEU	27	50.743	5.316	52.751		40.00
ATOM	259	CA	LEU	27	50.199	5.423	54.077	1.00	40.00
ATOM	260	СВ	LEU	27	49.203	4.300	54.426	1.00	40.00
ATOM	261	CG	LEU	27	47.799	4.468	53.815	1.00	40.00
ATOM	262	CD1	LEU	27	47.097	5.687	54.425		40.00
ATOM	263	CD2	LEU	27	47.820	4.503	52.280		40.00
ATOM	264	С	LEU	27	51.282	5.372	55.114		40.00
ATOM	265	0	LEU	27	51.125	5.920	56.202		40.00
ATOM	266	N	GLN	28	52.404	4.695	54.814		40.00
ATOM	268	CA	GLN	28	53.475	4.531	55.757		40.00
MOTA	269	СВ	GLN	28	54.656	3.726	55.191		40.00
MOTA	270	CG	GLN	28	55.794	3.551 2.750	56.199 55.531		40.00
ATOM	271	CD OF1	GLN	28 28	56.903 57.466	3.169	54.524		40.00
ATOM	272 273	OE1 NE2		28	57.222	1.561	56.110		40.00
ATOM	276	C	GLN	28	54.028	5.843	56.214		40.00
ATOM ATOM	277	0	GLN	28	54.444	5.978	57.363		40.00
ATOM	278	N	ARG	29	54.025	6.858	55.334		40.00
ATOM	280	CA	ARG	29	54.608	8.130	55.649		40.00
АТОМ	281	СВ	ARG	29	54.373	9.157	54.531	1.00	40.00
ATOM	282	CG	ARG	29	54.975	10.528	54.816		40.00
MOTA	283	CD	ARG	29	54.807	11.506	53.653		40.00
MOTA	284	NE	ARG	29	55.608	10.980	52.511		40.00
ATOM	286	cz	ARG	29	55.054	10.093	51.634		40.00
ATOM	287		ARG	29	53.754	9.702	51.785		40.00
ATOM	290		ARG	29	55.800	9.597	50.603		40.00
MOTA	293	C	ARG	29	53.987 54.629	8.647 9.325	56.906 57.707		40.00
ATOM	294	0	ARG	29 30	52.697	8.347	57.100		40.00
MOTA	295 297	N CA	MET MET	30	51.985	8.770	58.264		40.00
ATOM ATOM	298	CB	MET	30	50.510	8.341	58.207		40.00
ATOM	299	CG	MET	30	49.715	8.969	57.061		40.00
ATOM	300	SD	MET	30	49.219	10.693	57.345	1.00	40.00
ATOM	301	CE	MET	30	47.920	10.259	58.538		40.00
ATOM	302	С	MET	30	52.545	8.139	59.503	1.00	40.00
MOTA	303	0	MET	30	52.717	8.798	60.525		40.00
MOTA	304	N	PHE	31	52.864	6.835	59.432		40.00
MOTA	306	CA	PHE	31	53.208	6.092	60.610		40.00
ATOM	307	СВ	PHE	31	53.368	4.587	60.332		40.00
MOTA	308	CG	PHE	31	53.702	3.932	61.628		40.00
ATOM	309	CD1		31	52.704	3.584	62.509		40.00
MOTA	310	CD2	PHE	31	55.009	3.671	61.966		40.00
ATOM	311	CE1		31	53.005	2.991	63.712		40.00
ATOM	312	CE2		31	55.316	3.078	63.169 64.045		40.00
ATOM	313	CZ	PHE PHE	31 31	54.313 54.443	2.738 6.531	61.331		40.00
ATOM	314 315	C O	PHE	31	54.443	6.668	62.553		40.00
ATOM	315	N	ASN	32	55.545	6.784	60.607		40.00
MOTA MOTA	318	CA	ASN	32	56.765	7.029	61.316		40.00
MOTA	319	CB	ASN	32	57.986	7.127	60.383		40.00
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MOTA	320	CG	ASN	32	57.792	8.311	59.452		40.00
MOTA	321		ASN	32	56.702	8.526	58.926		40.00
MOTA	322		ASN	32	58.877	9.105	59.244		40.00
M	325	С	ASN	32	56.761	8.237	62.192		40.00
A.OM	326	0	ASN	32	57.023	8.132	63.389		40.00 40.00
ATOM	327	N	ASN	33	56.425 56.577	9.425 10.527	61.661 62.559		40.00
ATOM	329	CA	ASN	33 33	57.776	11.425	62.207		40.00
ATOM	330	CB CG	ASN ASN	33	59.052	10.651	62.509		40.00
ATOM	331 332		ASN	33	59.275	10.223	63.640		40.00
ATOM ATOM	333		ASN	33	59.912	10.462	61.473		40.00
MOTA	336	C	ASN	33	55.379	11.408	62.585		40.00
ATOM	337	o	ASN	33	55.411	12.515	62.049	1.00	40.00
MOTA	338	N	CYS	34	54.275	10.950	63.200	1.00	20.00
ATOM	340	CA	CYS	34	53.212	11.894	63.322	1.00	20.00
ATOM	341	CB	CYS ·	34	52.404	12.098	62.032		20.00
MOTA	342	SG	CYS	34	51.433	13.629	62.113		20.00
MOTA	343	С	CYS	34	52.283	11.462	64.407		20.00
ATOM	344	0	CYS	34	51.356	10.688	64.175		20.00
ATOM	345	N	GLU	35	52.542	11.933	65.642		20.00
ATOM	347	CA	GLU	35	51.663	11.649	66.735		20.00
MOTA	348	CB	GLU	35 35	52.196	12.161	68.084		20.00
ATOM	349	CG	GLU	35 35	53.439 53.851	11.425 12.052	68.585 69.908		20.00
ATOM	350	CD OF1	GLU GLU	35 35	54.873	11.593	70.485		20.00
MOTA	351 352		GLU	35 35	53.151	12.998	70.357		20.00
ATOM ATOM	353	C	GLU	35	50.420	12.415	66.450		20.00
MOTA	354	Õ	GLU	35	49.309	11.913	66.609		20.00
ATOM	355	N	VAL	36	50.591	13.679	66.015	1.00	20.00
ATOM	357	CA	VAL	36	49.445	14.482	65.726	1.00	20.00
ATOM	358	CB	VAL	36	49.255	15.619	66.686		20.00
MOTA	359	CG1	VAL	36	48.015	16.421	66.256		20.00
ATOM	360		VAL	36	49.162	15.045	68.110		20.00
ATOM	361	С	VAL	36	49.603	15.077	64.369		20.00
ATOM	362	0	VAL	36	50.572 48.640	15.778 14.818	64.091 63.471		20.00
ATOM	363 365	N CA	VAL VAL	37 37	48.745	15.411	62.175		20.00
ATOM ATOM	366	CB	VAL	37	47.997	14.656	61.101		20.00
MOTA	367		VAL	37	48.665	13.282	60.929		20.00
ATOM	368		VAL	37	46.508	14.540	61.476		20.00
ATOM	369	С	VAL	37	48.173	16.787	62.307		20.00
ATOM	370	0	VAL	37	47.002	16.964	62.634		20.00
MOTA	371	N	LEU	38	49.011	17.816	62.095		20.00
ATOM	373	CA	LEU	38	48.538	19.164	62.179		20.00
MOTA	374	CB	LEU	38	49.664	20.181	62.438		20.00
MOTA	375	CG	LEU	38	49.181	21.640	62.533		20.00
ATOM	376		LEU	38 38	48.220 50.372	21.843 22.614	63.715 62.561		20.00
MOTA	377 378	CD2	LEU LEU	38	47.938	19.486	60.856		20.00
ATOM ATOM	379	0	LEU	38	48.632	19.915	59.936		20.00
ATOM	380	N	GLY	39	46.610	19.300	60.738		20.00
ATOM	382	CA	GLY	39	45.961	19.543	59.485		20.00
MOTA	383	С	GLY	39	44.916	18.486	59.339	1.00	20.00
MOTA	384	o	GLY	39	44.326	18.039	60.319		20.00
ATOM	385	N	ASN	40	44.648	18.054	58.094		20.00
MOTA	387	CA	ASN	40	43.645	17.052	57.888		20.00
MOTA	388	СВ	ASN	40	42.481	17.526	57.002		20.00
MOTA	389	CG	ASN	40	43.047	17.898	55.638		20.00
MOTA	390		ASN	40	43.930	18.747	55.527		20.00
MOTA	391		ASN	40	42.529	17.239	54.568		20.00
MOTA	394	C	ASN	40 40	44.258 45.323	15.858 15.950	57.225 56.618		20.00
ATOM ATOM	395 396	O N	ASN LEU	41	43.591	14.697			20.00
MOTA MOTA	398	CA	LEU	41	44.106	13.504	56.750		20.00
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A	399	СВ	LEU	41	44.427	12.413	57.790	1.00 20.00
ATOM	400	CG	LEU	41	44.993	11.095	57.223	1.00 20.00
ATOM	401		LEU	41	43.917	10.281	56.495	1.00 20.00
MC	402	CD2		41	46.240	11.344	56.360	1.00 20.00
WO.W	403	С	LEU	41	43.081	13.013	55.786	1.00 20.00
MOTA	404	0	LEU	41	41.903	12.890	56.121	1.00 20.00
MOTA	405	N	GLU	42	43.503	12.746	54.530	1.00 20.00 1.00 20.00
MOTA	407	CA	GLU	42	42.576	12.236	53.573	1.00 20.00
ATOM	408	CB	GLU	42	42.343	13.151	52.357 51.362	1.00 20.00
MOTA	409	CG	GLU	42	41.341	12.557 13.525	50.199	1.00 20.00
MOTA	410	CD	GLU	42	41.171 41.827	14.601	50.222	1.00 20.00
ATOM	411		GLU GLU	42 42	40.384	13.201	49.271	1.00 20.00
ATOM	412	C C	GLU	42	43.131	10.961	53.033	1.00 20.00
MOTA	413 414	0	GLU	42	44.302	10.892	52.659	1.00 20.00
ATOM	415	N	ILE	43	42.304	9.899	53.011	1.00 20.00
ATOM ATOM	417	CA	ILE	43	42.752	8.662	52.445	1.00 20.00
ATOM	418	СВ	ILE	43	42.741	7.524	53.424	1.00 20.00
MOTA	419		ILE	43	43.059	6.230	52.657	1.00 20.00
ATOM	420		ILE	43	43.718	7.804	54.578	1.00 20.00
ATOM	421		ILE	43	45.176	7.902	54.129	1.00 20.00
ATOM	422	С	ILE	43	41.784	8.327	51.358	1.00 20.00
MOTA	423	0	ILE	43	40.727	7.756	51.616	1.00 20.00
MOTA	424	N	THR	44	42.126	8.643	50.096	1.00 20.00
MOTA	426	CA	THR	44	41.172	8.389	49.058	1.00 20.00
ATOM	427	CB	THR	44	40.818	9.607	48.256	1.00 20.00
ATOM	428	OG1	THR	44	39.737	9.316	47.382	1.00 20.00
MOTA	430	CG2	THR	44	42.053	10.050	47.453	1.00 20.00 1.00 20.00
ATOM	431	С	THR	44	41.667	7.354	48.098 47.968	1.00 20.00
MOTA	432	0	THR	44	42.868 40.704	7.121 6.690	47.429	1.00 20.00
ATOM	433	N	TYR	45 45	40.704	5.707	46.405	1.00 20.00
ATOM	435	CA CB	TYR TYR	45	41.028	6.314	44.994	1.00 20.00
ATOM	436 437	CG	TYR	45	39.706	6.904	44.639	1.00 20.00
MOTA MOTA	438		TYR	45	38.687	6.101	44.182	1.00 20.00
ATOM	439		TYR	45	37.480	6.645	43.808	1.00 20.00
ATOM	440	CD2		45	39.503	8.263	44.708	1.00 20.00
ATOM	441	CE2		45	38.298	8.812	44.337	1.00 20.00
ATOM	442	CZ	TYR	45	37.284	8.002	43.884	1.00 20.00
ATOM	443	OH	TYR	45	36.051	8.560	43.489	1.00 20.00
ATOM	445	C	TYR	45	42.127	4.854		1.00 20.00
MOTA	446	0	TYR	45	43.049	4.867		1.00 20.00
ATOM	447	N	VAL	46	42.169	4.080	47.723	1.00 20.00 1.00 20.00
MOTA	449	CA	VAL	46	43.301	3.215 3.641	47.895 48.988	1.00 20.00
ATOM	450	CB	VAL	46 46	44.235 43.474	3.627	50.320	1.00 20.00
ATOM	451		VAL VAL	46	45.461	2.713	48.965	1.00 20.00
MOTA	452 453	CGZ	VAL	46	42.811	1.841	48.220	1.00 20.00
MOTA	454	0	VAL	46	41.745	1.678	48.813	1.00 20.00
MOTA MOTA	455	N	GLN	47	43.573	0.802	47.815	1.00 20.00
ATOM	457	CA	GLN	47	43.130	-0.533	48.099	1.00 20.00
ATOM	458	СВ	GLN	47	42.333	-1.150	46.940	1.00 20.00
ATOM	459	CG	GLN	47	41.063	-0.367	46.607	1.00 20.00
ATOM	460	CD	GLN	47	40.429	-1.005	45.381	1.00 20.00
ATOM	461	OE1	GLN	47	39.658	-1.958	45.483	1.00 20.00
MOTA	462	NE2	GLN	47	40.771	-0.468	44.180	1.00 20.00
MOTA	465	С	GLN	47	44.309	-1.426	48.332	1.00 20.00
MOTA	466	0	GLN	47	45.210	-1.490	47.501	1.00 20.00
MOTA	467	N	ARG	48	44.353	-2.119	49.490	1.00 20.00
MOTA	469	CA	ARG	48	45.386	-3.099	49.670	1.00 20.00 1.00 20.00
MOTA	470	СВ	ARG	48	46.828	-2.580	49.817	1.00 20.00
MOTA	471	CG	ARG	48	47.112	-1.831	51.115 51.417	1.00 20.00
MOTA	472	CD	ARG	48	48.611	-1.746 -3.137	51.417	1.00 20.00
MOTA	473	NE	ARG	48	49.145	-2.13/	J 4. / 4.	1.00 20.00

MOTA	475	CZ	ARG	48	50.483	-3.358	51.318	1.00 20.00
MOTA	476		ARG	48	50.973	-4.631	51.348	1.00 20.00
ATOM	479	NH2		48	51.331	-2.307	51.125	1.00 20.00
MC	482	С	ARG	48	45.108	-3.855	50.928	1.00 20.00
A r OM	483	0	ARG	48	44.103	-3.633	51.600	1.00 20.00
ATOM	484	N	ASN	49	46.020	-4.783	51.272	1.00 20.00
MOTA	486	CA	ASN	49	45.864	-5.613	52.430	1.00 20.00
ATOM	487	CB	ASN	49	46.987	-6.657 -7.627	52.557 51.393	1.00 20.00 1.00 20.00
MOTA	488 489	CG	ASN ASN	49 49	46.858 45.806	-8.228	51.183	1.00 20.00
ATOM ATOM	490		ASN	49	47.957	-7.781	50.607	1.00 20.00
ATOM	493	C	ASN	49	45.891	-4.796	53.682	1.00 20.00
ATOM	494	ō	ASN	49	44.996	-4.901	54.518	1.00 20.00
ATOM	495	N	TYR	50	46.917	-3.937	53.835	1.00 20.00
ATOM	497	CA	TYR	50	47.034	-3.184	55.049	1.00 20.00
ATOM	498	СВ	TYR	50	48.313	-2.332	55.148	1.00 20.00
ATOM	499	CG	TYR	50	49.476	-3.249	55.318	1.00 20.00
MOTA	500	CD1	TYR	50	49.774	-3.761	56.559	1.00 20.00
ATOM	501	CE1	TYR	50	50.869	-4.574	56.740	1.00 20.00
ATOM	502	CD2	TYR	50	50.301	-3.547	54.258	1.00 20.00
ATOM	503	CE2	TYR	50	51.398	-4.359	54.433	1.00 20.00
ATOM	504	CZ	TYR	50	51.683	-4.873	55.675	1.00 20.00
ATOM	505	ОН	TYR	50	52.810	-5.702	55.857	1.00 20.00
ATOM	507	C	TYR	50 50	45.871 45.151	-2.269 -1.960	55.220 54.272	1.00 20.00 1.00 20.00
ATOM	508	O N	TYR ASP	50 51	45.151	-1.829	56.476	1.00 20.00
ATOM ATOM	509 511	CA	ASP	51	44.594	-0.929	56.799	1.00 40.00
ATOM	512	CB	ASP	51	43.591	-1.486	57.825	1.00 40.00
ATOM	513	CG	ASP	51	42.761	-2.572	57.151	1.00 40.00
ATOM	514		ASP	51	42.891	-2.734	55.908	1.00 40.00
ATOM	515		ASP	51	41.978	-3.250	57.869	1.00 40.00
ATOM	516	С	ASP	51	45.238	0.271	57.414	1.00 40.00
ATOM	517	0	ASP	51	46.447	0.299	57.629	1.00 40.00
ATOM	518	N	LEU	52	44.426	1.306	57.692	1.00 40.00
MOTA	520	CA	LEU	52	44.875	2.544	58.259	1.00 40.00
ATOM	521	CB	LEU	52	43.795	3.638	58.253	1.00 40.00
ATOM	522	CG	LEU	52	44.316	5.001	58.745	1.00 40.00
ATOM	523		LEU	52 52	45.417	5.540	57.819 58.947	1.00 40.00 1.00 40.00
ATOM	524		LEU	52 52	43.167 45.316	6.001 2.310	59.672	1.00 40.00
ATOM ATOM	525 526	С 0	LEU	52 52	46.083	3.086	60.238	1.00 40.00
ATOM	527	N	SER	53	44.838	1.207	60.272	1.00 40.00
ATOM	529	CA	SER	53	45.077	0.879	61.649	1.00 40.00
ATOM	530	СВ	SER	53	44.492	-0.484	62.049	1.00 40.00
ATOM	531	OG	SER	53	45.162	-1.527	61.355	1.00 40.00
ATOM	533	С	SER	53	46.536	0.824	61.965	1.00 40.00
ATOM	534	0	SER	53	46.923	1.047	63.111	1.00 40.00
ATOM	535	N	PHE	54	47.391	0.535	60.967	1.00 40.00
MOTA	537	CA	PHE	54	48.788	0.373	61.250	1.00 40.00
ATOM	538	CB	PHE	54	49.665	0.050	60.021	1.00 40.00
ATOM	539	CG	PHE	54	49.742	1.221	59.103	1.00 40.00
ATOM	540	CD1		54	50.664 48.995	2.219 1.254	59.322 57.950	1.00 40.00 1.00 40.00
ATOM	541 542	CD2 CE1		54 54	50.813	3.247	58.419	1.00 40.00
ATOM ATOM	543	CE2		54	49.127	2.284	57.049	1.00 40.00
ATOM	544	CZ	PHE	54	50.040	3.284	57.283	1.00 40.00
ATOM	545	C	PHE	54	49.319	1.607	61.908	1.00 40.00
ATOM	546	0	PHE	54	50.271	1.519	62.680	1.00 40.00
ATOM	547	N	LEU	55	48.738	2.790	61.609	1.00 40.00
ATOM	549	CA	LEU	55	49.180	4.002	62.248	1.00 40.00
MOTA	550	СВ	LEU	55	48.495	5.271	61.707	1.00 40.00
MOTA	551	CG	LEU	55	48.790	5.573	60.228	1.00 40.00
MOTA	552	CD1		55	50.281	5.855	60.008	1.00 40.00
ATOM	553	CD2	LEU	55	48.248	4.478	59.299	1.00 40.00



AUSTRALIA

Patents Act 1990

COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION

PROVISIONAL SPECIFICATION

Invention Title:

EGF family receptor agonists and antagonists

The invention is described in the following statement:

EGF FAMILY RECEPTOR AGONISTS AND ANTAGONISTS

Field of the Invention

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This invention relates to the field of receptor structure and receptor/ligand interactions. In particular it relates to the field of using receptor structure to predict the structure of related receptors and to use the determined structures and predicted structures to select and screen for agonists and antagonists of the polypeptide ligands.

Background of the Invention

Insulin is the peptide hormone that regulates glucose uptake and metabolism. The two types of diabetes are associated with either an inability to produce insulin because of destruction of the pancreatic islet cells (Homo-Delarche, F. & Boitard, C.,1996, Immunol. Today 10: 456-460) or poor glucose metabolism resulting from either insulin resistance at the target tissues, inadequate insulin secretion by the islets or faulty liver function (Taylor, S. I., et al., 1994, Diabetes, 43: 735-740).

Insulin-like growth factors-1 and 2 (IGF-1 and 2) are structurally related to insulin but are more important in tissue growth and development than in metabolism. They are primarily produced in the liver in response to growth hormone but are also produced in most other tissues where they function as paracrine/autocrine regulators. The IGFs are strong mitogens and are involved in numerous physiological states and certain cancers (Baserga, R., 1996, TibTech 14: 150-152).

Epidermal growth factor (EGF) is a small polypeptide cytokine that is unrelated to the insulin/IGF family. It stimulates marked proliferation of epithelial tissues and is a member of a larger family of structurally related cytokines such as transforming growth factor α, amphiregulin, betacellulin, heparin-binding EGF and some viral gene products. Abnormal EGF family signalling is a characteristic of certain cancers (Soler, C. & Carpenter, G., 1994 In Nicola, N. (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp194-197; Walker, F. & Burgess, A. W., 1994, In Nicola, N. (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp198-201).

Each of these growth factors mediate their biological actions through binding to the corresponding receptor. The IR, IGF-1R and insulin receptorrelated receptor (IRR), for which the ligand is not known, are closely related to each other and are referred to as the insulin receptor subfamily. There is a 5

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large body of information now available concerning the primary structure of these insulin receptor subfamily members (Ebina, Y., et al., 1985 Cell 40: 747-758; Ullrich, A., et al., 1985, Nature 313: 756-761; Ullrich, A. et al., 1986, EMBO J 5: 2503-2512; Shier, P. & Watt, V. M., 1989, J. Biol. Chem. 264: 14605-14608) and the identification of some of their functional domains (for reviews see De Meyts, P. 1994, Diabetologia 37: 135-148; Lee, J. & Pilch, P. F. 1994 Amer. J. Physiol. 266: C319-C334.; Schaffer, L. 1994, Eur. J. Biochem. 221: 1127-1132). IGF-1R, IR and IRR are members of the tyrosine kinase receptor superfamily and are closely related to the epidermal growth factor receptor (EGFR) subfamily, with which they share significant sequence identity in the extracellular region as well as in the cytoplasmic kinase domains (Ullrich, A. et al., 1984 Nature 309: 418-425; Ward, C. W. et al., 1995 Proteins: Structure Function & Genetics 22: 141-153). Both the insulin and EGF receptor subfamilies have a similar arrangement of two homologous domains (L1 and L2) separated by a cys-rich region of approximately 160 amino acids containing 22-24 cys residues (Bajaj, M., et al., 1987 Biochim. Biophys. Acta 916: 220-226; Ward, C. W. et al., 1995 Proteins: Structure Function & Genetics 22: 141-153). The C-terminal portion of the IGF-1R ectodomain (residues 463 to 906) is comprised of four domains: a connecting domain, two fibronectin type 3 (Fn3) repeats, and an insert domain (O'Bryan, J. P., et al., 1991 Mol Cell Biol 11: 5016-5031); the C-terminal portion of the EGFR ectodomain (residues 477-621) consists solely of a second cys-rich region containing 20 cys residues (Ullrich, A. et al., 1984, Nature 309: 418-425).

Little is known about the secondary, tertiary and quaternary structure of the ectodomains of these receptor subfamilies. Unlike the members of the EGFR subfamily which are transmembrane monomers which dimerise on binding ligand, the IR subfamily members are homodimers, held together by disulphide bonds. The extracellular region of the IR/IGF-1R/IRR monomers contains an α-chain (~ 703 to 735 amino acid residues) and 192-196 residues of the β-chain. There is a ~23 residue transmembrane segment, followed by the cytoplasmic portion (354 to 408 amino acids) which contains the catalytic tyrosine kinase domain flanked by juxtamembrane and C-tail regulatory regions and is responsible for mediating all receptor-specific functions (White, M. F. & Kahn, C. R. 1994 J. Biol. Chem. 269: 1-4). Chemical analyses of the receptor suggest that the α-chains are linked to the β-chains

via a single disulphide bond with the IR dimer being formed by at least two α-α disulphide linkages (Finn, F. M., et al., 1990, Proc. Natl. Acad. Sci. 87: 419-423; Chiacchia, K. B., 1991, Biochem. Biophys. Res. Commun. 176, 1178-1182; Schaffer, L. & Ljungqvist, L., 1992, Biochem. Biophys. Res. Comm. 189: 650-653; Sparrow, L. G., et al., 1997, J. Biol. Chem. 47: 29460-29467).

Although the 3D structures of the ligands EGF, TGF-alpha (Hommel, U., et al., 1992, J. Mol. Biol. 227:271-282), insulin (Dodson, E. J., et al., 1983, Biopolymers 22:281-291), IGF-1 (Sato, A., et al., 1993, Int J Peptide Protein Res 41:433-440) and IGF-2 (Torres, A. M., et al., 1995, J. Mol. Biol. 248:385-401) are known and numerous analytical and functional studies of ligand binding to EGFR (Soler, C. & Carpenter, G., 1994 In Nicola (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp194-197), IGF-1R and IR (see De Meyts, P., 1994 Diabetologia, 37:135-148) have been carried out, the mechanisms of ligand binding and subsequent transmembrane signalling have not been resolved.

Ligand-induced, receptor-mediated phosphorylation is the signalling mechanism by which most cytokines, polypeptide hormones and membrane-anchored ligands exert their biological effects. The primary kinase may be part of the intracellular portion of the transmembrane receptor protein as in the tyrosine kinase receptors (for review see Yarden, Y., et al., 1988, Ann. Rev. Biochem. 57:443-478) or the Ser/Thr kinase receptors (Alevizopoulos, A. & Mermod, N., 1997, BioEssays, 19:581-591) or be non-covalently associated with the cytoplasmic tail of the transmembrane protein(s) making up the receptor complex as in the case of the haemopoietic growth factor receptors (Stahl, N., et al., 1995, Science 267:1349-1353). The end result is the same, ligand binding leads to receptor dimerization or oligomerization or a conformational change in pre-existing receptor dimers or oligomers resulting in activation by transphosphorylation, of the covalently attached or non-covalently associated protein kinase domains (Hunter, T., 1995, Cell, 80:225-236).

Many oncogenes have been shown to be homologous to growth factors, growth factor receptors or molecules in the signal transduction pathways (Baserga, R., 1994 Cell, 79:927-930; Hunter, T., 1997 Cell, 88:333-346). One of the best examples is v-Erb (related to the EGFR). Since overexpression of a number of growth factor receptors results in ligand-dependent transformation an alternate strategy for oncogenes is to regulate

the expression of growth factor receptors or their ligands or to directly bind to the receptors to stimulate the same effect (Baserga, R., 1994 Cell, 79:927-930). Examples are v-Src, which activates IGF-1 R intracellularly; c-Myb, which transforms cells by enhancing the expression of IGF1R and SV40 T antigen which interacts with the IGF-1R and enhances the secretion of IGF-1 (see Baserga, R.,1994 Cell, 79:927-930 for review). Cells in which the IGF-1 receptor has been knocked out cannot be transformed by SV40 T antigen. If oncogenes activate growth factors and their receptors then tumour suppressor genes should have the opposite effect. One good example of this is WT1, the Wilm's tumour suppressor gene which suppresses the expression of IGF-1R (Drummond, J. A., et al., 1992, Science, 257:275-277). Cells that are driven to proliferate by oncogenes undergo massive apotosis when growth factor receptors are ablated since unlike normal cells, they appear unable to withdraw from the cell-cycle and enter into the G0 phase (Baserga, R.,1994 Cell, 79:927-930).

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The insulin-like growth factor-1 receptor (IGF-1R) is one of several growth-factor receptors that regulate the proliferation of mammalian cells. However, its ubiquitousness and certain unique aspects of its function make IGF-1R an ideal target for therapeutic interventions against abnormal growth, with very little effect on normal cells (see Baserga, R., 1996 TIBTECH, 14:150-152). The receptor is activated by IGF1, IGF2 and insulin and plays a major role in cellular proliferation in at least three ways: it is essential for optimal growth of cells in vitro and in vivo; several cell types require IGF-1R to maintain the transformed state and activated IGF-1R has a protective effect against apoptotic cell death (Baserga, R., 1996 TIBTECH, 14:150-152). These properties alone make it an ideal target for therapeutic interventions. Transgenic experiments have shown that IGF-1R is not an absolute requirement for cell growth but is essential for the establishment of the transformed state (Baserga, R., 1994 Cell, 79: 927-930). In several cases (human glioblastoma, human melanoma; human breast carcinoma; human lung carcinoma; human ovaraian carcinoma; human rhabdomyosarcoma; mouse melanoma, mouse leukaemia; rat glioblastoma; rat rhabdomyosarcoma; hamster mesothelioma) the transformed phenotype can be reversed by decreasing the expression of IGF-1R using antisense to IGF-1R (Baserga. R., 1996 TIBTECH 14:150-152); or interfering with its function by antibodies to IGF-1R (human breast carcinoma; human rhabdomyosarcoma)

or by dominant negatives of IGF-1R (rat glioblastoma; Baserga, R.,1996 TIBTECH 14:150-152).

Three effects are observed when the function of IGF-1R is impaired: tumour cells undergo massive apoptosis which results in inhibition of tumourogenesis; surviving tumour cells are eliminated by a specific immune response; and such a host response can cause a regression of an established wild-type tumour (Resnicoff, M., et al., 1995, Cancer Res. 54:2218-2222). These effects, plus the fact that interference of IGF-1R function has a limited effect on normal cells (partial inhibition of growth without apoptosis) makes IGF-1R a unique target for therapeutic interventions (Baserga, R., 1996 TIBTECH 14:150-152). In addition IGF-1R is downstream of many other growth factor receptors, which makes it an even more generalised target. The implication of these findings is that if you can decrease the number of IGF-1 receptors on cells or antagonise their function then tumours cease to grow and can be removed immunologically. These studies establish that IGF-1R antagonists will be extremely important therapeutically.

Many cancer cells have constitutively active EGFR (Sandgreen, E. P., et al., 1990, Cell, 61:1121-135; Karnes, W. E. J., et al., 1992, Gastroenterology, 102:474-485) or other EGFR family members (Hines, N. E.,1993, Semin. Cancer Biol. 4:19-26). Elevated levels of activated EGFR occur in bladder, breast, lung and brain tumours (Harris, A. L., et al., 1989, In Furth & Greaves (eds) The Molecular Diagnostics of human cancer. Cold Spring Harbor Lab. Press, CSH, NY, pp353-357). Antibodies to EGFR can inhibit ligand activation of EGFR (Sato, J. D., et al., 1983 Mol. Biol. Med. 1:511-529) and the growth of many epithelial cell lines (Aboud-Pirak E., et al., 1988, J. Natl Cancer Inst. 85:1327-1331). Patients receiving repeated doses of a humanised chimeric anti-EGFR antibody showed signs of disease stabilization. The large doses required and the cost of production of humanised Mab is likely to limit the application of this type of therapy. These findings indicate that the development of EGF antagonists will be attractive anticancer agents.

Summary of the Invention

The present inventors have now obtained 3D structural information concerning the insulin-like growth factor receptor (IGF-1R) and the insulin receptor (IR) which provides a rational basis for the development of antagonists and agonists of the polypeptide ligands for specific therapeutic applications. This information can be used to predict the structure of related

members of the insulin receptor family and epidermal growth factor family and to develop agonists and antagonists of their respective polypeptide ligands.

Accordingly, in a first apsect the present invention provides a method of screening for, or designing, an agonist of a ligand of an insulin receptor family member or EGF receptor family member which method includes

- (i) selecting or designing a substance which possesses stereochemical complementarity to a receptor site, wherein the receptor site is characterised by
- (a) amino acids 1-462 of IGF-1R positioned at atomic coordinates substantially as shown in Figure 1 or a subset thereof; or
- (b) amino acids derived from an insulin receptor family member or EGF receptor family member which form an equivalent structure to the amino acids defined in paragraph (a); and
- (ii) testing the substance for the ability to act as an agonist of the ligand of an insulin receptor family member or EGF receptor family member.

In a second apsect the present invention provides a method of screening for, or designing, an antagonist of a ligand of an insulin receptor family member or EGF receptor family member which method includes

- (i) selecting or designing a substance which possesses stereochemical complementarity to a receptor site, wherein the receptor site is characterised by
- (a) amino acids 1-462 of IGF-1R positioned at atomic coordinates substantially as shown in Figure 1 or a subset thereof; or
- (b) amino acids derived from an insulin receptor family member or an EGF receptor family member which form an equivalent structure to the amino acids defined in paragraph (a); and
- (ii) testing the substance for the ability to act as an antagonist of the ligand of an insulin receptor family member or EGF receptor family member.

The phrase "insulin receptor family" encompasses, for example, IGF-1R. IR and IRR. The phrase "EGF receptor family" encompasses for example, EGFR, ErbB2, ErbB3 and ErbB4. In general, insulin receptor family members and EGF receptor family members show similar domain arrangements and share significant sequence identity (preferably at least 20% identity between the families and at least 40% identity within each family).

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The receptor site defined in the first and second aspects of the present invention comprises the L1-cysteine rich-L2 region (residues 1-462) of the ectodomain of IGF-1R. At the centre of this structure is a groove, bounded by all three domains, of sufficient size to accommodate a ligand molecule. By "stereochemical complementarity" we mean that the biologically active substance or a portion thereof correlates, in the manner of the classic "lock-and-key" visualisation of ligand-receptor interaction, with the groove in the receptor site. Preferably, the stereochemical complementarity is such that the compound has a K_I for the receptor site of less than 10⁻⁶M. More preferably, the K_I value is less than 10⁻⁸M and more preferably less than 10⁻⁹M.

In preferred embodiments of the first and second aspects of the present invention, the method further involves selecting or designing a substance which has portions that match residues positioned on the surface of the receptor site which faces the groove. By "match" we mean that the identified portions interact with the surface residues, for example, via hydrogen bonding or by enthalpy-reducing Van der Waals interactions which promote desolvation of the biologically active substance within the site, in such a way that retention of the biologically active substance within the groove is favoured energetically.

In a preferred embodiment of the first aspect of the present invention, the method includes screening for, or designing, a substance which possesses a stereochemistry and/or geometry which allows it to interact with both the L1 and L2 domains of the receptor site. As described above, the insulin receptor exists as homodimers held together by disulphide bonds. Electron miscroscopy studies described herein indicate that the insulin receptor monomers dimerise in nature in such a manner that the grooves of each monomer may face each other. Accordingly, the method of the first aspect of the present invention may involve screening for, or designing, a biologically active substance which interacts with the L1 domain of one monomer and the L2 domain of the other monomer.

In a third aspect the present invention provides a method of selecting or designing an agonist of a ligand of an insulin receptor family member or EGF receptor family member which method includes

(i) selecting or designing a substance which interacts with

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(a) a fragment of IGF-1R characterised by amino acids 1-462 positioned at atomic coordinates substantially as shown in Figure 1 or a subset thereof; or

(b) a fragment derived from an insulin family receptor member or EGF receptor family member which is equivalent to the fragment defined in paragraph (a);

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wherein the interaction of the substance with the fragment alters the position of at least one of the L1, L2 or cys-rich domains of the fragment relative to the position of at least one of the other domains; and

(ii) testing the substance for the ability to act as an agonist of the ligand of an insulin receptor family member or EGF receptor family member.

In a preferred embodiment of the third aspect of the present invention the substance interacts with the fragment in the region of the L1 domain-cys rich domain interface, causing the L1 and cys-rich domains to move away from each other. In a further preferred embodiment the substance interacts with the hinge region between the L2 domain and the cys-rich domain causing an alteration in the positions of the domains relative to each other. In a further preferred embodiment the substance interacts with the beta sheet of the L1 domain causing an alteration in the position of the L1 domain relative to the position of the cys-rich domain or L2 domain.

In a fourth aspect the present invention provides an agonist of a ligand of an insulin receptor family member or EGF receptor family member obtained by a method according to the first or third aspects of the present invention.

In a fifth aspect the present invention provides an antagonist of ligand of an insulin receptor family member or EGF receptor family member obtained by a method according to the second aspect of the present invention.

The agonists or antagonists of the fourth and fifth aspects of the present invention may be mutant insulin family member or EGF family member ligands where at least one mutation occurs in the region of the ligand which interacts with residues on the surface of the receptor site facing toward the groove. For example, the IGF-1 ligand has a predominance of basic residues in the C region which may interact with the acidic patch of the cys-rich region near L1. An acidic patch on the other side of the ligand may interact with the patch of basic residues (residues 307-310) on the N-terminal

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end of L2. Accordingly, mutants of IGF-1 which exhibit altered activity may be generated by introducing modifications in the C region of IGF-1 or residues in the acidic patch on the other side of the hormone.

In a sixth aspect the present invention provides a substance which possesses stereochemical complementarity to a receptor site, wherein the receptor site is characterised by

- (a) amino acids 1-462 of IGF-1R positioned at atomic coordinates substantially as shown in Figure 1 or a subset thereof; or
- (b) amino acids derived from an insulin receptor family member or an EGF receptor family member which form an equivalent structure to the amino acids defined in paragraph (a);

with the proviso that the substance is not a naturally occurring ligand of an insulin receptor family member or EGF receptor family member or a mutant thereof.

By "mutant" we mean a ligand which has been modified by one or more point mutations, insertions of amino acids or deletions of amino acids.

In a preferred embodiment of the sixth aspect of the present invention, the stereochemical complementarity is such that the compound has a K_I for the receptor site of less than $10^{-6}M$. More preferably, the K_I value is less than $10^{-8}M$ and more preferably less than $10^{-9}M$.

In a seventh aspect the present invention provides a pharmaceutical composition for treatment of a disease associated with reduced activity of a ligand of an insulin receptor family member or EGF receptor family member which includes an agonist obtained by a method according to the first or third aspects of the present invention and a pharmaceutically acceptable carrier or diluent.

In an eighth aspect the present invention provides a pharmaceutical composition for treatment of a disease associated with activity of a ligand of an insulin receptor family member or EGF receptor family member which includes an antagonist obtained by a method according to the second aspect of the present invention and a pharmaceutically acceptable carrier or diluent.

In a ninth aspect the present invention provides a method of preventing or treating a disease associated with reduced activity of a ligand of an insulin receptor family member or EGF receptor family member which method includes administering to a subject in need thereof an agonist

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obtained by a method according to the first or third aspects of the present invention.

Diseases associated with reduced activity of a ligand of an insulin receptor family member or EGF receptor family member include diabetes, osteoporosis, nerve degeneration and a range of catabolic states.

In a tenth aspect the present invention provides a method of preventing or treating a disease associated with activity of a ligand of an insulin receptor family member or EGF receptor family member which method includes administering to a subject in need thereof an antagonist obtained by a method according to the second aspect of the present invention.

Diseases associated with activity of a ligand of an insulin receptor family member or EGF receptor family member include cancer, leukaemia and many types of tumour states including but not restricted to breast cancer, brain tumours, ovarian cancer, pancreatic tumours, lung cancer, melanoma, rhabdomyosarcoma, mesothelioma and glioblastoma.

Brief Description of the Drawings

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- Figure 1. IGF-1R residues 1-462, in terms of atomic coordinates refined to a resolution of 2.6 Å (average accuracy \approx 0.3Å). The coordinates are in relation to a Cartesian system of orthogonal axes.
- Figure 2. Depiction of the residues lining the groove of the IGF-1R receptor fragment 1-462.
 - Figure 3. Gel filtration chromatography of affinity-purified IGF-1R/462 protein. The protein was purified on a Superdex S200 column (Pharmacia) fitted to a BioLogic L.C. system (Biorad), equilibrated and eluted at 0.8 ml/min with 40 mM Tris/150 mM NaCl/0.02% NaN3 adjusted to pH 8.0. (a) Protein eluting in peak 1 contained aggregated IGF-1R/462 protein, peak 2 contained monomeric protein and peak 3 contained the c-myc undecapeptide used for elution from the Mab 9E10 immunoaffinity column. (b) Non-reduced SDS-PAGE of fraction 2 from IGF-1R/462 obtained following Superdex S200 (Fig.1a). Standard proteins are indicated.

Figure 4. Ion exchange chromatography of affinity-purified, truncated IGF-1R ectodomain. A mixture of gradient and isocratic elution chromatography was performed on a Resource Q column (Pharmacia) fitted to a BioLogic System (Biorad), using 20 mM Tris/pH 8.0 as buffer A and the same buffer containing 1M NaCl as buffer B. Protein solution in TBSA was diluted at least 1:2 with water and loaded onto the column at 2 ml/min. Elution was monitored by absorbance (280 nm) and conductivity (mS/cm). Target protein (peak 2) eluted isocratically with 20 mM Tris/0.14 M NaCl pH 8.0. Inset: Isoelectric focusing gel (pH 3 - 7; Novex Australia Pty Ltd)of fraction 2. The pI was estimated at 5.1 from standard proteins (not shown).

Figure 5. Gel filtration chromatography of affinity purified IR/485 protein. Affinity-purified material at 1 mg/ml produced a dominant peak at apparent mass ~ 140 kDa (interpreted as a dimer) (a); whereas affinity-purified material at 0.02 mg/ml produced a dominant peak at apparent mass ~ 85kDa (interpreted as a monomer) (b).

Figure 6. (a) SDS-PAGE of IR/485 following gel filtration chromatography. The protein migrated as a single broad band of apparent molecular mass ~ 78 kDa (reduced - lane A) or ~ 68kDa (non-reduced - lane B). (b) Isoelectric focussing of the IR/485 protein. The IR/485 fragment reacted positively in an ELISA with Mab 83-7, gave a single sequence corresponding to the N-terminal 10 residues of IR, showing several isoforms on isoelectric focussing from pI6.0-6.8. The fragment was further purified by ion-exchange chromatography on Uno Q (BioRad, USA), using stepwise isocratic elution with incremental changes in salt concentrations (see Figure 7). Fractions A and D were each enriched in a component isoform from the ladder of isoforms present in the unfractionated mixture. Both these fractions produced crystals, whereas no crystals were obtained from fractions B and C.

Figure 7. Purification of the IR/485 protein by ion-exchange chromatography on Uno Q (BioRad, USA), using stepwise isocratic elution with incremental changes in salt concentrations.

Figure 8. Polypeptide fold for residues 1-462 of IGF-1R. The L1 domain is at the top, viewed from the N-terminal end and L2 is at the bottom. The space

at the centre is of sufficient size to accommodate IGF-1. Helices are indicated by curled ribbon and b-strands by arrows. Cysteine side chains are drawn as ball-and-stick with lines showing disulfide bonds. The arrow points in the direction of view for Figure 9.

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Figure 9. Amino acid sequences of IGF-1R and related proteins. a, L1 and L2 domains of human IGF-1R and IR are shown based on a sequence alignment for the two proteins and a structural alignment for the L1 and L2domains. Positions showing conservation physico-chemical properties of amino acids are boxed, residues used in the structural alignment are shaded yellow and residues which form the Trp 176 pocket are in red. Secondary structure elements for L1 (above the sequences) and L2 (below) are indicated as cylinders for helices and arrows for b-strands. Strands are colour coded according to the b-sheet to which they belong. Disulfide bonds are also indicated. b, Cys-rich domains of human IGF-1R, IR and EGFR (domains 2 and 4) are aligned based on sequence and structural considerations. Secondary structural elements and disulfide bonds are indicated above the sequences. The dashed bond is only present in IR. Different types of disulfide bonded modules are labelled below the sequences as open, filled or broken lines. Boxed residues show conservation of physico-chemical properties and structurally conserved residues for modules 4-7 are shaded yellow. Residues from EGFR which do not conform to the pattern are shaded grey and the conserved Trp 176 and the semi-conserved Gln 182 are shaded red. This figure was prepared using ALSCRIPT (Barton, G. J., 1993, Prot. Engineering, 6:37-40).

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Figure 10. Stereo view of a superposition of the L1 (white) and L2 (black) domains. Residues numbers above are for L1 and below for L2. The side chain of Trp 176 which protrudes into the core of L1 is drawn as ball-and-stick.

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Figure 11. Schematic diagram showing the association of three β -finger motifs. β -strands are drawn as arrows and disulfide bonds as zigzags.

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Figure 12. GRASP [Nicolls, A. et al., 1993, Biophys. J. 64, 166-170] surface diagram of the L1 domain of IGF-1R shown in a similar view to Figure 8. The

N-terminal β -strand is at the top. The mutation L87A [Nakae, J. et al., 1995, J. Biol. Chem. 270, 22017-22022] and four regions (residues 12-15, 34-44, 64-67 and 89-91 of IR) shown to be important in insulin binding to IR [Williams, P. F. et al., 1995, J. Biol. Chem. 270, 3012-3016] correspond to a patch of residues on the large β -sheet. Residues numbers for IR/IGF-1R are given and residues are coloured according to the magnitude of Kd(mutant)/Kd(wild type), red, > 40; orange, 10-40; yellow, 2.5-10; green, < 2.5; non-secreting, white; untested, blue. All mutants on the opposite face of the domain do not affect insulin affinity.

Figure 13: Sequence Alignment of hIGF-1R, hIR and hIRR Ectodomains.

Derived by use of the PileUp program in the software package of the Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA.

For assignment of homologous 3D structures see Figure 9.

Figure 14: Sequence Alignment of EGFR, ErbB2, ErbB3 and ErbB4 Ectodomains. Derived by use of the PileUp program in the software package of the Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA. For alignment on the IGF-1R fragment and assignment of homologous 3D structures, see Figure 9.

Figure 15 Sequence Alignment and Classification of the Disulphide-bonded Modules in the Cys-rich domains of IGF-1R, IR, IRR, EGFR, ErbB2, ErbB3 and ErbB4.

Figure 16. Gel filtration chromatography of insulin receptor ectodomain and MFab complexes. hIR -11 ectodomain dimer (5 - 20 mg) was complexed with MFab derivatives (15-25 mg each) of the anti-hIR antibodies 18-44, 83-7 and 83-14 (Soos et al., 1986). Elution profiles were generated from samples loaded onto a Superdex S200 column (Pharmacia), connected to a BioLogic chromatography system (Biorad) and monitored at 280 nm. The column was eluted at 0.8 ml/min with 40 mM Tris/150 mM sodium chloride/0.02% sodium azide buffer adjusted to pH 8.0: Profile 0, hIR -11ectodomain, Profile 1, ectodomain mixed with MFab 18-44; Profile 2, ectodomain mixed with MFab 18-44 and MFab 83-14; Profile 3, ectodomain mixed with MFab 18-44, MFab 83-14 and MFab 83-7. The apparent mass of each complex was

determined from a plot of the following standard proteins: thyroglobulin (660 kDa), ferritin (440 kDa), bovine gammaglobulin (158 kDa), bovine serum albumin (67 kDa), chicken ovalbumin (44 kDa) and equine myoglobin (17 kDa).

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Figure 17. Micrographs of hIR and hIGF-1R ectodomains.(a) Undecorated hIR ectodomain dimer stained with methylamine tungstate showing parallel bars. (b) Undecorated hIR ectodomain dimer stained with uranyl formate, showing well-spaced parallel bars corresponding to the cartoon below. (c) Undecorated hIGF-1R ectodomain dimer stained with uranyl formate. Magnification bars for (a), (b) and (c) 50nm.

Figure 18. Micrographs of hIR and hIGF-1R ectodomains. (a) Thinly stained region of undecorated hIR ectodomain dimers in uranyl formate, showing Ushaped particles (circled) as well as parallel bars as in the cartoon below. (b) Undecorated hIGF-1R ectodomain dimer under similar staining conditions. Magnification bars 50 nm.

Figure 19. hIR ectodomain dimer complexed with MFab 83-7 and stained with KPT. Three projections can be recognised: circled particles have the Fab arms displaced either clockwise as in the cartoon below left, or anticlockwise as in the cartoon below middle; arrowed particles have the Fab arms in a central position, cartoon below right. Magnification bar 50 nm.

Figure 20. hIR ectodomain dimer complexed with MFab 83-7 and stained 25 with uranyl formate showing the parallel bar structure in particles having the Fab arms displaced (circled). Magnification bar 50 nm.

Figure 21. (a) hIR ectodomain dimer complexed with MFab 83-14 stained with potassium phosphotungstate, showing Fab arms attached near the 30 bottom of U-shaped particles (circled). The corresponding cartoon is shown below left. (b) hIR ectodomain dimer complexed with MFab 83-14 stained with uranyl acetate, showing both the view described above (circled) and the parallel-bar view with diagonally projecting Fab arms (arrowed), as in the cartoon below right. Magnification bars 50 nm.

Figure 22. Double complex of hIR ectodomain dimer with MFabs 83-7 and 18-44 showing particles of complex shape (circled) with four Fab arms attached, consistent with the cartoon below. Magnification bar 50 nm.

- Figure 23. Images of hIR ectodomain dimer co-complexed with MFabs 83-7, 83-14 and 18-44 showing examples of complex particles (circled) where it is possible to identify that there are more than four MFabs bound to the dimeric central region. Magnification bar 50 nm.
- Figure 24. Schematic illustrating the proposed model of the hIR ectodomain dimer. The dimensions of the molecular envelope are as shown in the diagram, as is the position of the two-fold axis.

Detailed Description of the Invention

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We describe herein the expression, purification, and crystallization of a recombinant IGF-1R fragment (residues 1-462) containing the L1-cysteinerich-L2 region of the ectodomain. The selected truncation position is just downstream of the exon 6/exon 7 junction (Abbott, A. M., et al., 1992. J Biol Chem., 267:10759-10763) and occurs at a position where the sequences of the IR and EGFR families diverge markedly (Ward, C. W., et al., 1995, Proteins: Struct., Funct., Genet. 22:141-153; Lax, I., et al., 1988, Molec. Cellul. Biol. 8:1970-1978) suggesting it represents a domain boundary. To limit the effects of glycosylation, the IGF-1R fragment was expressed in Lec8 cells, a glycosylation mutant of Chinese hamster ovary (CHO) cells, whose defined glycosylation defect produces N-linked oligosaccharides truncated at N-acetyl glucosamine residues distal to mannose residues (Stanley, P. 1989, Molec. Cellul. Biol. 9:377-383). Such an approach has facilitated glycoprotein crystallization (Davis, S. J., et al., 1993, Protein Eng. 6:229-232; Liu, J., et al., 1996, J. Biol. Chem. 271:33639-33646).

The IGF-1R construct described herein included a c-myc peptide tag (Hoogenboom, H. R., et al.,1991, Nucleic Acids Res. 19:4133-4137) that is recognised by the Mab 9E10 (Evan, G. I., et al., 1985, Mol. Cell. Biol. 5:3610-3616) enabling the expressed product to be purified by peptide elution from an antibody affinity column followed by gel filtration over Superdex S200. The purified proteins crystallized under a sparse matrix screen (Jancarik, J. & Kim. S.-H., 1991, J. Appl. Cryst. 24:409-411) but the crystals were of variable

quality, with the best diffracting to 3.0-3.5A. Isocratic gradient elution by anion-exchange chromatography yielded protein that was less heterogenous and gave crystals of sufficient quality to determine the structure of the first three domains of the human IGF-1R.

The IGF-1R fragment consisted of residues 1-462 of IGF-1R linked via an enterokinase-cleavable pentapeptide sequence to an eleven residue c-myc peptide tag at the C-terminal end. The fragment was expressed in Lec8 cells by continuous media perfusion in a bioreactor using porous carrier disks. It was secreted into the culture medium and purified by peptide elution from an anti-c-myc antibody column followed by Superdex S200 gel filtration. The receptor fragment bound two anti-IGF-1R monoclonal antibodies, 24-31 and 24-60, which recognize conformational epitopes, but could not be shown to bind IGF-1 or IGF-2. Crystals of variable quality were grown as rhombic prisms in 1.7 M ammonium sulfate at pH 7.5 with the best diffracting to 3.0-3.5 Å. Further purification by isocratic elution on an anion-exchange column gave protein which produced better quality crystals, diffracting to 2.6 Å, that were suitable for X-ray structure determination.

The structure of this fragment (IGF-1R residues 1-462; L1-cys rich-L2domains) has been determined to 2.6 Å resolution by X-ray diffraction. The L domains each adopt a compact shape consisting of a single stranded right-handed β-helix. The cys-rich region is composed of eight disulphide-bonded modules, seven of which form a rod-shaped domain with modules associated in a novel manner. At the centre of this reasonably extended structure is a space, bounded by all three domains, and of sufficient size to accommodate a ligand molecule. Functional studies on IGF-1R and other members of the insulin receptor family show that the regions primarily responsible for hormone-binding map to this central site. Thus this structure gives a first view of how members of the insulin receptor family might interact with their ligands.

Another group has reported the crystallization of a related receptor, the EGFR in a complex with its ligand EGF (Weber, W., et al., 1994, J Chromat. 679:181-189). However difficulties were encountered with these crystals which diffracted to only 6 Å, insufficient for the determination of an atomic resolution structure of this complex (Weber, W., et al., 1994, J Chromat 679:181-189) or the generation of accurate models of structurally related receptor domains such as IGF-1R and IR by homology modelling.

The present inventors have applied the same process to the IR and generated a fragment (residues 1-485) that covers the first three domains of the IR. This fragment has been expressed in transformed Lec8 cells, purified, and crystallized by similar methodologies to yield crystals suitable for X-ray diffraction.

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The present inventors have therefore developed 3D structural information about cytokine receptors to enable a more accurate understanding of how the binding of ligand leads to signal transduction. Such information provides a rational basis for the development of antagonists or agonists for specific therapeutic applications, something that heretofore could not have been predicted de novo from available sequence data.

The precise mechanisms underlying the binding of agonists and antagonists to the IGF-1 receptor site are not fully clarified. However, the binding of the agonists or antagonists to the receptor site, preferably with an affinity in the order of 10⁻⁸M or higher, is understood to arise from enhanced stereochemical complementarity, relative to naturally occurring IGF-1 ligands.

Such stereochemical complementarity, pursuant to the present invention, is characteristic of a molecule that matches intra-site surface residues lining the groove of the receptor site as eneumerated by the coordinates set out in Figure 1. The residues lining the groove are depicted in Figure 2. Substances which are complementary to the shape of the receptor site characterised by amino acids positioned at atomic coordinates set out in Figure 1 may be able to bind to the receptor site and, when the binding is sufficiently strong, substantially prohibit binding of the naturally occurring ligands to the site.

It will be appreciated that it is not necessary that the complementarity between agonists or antagonists and the receptor site extend over all residues lining the groove in order to inhibit binding of the natural ligand. Accordingly, agonists or antagonists which bind to a portion of the residues lining the groove are encompassed by the present invention.

In general, the design of a molecule possessing stereochemical complementarity can be accomplished by means of techniques that optimize, either chemically or geometrically, the "fit" between a molecule and a target receptor. Known techniques of this sort are reviewed by Sheridan and Venkataraghavan, Acc. Chem Res. 1987 20 322; Goodford, J. Med. Chem.

1984 <u>27</u> 557; Beddell, Chem. Soc. Reviews 1985, 279; Hol, Angew. Chem. 1986 <u>25</u> 767 and Verlinde C.L.M.J & Hol, W.G.J. Structure 1994, <u>2</u>, 577, the respective contents of which are hereby incorporated by reference. See also Blundell et al., Nature 1987 <u>326</u> 347 (drug development based on information regarding receptor structure).

Thus, there are two preferred approaches to designing a molecule, according to the present invention, that complements the shape of IGF-1R or a related receptor molecule. By the geometric approach, the number of internal degrees of freedom (and the corresponding local minima in the molecular conformation space) is reduced by considering only the geometric (hard-sphere) interactions of two rigid bodies, where one body (the active site) contains "pockets" or "grooves" that form binding sites for the second body (the complementing molecule, as ligand). The second preferred approach entails an assessment of the interaction of respective chemical groups ("probes") with the active site at sample positions within and around the site, resulting in an array of energy values from which three-dimensional contour surfaces at selected energy levels can be generated.

The geometric approach is illustrated by Kuntz et al., J. Mol. Biol. 1982 161 269, the contents of which are hereby incorporated by reference, whose algorithm for ligand design is implemented in a commercial software package distributed by the Regents of the University of California and further described in a document, provided by the distributor, which is entitled "Overview of the DOCK Package, Version 1.0,", the contents of which are hereby incorporated by reference. Pursuant to the Kuntz algorithm, the shape of the cavity represented by the IGF-R1 site is defined as a series of overlapping spheres of different radii. One or more extant data bases of crystallographic data, such as the Cambridge Structural Database System maintained by Cambridge University (University Chemical Laboratory, Lensfield Road, Cambridge CB2 1EW, U.K.) and the Protein Data Bank maintained by Brookhaven National Laboratory (Chemistry Dept. Upton, NY 11973, U.S.A.), is then searched for molecules which approximate the shape thus defined.

Molecules identified in this way, on the basis of geometric parameters, can then be modified to satisfy criteria associated with chemical complementarity, such as hydrogen bonding, ionic interactions and Van der Waals interactions.

The chemical-probe approach to ligand design is described, for example, by Goodford, J. Med. Chem. 1985 28 849, the contents of which are hereby incorporated by reference, and is implemented in several commercial software packages, such as GRID (product of Molecular Discovery Ltd., West Way House, Elms Parade, Oxford OX2 9LL, U.K.). pursuant to this approach, the chemical prerequisites for a site-complementing molecule are identified at the outset, by probing the active site (as represented via the atomic coordinates shown in Fig. 1) with different chemical probes, e.g., water, a methyl group, an amine nitrogen, a carboxyl oxygen, and a hydroxyl. Favored sites for interaction between the active site and each probe are thus determined, and from the resulting three-dimensional pattern of such sites a putative complementary molecule can be generated.

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The chemical-probe approach is especially useful in defining variants of a molecule known to bind the target receptor. Accordingly, crystallographic analysis of IGF-1 bound to the receptor site may provide useful information regarding the interaction between the archetype ligand and the active site of interest.

A further use of the structure of IGF-1R fragment described here is in facilitating structure determination of a related protein such as a larger fragment of this receptor, another member of the insulin receptor family or a member of the EGF receptor family. This new structure could be either alone or in complex with its ligand. For crystallographic analysis this is achieved using the method of molecular replacement (Brunger, Meth. Enzym. 1997 276 558-580, Navaza and Saludjian, ibid. 581-594, Tong and Rossmann, ibid. 594-611, Bentley, ibid. 611-619) in a program such as XPLOR. In this procedure diffraction data is collected from a crystalline protein of unknown structure. A transform of these data (Patterson function) is compared with a Patterson function calculated from a known structure. Firstly, the one Patterson function is rotated on the other to determine the correct orientation of the unknown molecule in the crystal. The translation function is then calculated to determine the location of the molecule with respect to the crystal axes. Once the molecule has been correctly positioned in the unit cell initial phases for the experimental data may be calculated. These phases are necessary for calculation of an electron density map from which structural differences may be observed and for refinement of the structure. Due to limitations in the method the search molecule must be structurally related to

that which is to be determined. However it is sufficient for only part of the unknown structure (e.g. < 50%) to be similar to the search molecule. Thus the three dimensional structure of IGF-1R residues 1-462 may be used to solve structures consisting of related receptors, enabling a program of drug design as outlined above.

In summary, the general principles of receptor-based drug design can be applied by persons skilled in the art, using the crystallographic results presented above, to produce agonists or antagonists of IGF-1R or other related receptors, having sufficient stereochemical complementarity to exhibit high affinity binding to the receptor site.

The present invention is further described below with reference to the following, non-limiting examples.

EXAMPLE 1

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Expression, Purification and Crystalization of the IGF-1R Fragment.

Several factors hamper macromolecular crystallization including sample selection, purity, stability, solubility (McPherson, A., et al., 1995, Structure 3:759-768); Gilliland, G. L., & Ladner, J. E., 1996, Curr. Opin. Struct. Biol. 6:595-603), and the nature and extent of glycosylation (Davis, S. J., et al., 1993, Protein Eng. 6:229-232). Initial attempts to obtain structural data from soluble IGF-1R ectodomain (residues 1-906) protein, expressed in Lec8 cells (Stanley, P. 1989, Molec. Cellul. Biol. 9:377-383) and purified by affinity chromatography, produced large, well-formed crystals (1.0 mm x 0.2 mm x 0.2 mm) which gave no discernable X-ray diffraction pattern (unpublished data). Similar difficulties have been encountered with crystals of the structurally related epidermal growth factor receptor (EGFR) ectodomain which diffracted to only 6 Å, insufficient for the determination of an atomic resolution structure (Weber, W. et al., 1994, J Chromat 679:181-189). This prompted us to search for a fragment of IGF-1R that was more amenable to X-ray crystallographic studies.

The fragment expressed (residues 1-462) comprises the L1-cysteinerich-L2 region of the ectodomain. The selected truncation position at Val462 is four residues downstream of the exon 6/exon 7 junction (Abbott, A. M., et al., 1992, J Biol Chem. 267:10759-10763) and occurs at a position where the sequences of the IR and the structurally related EGFR families diverge markedly (Lax, I., et al., 1988, Molec Cell Biol. 8:1970-1978; Ward, C. W., et

al., 1995, Proteins: Struct., Funct., Genet. 22:141-153), suggesting it represents a domain boundary. The expression strategy included use of the pEE14 vector (Bebbington, C. R. & Hentschel, C. C. G., 1987, In: Glover, D. M., ed. DNA Cloning. Academic Press, San Diego. Vol 3, p163) in glycosidase-defective Lec8 cells (Stanley, P., 1989, Molec. Cellul. Biol. 9:377-5 383), which produce N-linked oligosaccharides lacking the terminal galactose and N-acetylneuraminic acid residues (Davis, S. J., et al., 1993, Protein Eng. 6:229-232; Liu, T., et al., 1996, J Biol Chem 271:33639-33646.). The construct contained a C-terminal c-myc affinity tag (Hoogenboom, H. R., et al., 1991, Nucl Acids Res. 19:4133-4137), which facilitated immunoaffinity purification 10 by specific peptide elution and avoided aggressive purification conditions. These procedures yielded protein which readily crystallized after a gel filtration polish. This provided a general protocol to enhance crystallisation prospects for labile, multidomain glycoproteins.

The structure of this fragment is of considerable interest since it contains the major determinants governing insulin and IGF-1 binding specificity (Gustafson, T. A. & Rutter, W. J., 1990, J. Biol. Chem. 265:18663-18667; Andersen, A. S., et al., 1990, Biochemistry, 29:7363-7366; Schumacher, R., et al., 1991, J. Biol. Chem. 266:19288-19295; Schumacher, R., et al., 1993, J. Biol. Chem. 268:1087-1094; Schäffer, L., et al., 1993, J. Biol. Chem. 268:3044-3047; Williams, P. F., et al., 1995, , J. Biol. Chem. 270:3012-3016) and is very similar to an IGF-1R fragment (residues 1-486) reported to act as a strong dominant negative for several growth functions and which induces apoptosis of tumour cells in vivo (D'Ambrosio, C., et al., 1996, Cancer Res. 56:4013-4020).

The expression plasmid pEE14/IGF-1R/462 was constructed by inserting the oligonucleotide cassette:

AatII 5' GACGTC GACGATGACGATAAG GAACAAAAACTCATC 30 D V D D D K Ε Q K L I (EK cleavage) (c-myc tail) Ε E L Ν (Stop) TCAGAAGAGGATCTGAAT TAGAATTC GACGTC 3' 35 **EcoRI AatII**

encoding an enterokinase cleavage site, c-myc epitope tag (Hoogenboom, H. R., et al., 1991, Nucleic acids Res. 19:4133-4137) and stop codon into the AatII site (within codon 462) of IGF-1 receptor cDNA in the mammalian expression vector pECE (Ebina, Y., et al., 1985, Cell, 40:747-758; kindly supplied by W. J. Rutter, UCSF, USA), and introducing the DNA comprising 5 the 5' 1521 bp of the cDNA (Ullrich, A., et al., 1986, EMBO J. 5:2503-2512) ligated to the oligonucleotide cassette into the EcoRI site of the mammalian plasmid expression vector pEE14 (Bebbington, C. R. & Hentschel, C. C. G., 1987, In: Glover, D. M., ed. DNA Cloning. Academic Press, San Diego. Vol 3, 10 p163; Celltech Ltd., UK). Plasmid pEE14/IGF-1R/462 was transfected into Lec8 mutant CHO cells (Stanley, P. 1989, Molec. Cellul. Biol. 9:377-383) obtained from the American Tissue Culture Collection (CRL:1737) using Lipofectin (Gibco-BRL). Cell lines were maintained after transfection in glutamine-free medium (Glascow modification of Eagle's medium (GMEM; ICN Biomedicals, Australia) and 10% dialysed FCS (Sigma, Australia) 15 containing 25 µM methionine sulphoximine (MSX; Sigma, Australia) as described (Bebbington, C. R. & Hentschel, C. C. G., 1987, In: Glover, D. M., ed. DNA Cloning. Academic Press, San Diego. Vol 3, p163). Transfectants were screened for protein expression by Western blotting and sandwich enzyme-linked immunosorbant assay (ELISA) (Cosgrove, L., et al., 1995,) 20 using monoclonal antibody (Mab) 9E10 (Evan et al., 1985) as the capture antibody and either biotinylated anti-IGF-1R Mab 24-60 or 24-31 for detection(Soos et al., 1992; gifts from Ken Siddle, University of Cambridge, UK). Large-scale cultivation of selected clones expressing IGF-1R/462 was carried out in a Celligen Plus bioreactor (New Brunswick Scientific, USA) 25 containing 70 g Fibra-Cel Disks (Sterilin, UK) as carriers in a 1.25 L working volume. Continuous perfusion culture using GMEM medium supplemented with non-essential amino acids, nucleosides, 25 μ M MSX and 10% FCS was maintained for 1 to 2 weeks followed by the more enriched DMEM/F12 30 without glutamine, with the same supplemention for the next 4-5 weeks. The fermentation production run was carried out three times under similar conditions and resulted in an estimated overall yield of 50 mg of receptor protein from 430 L of harvested medium. Cell growth was poor during the initial stages of the fermentation when GMEM medium was employed, but improved dramatically following the switch to the more enriched medium. 35 Target protein productivity was essentially constant during the period from

~100 to 700 h of the 760 h fermentation, as measured by ELISA using Mab 9E10 as the capture antibody and biotinylated Mab 24-31 as the developing antibody.

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Soluble IGF-1R/462 protein was recovered from harvested fermentation medium by affinity chromatography on columns prepared by coupling Mab 9E10 to divinyl sulphone-activated agarose beads (Mini Leak; Kem En Tec, Denmark) as recommended by the manufacturer. Mini-Leak Low and Medium affinity columns with antibody loadings of 1.5-4.5 mg/ml of hydrated matrix were obtained, with the loading range of 2.5-3 mg/ml giving optimal performance (data not shown). Mab 9E10 was produced by growing hybridoma cells (American Tissue Culture Collection) in serum-free medium in the Celligen Plus bioreactor and recovering the secreted antibody (4 g) using protein A glass beads (Prosep-A, Bioprocessing Limited, USA). Harvested culture medium containing IGF-1R/462 protein was adjusted to pH 8.0 with Tris-HCl (Sigma), made 0.02% (w/v) in sodium azide and passed at 3-5 ml/min over 50 ml Mab 9E10 antibody columns at 4° C. Bound protein was recovered by recycling a solution of 2-10 mg of the undecamer c-myc peptide EQKLISEEDLN (Hoogenboom et al., 1991) in 20 ml of Tris-buffered saline containing 0.02% sodium azide (TBSA). Between 65% and 75% of the product was recovered from the medium as estimated by ELISA, with a further 15-25% being recovered by a second pass over the columns. Peptide recirculation (~10 times) through the column eluted bound protein more efficiently than a single, slower elution. Residual bound protein was eluted with sodium citrate buffer at pH 3.0 into 1 M Tris HCl pH 8.0 to neutralize the eluant, and columns were re-equilibrated with TBSA.

Gel filtration over Superdex S200 (Pharmacia, Sweden), of affinity-purified material showed a dominant protein peak at ~63 kDa, together with a smaller quantity of aggregated protein (Figure 3a). The peak protein migrated primarily as two closely spaced bands on reduced, sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE; Figure 3b), reacted positively in the ELISA with both Mab 24-60 and Mab 24-31, and gave a single sequence corresponding to the N-terminal 14 residues of IGF-1R. No binding of IGF-1 or IGF-2 could be detected in the solid plate binding assay (Cosgrove et al., 1995, Protein Express Purif. 6:789-798). The IGF-1R/462 fragment was further purified by ion-exchange chromatography on Resource Q (Pharmacia, Sweden). Using shallow salt gradients, protein enriched in the

slowest migrating SDS-PAGE band was obtained (data not shown), which formed relatively large, well-formed crystals (see below). Isoelectric focusing showed the presence of one major and two minor isoforms. Protein purified on Resource Q with an isocratic elution step of 0.14 M NaCl in 20 mM TrisCl at pH 8.0 (fraction 2, Figure 4) showed less heterogeneity on isoelectric focusing (Figure 4 inset) and SDS-PAGE (data not shown) and produced crystals of sufficient quality for structure determination (see below).

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Crystals were grown by the hanging drop vapour diffusion method using purified protein concentrated in Centricon 10 concentrators (Amicon Inc, USA) to 5-10 mg/ml in 10-20 mM Tris-HCl pH 8.0 and 0.02% (w/v) azide, or 100 mM ammonium sulfate and 0.02% (w/v) azide. A search for crystallization conditions was performed initially using the factorial screen (Jancarik, J. & Kim, S.-H.,1991, J Appl Cryst 24:409-411) and subsequently optimised. Crystals were examined on an M18XHF rotating anode generator (Siemens, Germany) equipped with Franks mirrors (MSC, USA) and RAXIS IIC and IV image plate detectors (Rigaku, Japan).

From the initial crystallization screen of this protein, crystals of about 0.1 mm in size grew in one week. Upon refining conditions, crystals of up to $0.6 \times 0.4 \times 0.4$ mm could be grown from a solution of 1.7-2.0 M ammonium sulfate, 0.1 M HEPES pH 7.5. The crystals varied considerably in shape and diffraction quality, growing predominantly as rhombic prisms with a length to width ratio of up to 5:1, but sometimes as rhombic bipyramids, the latter form being favoured when using material which had been eluted from the Mab 9E10 column at pH 3.0. Each crystal showed a minor imperfection in the form of very faint lines from the centre to the vertices. Protein from dissolved crystals did not appear to be different from the protein stock solution when run on an isoelectric focusing gel. Upon X-ray examination, the crystals diffracted to 3.0-4.0 Å and were found to belong to the space group $P2_12_12_1$ with a = 76.8 Å, b = 99.0 Å, c = 119.6 Å. In the diffraction pattern, the crystal variability noted above was manifest as a large (1-2°) and anisotropic mosaic spread, with concomitant variation in resolution. To improve the quality of the crystals, they were grown in the presence of various additives or were recrystallized. These methods failed to substantially improve the crystal quality although bigger crystals were obtained by recrystallization. The variability in crystal quality appeared to be due to protein heterogeneity, as demonstrated by the observation that more

highly purified protein, eluted isocratically from the Resource Q column and showing one major band on isoelectric focusing (Figure 4 inset), produced crystals of sufficient quality for structure determination. These crystals diffracted to 2.6 Å resolution with cell dimensions, a = 77.0 Å, b = 99.5 Å, c = 120.1 Å and mosaic spread of 0.5°. Heavy metal derivatives of the IGF-1R/462 crystals have been obtained and are leading to the determination of an atomic resolution structure of this fragment, which contains the L1, cysteine-rich and L2 domains of human IGF-1R.

EXAMPLE 2

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10 Expression, Purification and Crystalization of the IR Fragment

A similar strategy was adopted for the human insulin receptor. The fragment expressed (residues 1-485) comprises the L1-cysteine-rich-L2 region of the IR ectodomain but extends 13 residues further before the attachment of the 17 residue EK cleavage site linker and c-myc tail. The selected truncation position corresponds to a unique and convenient Bgl II restriction site. The expression strategy was also based on the pEE14 expression vector in glycosidase-defective Lec8 cells and use of a C-terminal c-myc affinity tag for immunoaffinity purification by specific peptide elution. These procedures yielded IR protein which readily crystallized after a gel filtration polish.

The expression plasmid pHIR485 was constructed by ligating the double-stranded oligonucleotide cassette:

Bgl II

25 5' AGATC TCCGACGATGACGATAAG GAACAAAAACTCATCTCAGAAGAGGATCTGAAT TAG TCTAGA 3'

K I S D D D K E Q K L I S E E D L N

EK cleavage c-myc tail Stop

encoding an enterokinase cleavage site, c-myc epitope tag (Hoogenboom, H. R., et al., 1991, Nucleic acids Res. 19:4133-4137) and stop codon, to the larger 11.1 kilobasepair Bgl II / Xba I fragment isolated from digestion of the mammalian expression plasmid pEH3 (a derivative of the mammalian plasmid expression vector pEE14 [Bebbington, C. R. & Hentschel, C. C. G., 1987. In: Glover, D. M., ed. DNA Cloning. Academic Press. San Diego. Vol 3, p163: Celltech Ltd., UK] which holds the entire coding sequence of human insulin receptor within a Hind III /Xba I fragment). Lec8 mutant CHO cells

(Stanley, P. 1989, Molec. Cellul. Biol. 9:377-383) obtained from the American Tissue Culture Collection (CRL:1737) were transfected with pHIR485 using Lipofectamine (Gibco-BRL). Cell lines were maintained after transfection in glutamine-free medium (Glascow modification of Eagle's medium - GMEM; ICN Biomedicals, Australia) and 10% dialysed FCS (Sigma, Australia) containing 25 µM methionine sulphoximine (MSX; Sigma, Australia) as described (Bebbington, C. R. & Hentschel, C. C. G., 1987, In: Glover, D. M., ed. DNA Cloning. Academic Press, San Diego. Vol 3, p163). Transfectants were screened for protein expression by Western blotting and sandwich enzyme-linked immunosorbant assay (ELISA) (Cosgrove, L., et al., 1995,) using anti-hIR (Mab) 83.7 as the primary antibody and biotinylated monoclonal antibody (Mab) 9E10 (Evan et al., 1985) for detection (Soos et al., 1986; gifts from Ken Siddle, University of Cambridge, UK). Large-scale cultivation of selected clones expressing IR/485 was carried out in a Celligen Plus bioreactor (New Brunswick Scientific, USA) containing 70 g Fibra-Cel Disks (Sterilin, UK) as carriers in a 1.25 L working volume. Continuous perfusion culturé was carried out using DMEM/F12 without glutamine medium (ICN), supplemented with non-essential amino acids, nucleosides, 25 μM MSX and 5 - 10% FCS and resulted in an estimated overall yield of 115 mg of receptor protein from 165 L of harvested medium. Target protein productivity was essentially constant during the fermentation, as measured by ELISA.

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Soluble IR/485 protein was recovered from harvested fermentation medium by affinity chromatography on columns of Mab 9E10 essentially as described in Example 1. Between 92 -98% of the product was recovered from the medium by this affinity-chromatography step, as estimated by ELISA.

Gel filtration over Superdex 200 (Pharmacia, Sweden), of the affinity-purified material at 1mg/ml produced a dominant protein peak at apparent mass ~140 kDa (Figure 5a - interpreted as dimer), whereas a peak at apparent mass ~85 kDa was obtained (Figure 5b - interpreted as monomer) at 0.02 mg/ml. The protein migrated as a single broad band of apparent molecular mass ~78 kDa (reduced- lane A) or ~68 kDa (non-reduced - lane B) on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE; Figure 6a) The IR/485 fragment reacted positively in the ELISA with Mab 83-7, gave a single sequence corresponding to the N-terminal 10 residues of IR, showing several isoforms on isoelectric focussing from pI 6.0 - 6.8 (Figure

6b). Crystallisation screening trials of the fragment produced crystals too small for X-ray diffraction studies. The fragment was further purified by ion-exchange chromatography on Uno Q (BioRad, USA), using stepwise isocratic elution with incremental changes in salt concentrations (Figure 7). Fractions A and D were each enriched in a component isoform from the ladder of isoforms present in the unfractionated mixture (Figure 6b). Both these fractions produced crystals, whereas no crystals were obtained from fractions B and C.

Crystals were grown by the hanging drop vapour diffusion method using purified protein concentrated in Centricon 10 concentrators (Amicon Inc, USA) to 5-10 mg/ml in 10mM Tris-HCl pH 8.0 and 0.02% (w/v) azide. A search for crystallization conditions was performed initially using the factorial screen (Jancarik, J. & Kim, S.-H.,1991, J Appl Cryst 24:409-411) and subsequently optimised. Crystals were examined on an M18XHF rotating anode generator (Siemens, Germany) equipped with Franks mirrors (MSC, USA) and an RAXIS IIC image plate detector (Rigaku, Japan).

From the initial crystallization screen of this protein fraction D fine needles grew in about one week. In further experiments, crystals of up to $0.04 \times 0.04 \times 0.2$ mm could be grown from a solution of 1.9-2.0 M ammonium sulfate, 2% PEG 400, 0.1 M HEPES pH 7.5. Upon X-ray examination, the crystals diffracted to 4 Å and were found to belong to the space group $P2_12_12_1$ with a = 103.2 Å, b = 130.0 Å, c = 161.6 Å. Despite their small size these crystals diffracted sufficiently well to allow collection of a low resolution data set. Further purification of the protein and refinement of crystallisation conditions should yield larger crystals, providing data to determine the structure of this fragment at medium resolution or better.

EXAMPLE 3

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Structure of the IGF-1R/1-462

Crystals were cryo-cooled to-170°C in a mother liquor containing 20% glycerol, 2.2 M ammonium sulfate and 100 mM Tris at pH 8.0. Native and derivative diffraction data were recorded on Rigaku RAXIS IIc or IV area detectors using copper $K\alpha$ radiation from a Siemens rotating anode generator with Yale/MSC mirroroptics. The space group was $P2_12_12_1$ with a = 77.39 Å, b = 99.72 Å. and c = 120.29 Å. Data were reduced using DENZO and SCALEPACK (Otwinowski, Z. & Minor, W., 1996, Mode.Meth. Enzym. 276:307-326). Diffraction was notably anisotropic for all crystals examined.

Phasing by multiple isomorphous replacement(MIR) was performed with PROTEIN (Steigeman, W. Dissertation (Technical Univ. Munich, 1974) using anomalous scattering for both UO2 and PIP derivatives. Statistics for data collection and phasing are given in Table 1. In the initial MIR map regions of protein and solvent could clearly be seen but the path of the polypeptide was by no means obvious. That map was subject to solvent flattening and histogram matching in DM (Cowtan, K., 1994, Joint CCP4 and ESF-EACBM newslett. Protein Crystallogr. 31:34-38). The structure was traced and rebuilt using O (Jones, T. A., et al., 1991, Acta Crystallogr. A47:110-119) and refined with X-PLOR 3.851 (Brunger, A. T., 1996, X-PLOR ReferenceManual 3.851, Yale Univ., New Haven, CT). After 5 rounds of rebuilding and energy minimisation the R-factor dropped to 0.279 and Rfree = 0.359 for data 7-2.6 Å resolution. The current model contains 458 amino acids and 3 N-linked carbohydrates but no solvent molecules. For residues with B(Ca) > 70 Å2atomic positions are less reliable (37-42, 155-159, 305, 336-341, 404-406,453-458). There is weak electron density for residues 459-461 but the c-myc tail appears completely disordered.

The 1-462 fragment consists of the N-terminal three domains of IGF-1R (L1, cys-rich, L2) and contains regions of the molecule which dictate ligand specificity (17-23). The molecule adopts a reasonably extended structure (approximately $40 \times 48 \times 105 \text{ Å}$) with domain 2 (cys-rich region) making contact along the length of domain 1 (L1) but very little contact with the third domain (L2) (see Figure 8). This leaves a space at the centre of the molecule of approximately $24 \text{ Å} \times 24 \text{ Å} \times 24 \text{ Å}$ which is bounded on three sides by the three domains of the molecule. The space is of sufficient size to accommodate the ligand, IGF-1.

The L domains

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Each of the L domains (residues 1-150 and 300-460) adopt a compact shape (24 x 32 x 37 Å) consisting of a single-stranded right handed β -helix and capped on the ends by short a-helices and disulfide bonds. The body of the domain looks like a loaf of bread with the base formed from a flat six-stranded β -sheet, 5 residues long and the sides being β -sheets three residues long (Figures 8 & 9). The top is irregular but in places is similar for the two domains. The two domains are superposable with an rms deviation in Ca positions of 1.6 Å for 109 atoms (Figure 10). Although this fold is reminiscent of other β -helix proteins it is much simpler and smaller with very few

elaborations and thus it represents a new superfamily of domains. One notable difference between the two domains is that the indole ring of Trp 176 from the cys-rich region (Figure 9b) is inserted into the hydrophobic core of L1 and the C-terminal helix is only vestigial (Figure 8). For the insulin receptor family the sequence motif of residues which form the Trp pocket in L1 does not occur in L2 (Figure 9a). However in the EGF receptor, which has an additional cys-rich region after the L2 domain (14, 15), the pocket motif can be found in both L domains and the Trp is conserved in both cys-rich regions (Figure 9b).

The repetitive nature of the β-helix is reflected in the sequence and the first five turns were correctly identified by Bajaj, M., et al. (1987, Biochim.Biophys. Acta 916:220-226), the conserved Gly residues being found in turns making one bottom edge of the domain. However, their conclusions about the fold were incorrect. The"helix-like" repeat is actually a pair of bends at the top edge of the domain. In their Motif V, the Gly is not in a bend but is followed by the insertion of a conserved loop of 7-8 residues (see Figure 9a). Glycine is structurally important in the Gly bends as mutation of these residues compromises folding of the receptor [van der Vorm, E.R., et al., 1992, J. Biol. Chem. 267, 66-71; Wertheimer, E. et al., 1994, J. Biol. Chem. 269, 7587-7592].

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Upon comparing the L domains with other right-handed β-helix structures such as pectate lyase (Yoder, M. D., et al., 1993,.Structure, 1:241-251-1507) and the p22 tailspike protein (Steinbacher, S., et al., 1997, J.Mol. Biol. 267:865-880) there are some striking similarities as well as differences. In all cases the ends of the domain are capped by $\alpha\text{-helices}$ but the L domains also have a disulphide bond at each end to hold the termini. The other βhelix domains are considerably longer and have significant twist to their sheets while the L domains have flat sheets. Although the sizes of the helix repeats are similar (here 24-25 residues vs 22-23 for pectate lyase) the crosssections are quite different. The L domains have a rectangular cross-section while pectate lyase and p22 tailspike protein are V-shaped and have many, and sometimes quite large, insertions (Yoder, M. D., et al., 1993,.Structure, 1:241-251-1507; Steinbacher, S., et al., 1997, J.Mol. Biol. 267:865-880). In the hydrophobic core a common feature is the stacking of aliphatic residues from successive turns of the \beta-helix and near the C-terminus of each L domain there is also a short Asn ladder, reminiscent of the long Asn ladder

observed in pectate lyase (Yoder, M. D., et al., 1993,.Structure 1:241-251-1507). On the opposite side of the L domains the Gly bend as well as the two bends and sheet preceding it have no counterpart in the other β -helix domains. Thus although the L domains are built on similar principles to the other β -helix domains they constitute a separate superfamily.

The cys-rich domain

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The cys-rich domain is composed of eight disulfide-bonded modules (Figure 9b), the first of which sits at the end of L1 while the remainder make a curved rod running diagonally across L1 and reaching to L2 (Figure 8). The strands in modules 2-7 run roughly perpendicular to the axis of the rod in a manner more akin to laminin (Stetefeld, J., et al., 1996, J.Mol. Biol. 257:644-657) than to TNF receptor (Banner, D. W., et al., 1993, Cell, 73:431-445) but the modular arrangement of the cys-rich domain is different to other cys-rich proteins for which structures are known. The first 3 modules of IGF-1R have a common core, containing a pair of disulfide bonds, but show considerable variation in the loops (Figure 9b). The connectivity of these modules is the same as the first half of EGF (Cys 1-3and 2-4) but their structures do not appear to be closely related to any member of the EGF family. Modules 4 to 7 have a different motif, β-finger, and best match residues 2152-2168 of fibrillin (Dowling, A. K., et al., 1996, Cell, 85:597-605). Each is composed of three polypeptide strands, the first and third being disulfide bonded and the latter two forming a β -ribbon. The β -ribbon of each β - finger module lines up antiparallel to form a tightly twisted 8-stranded β-sheet (Figures 8 and 11). Module 6 deviates from the common pattern with the first segment being replaced by an α -helix followed by a large loop that is likely to have a role in ligand binding (see below). As module 5 is most similar to module 7 it is possible that the four modules arose from serial gene duplications. The final module is a disulfide linked bend of five residues.

The fact that the two major types of cys-rich modules occur separately implies that these are the minimal building blocks of cys-rich domains found in many proteins. Although it can be as short as 16 residues, the motif of modules 4-7 is clearly distinct and capable of forming a regular extended structure. Thus cys-rich domains such as these can be considered as made of repeat units each composed of a small number of modules.

Hormone binding

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Attempts have been made to locate the IGF-1 (and insulin) binding site by examining natural (Taylor, S. I., 1992, Diabetes, 41:1473-1490) and site-directed mutants (Williams, P. F., et al., 1995, J. Biol. Chem. 270:3012-3016; Mynarcik, D. C et al., 1996, J. Biol. Chem. 271:2439-2442; Mynarcik, D. C., et al., 1997, J. Biol. Chem. 272:2077-2081), chimeric receptors (Andersen, A. S., et al., 1990, Biochemistry 29:7363-7366; Gustafson, T. A., & Rutter, W. J., 1990, J. Biol. Chem. 265:18663-18667; Schäffer, L., et al., 1993, J. Biol. Chem. 268:3044-3047; Schumacher, R., 1993, J. Biol. Chem. 268:1087-1094; Kjeldsen, T., et al., 1991, Proc. Natl Acad. Sci. USA, 88:4404-4408) and by crosslinking studies (Wedekind, F., et al., 1989, Biol. Chem Hoppe-Seyler, 370:251-258; Fabry, M., 1992, J. Biol. Chem. 267:8950-8956; Waugh, S. M., et al., 1989, Biochemistry, 28:3448-3458; Kurose, T., et al., 1994), J. Biol. Chem.269:29190-29197-34). IGF-1R/IR chimeras not only show which regions of the receptors account for ligand specificity but also provide an efficient means of identifying some parts of the hormone binding site. Paradoxically regions controlling specificity are not the same for insulin and IGF-1. Replacing the first 68 residues of IGF-1R with those of IR confers insulin binding ability on the chimeric IGF-1R (Kjeldsen, T., et al., 1991, Proc. Natl Acad. Sci. USA, 88:4404-4408) and replacing residues 198-300 in the cys-rich region of IR with the corresponding residues 191-290 of IGF-1R allows the chimeric receptor to bind IGF-1 (Schäffer, L., et al.,1993, J. Biol. Chem. 268:3044-3047). Thus a receptor can be constructed which binds both IGF-1 and insulin with near native affinity. From the structure it is clear that if the hormone bound in the central space it could contact both these regions.

From analysis a series of chimeras examined by Gustafson, T. A., & Rutter, W. J. (J. Biol. Chem. 265:18663-18667, 1990) the specificity determinant in the cys-rich region can be limited further to residues 223-274. This region corresponds to modules 4-6 and includes a large and somewhat mobile loop (residues 255-263, mean B[Ca atoms] = 57 Å2) which extends into the central space (see Figure 8). In IR this loop is four residues bigger and is stabilised by an additional disulfide bond (Schäffer, L. & Hansen, P.H..1996, Exp. Clin. Endocrinol. Diabetes, 104: Suppl. 2, 89). The larger loop of IR may serve to exclude IGF-1 from the hormone binding site but allow the smaller insulin molecule to bind. It is interesting to note that mosquito IR homologue, which has a loop two residues larger than the

mammalian IRs, also appears to bind insulin but not IGF-1 (Graf, R., et al., 1997, Insect Molec.Biol. 6:151-163). Analysis of the structure indicates that the insulin/IGF-1 specificity is controlled by residues in this loop (amino acids 253-272 in IGF-1R; amino acids 260-283 in IR)

As chimeras only address residues which differ between the two receptors a more precise analysis of the site can be obtained from single site mutants. In particular, from an alanine-replacement study, four regions of L1 important for insulin binding were identified (Williams, P. F., et al., 1995, J. Biol. Chem. 270:3012-3016). The first three are at similar positions on successive turns of the b-helix and the fourth lies on the conserved bulge on the large b-sheet (Figure 12). Thus there is a footprint for insulin binding to the L1 domain which lies on the first half of large b-sheet facing into the central space. Residues further along the sheet which are conserved in IGF-1R and could also be important. The conservative substitution of leucine for methionine at residue 119 of IR (113 of IGF-1R) causes a mild form of leprechaunism [Hone, J. et al., 1994, J. Med. Genet. 31, 715-716]. This residue is buried and the mutation could perturb neighbouring residues to affect insulin binding.

The axis of the L2 domain is perpendicular to that of the L1 domain and N-terminal end of its β-helix is presented to the hormone-binding site. On this face of the L2 domain the only mutation studied so far is the naturally occurring IR mutant, S323L, which gives rise to Rabson-Mendehall syndrome and severe insulin resistance (Roach, P.,1994, Diabetes 43:1096-1102). As this mutant only affects insulin binding and not cell-surface expression, residue 323 of IR (residue 313 of IGF-1R) is probably at or near the binding site. Structurally this residue lies in the middle of a region (residues 309-318 of IGF-1R) which is conserved in both IR and IGF-1R and the surrounding region, 332-345 (of IGF-1R), is also quite well conserved in the these receptors (Figure 9a). Therefore this region is quite likely to form part of the hormone-binding site but would not have been detected by chimeras. It is interesting to note that in this region IRR is not as well conserved as the other two receptors (Shier, P. & Watt, V.M., 1989, J.Biol.Chem. 264:4605-14608).

The distance from this putative hormone-binding region on L2 to that found on L1 is about 30 Å (Figure 8). Thus L1 and L2 appear too far apart to bind IGF-1 or insulin. However, in the crystal structure there is a deep cleft

between part of the cys-rich domain (residue 262) and L2 (residue 305) and this cleft is occupied by a loop from a neighbouring molecule. Thus it seems probable that the position of the L2 domain in the receptor structure or the hormone-receptor complex adopts a different position with respect to the cys-rich domain than that found in the crystal. The movement required to bring L2 sufficiently close to L1 is small, namely a rotation of approximately 25° about residue 298.

A number of IR mutants have been identified which constitutively activate the receptor and the majority of these are found in the α chain. Curiously all α chain mutants involve changes to or from proline or the 10 deletion of an amino acid, implying that they cause local structural rearrangements. The mutation R86N is similar to wild type but R86P reduces cell-surface expression and insulin binding while constitutively activating autophosphorylation [Grønskov, K. et al., 1993, Biochem. Biophys. Res. 15 Commun. 192, 905-911]. The proline mutation probably disturbs residues preceding 87 which lie in the interface between the L1 and cys-rich domains but it could also affect insulin binding. In the cys-rich domain residues 233, 281, 244 and 247 of IR are not conserved in IGF-1R (Figure 9b) yet L233P [Klinkhamer, M.P. et al., 1989, EMBO J. 8, 2503-2507], deletion of N281 [Debois-Mouthon, C. et al., 1996, J. Clin. Endochronol. Metab. 81, 719-727] or 20 the triple mutant P243R, P244R and H247D [Rafaeloff, R. et al., 1989, J. Biol. Chem. 264, 15900-15904] cause constitutive kinase activation. Due to their locations each of these three mutants appears likely to compromise the folding of a β -finger domain and, in turn, the structural integrity of the rodlike cys-rich domain. The structural ramifications of these mutations could be significant for the whole receptor ectodomain as disturbing the L1/cys-rich interface or distorting the rod-like domain could affect the relative position of L1 and the cys-rich domain in this context.

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L1 has been further implicated as deletion of K121 on the opposite side of L1 from the cys-rich domain was also found to cause autophosphorylation [Jospe, N. et al., 1994, J. Clin. Endochronol. Metab. 79, 1294-1302]. By contrast this mutation does not affect insulin binding. Thus a possible mechanism emerges for insulin binding and signal transduction. When insulin binds between L1 and L2 it modifies the relative position of L1 and the cys-rich domain in the receptor, perhaps by hinge motion between L2 and the cys-rich domain like that suggested above, and the structural

rearrangement is transmitted across the plasma membrane. In the absence of insulin the same signal can be initiated by mutations in the cys-rich region or at the L1/cys-rich interface but at the expense on insulin binding. The signal can also be initiated more directly by mutations on the opposite side of L1 which affect the interaction of L1 with other parts of the ectodomain, possibly the other half of the receptor dimer.

Ligand Studies

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Although there is no structural information about an IGF-1/IGF-1R complex a number of studies have probed the nature of this interaction. Results from cross-linking experiments with IGF-1 and insulin and their cognate receptors are consistent with the hormone binding site proposed above. For example B29 of insulin can be cross-linked to the cys-rich region (residues 205-316((Yip, C. C., et al., 1988, Biochim. Biophys. Res. Commun. 157:321-329) or the L1 domain (Wedekind, F., et al., 1989, Biol. Chem Hoppe-Seyler, 370:251-258). However these two regions are reasonably well separated and those studies may indicate that B29 is mobile. Other studies unfortunately do not map the site any more precisely.

Analogues and site-directed mutants of IGF-1 and -2 have been more fruitful. Relative to insulin IGF-1 and -2 contain two extra regions, the C region between B and A and a D peptide at the C-terminus. For IGF-1 replacement of the C region by a four Gly linker reduced affinity for IGF-1R by a factor of 40 but increased affinity for IR 5-fold (Bayne, M.L., et al., 1988, J. Biol.Chem. 264:11004-11008). Changes in affinity are consistent with the deletion in IGF-1 complementing differences in the cys-rich regions of IGF-1R and IR noted above. Mutation of residues either side of the C region (residue 24 for IGF-1 [Cascieri, M.A., et al., 1988, Biochemistry 27:3229-3233], residues 27,43 for IGF-2, [Sakano, K., et al., 1991, J. Biol. Chem. 266:20626-20635]) also have deleterious effects on the affinity of the hormone for IGF-1R as has truncation of the nearby D peptide in IGF-2 (Roth, B.V., et al., 1991, Biochem. Biophys. Res. Commun. 181:907-914). Insulin has been extensively mutated. Binding studies [summarised in Kristensen, C. et al., 1997, J. Biol. Chem. 272, 12978-12983] indicate that insulin may bind its receptor via a hydrophobic patch (residues A2, A3, A19, B8, B11. B12. B15 and possibly B23 & B24). However this patch is normally buried and requires the removal of the B chain's C-terminus from the observed position. Assuming IGF-1, -2 and insulin bind their receptors in the same

orientation, these data suggest an approximate orientation for the hormone when bound to the receptor.

One notable feature of IGF-1 and -2 is the large number of charged residues and their uneven distribution over the surface. Basic residues are predominantly found in the C region and, in solution, this region is not well ordered in either IGF-1 or -2 (Sato, A., et al., 1993, Int J Peptide Protein Res. 41:433-440; Torres, A. M., et al., 1995, J. Mol. Biol. 248:385-401). In contrast the binding site of the receptor has a sizable patch of acidic residues in the corner where the cys-rich domain departs from L1. Other acidic residues which are specific to this receptor are found along the inside face of the cys-rich domain and the loop (residues 255-263) extending from module 6. Thus it is possible that electrostatics play an important part in IGF-1 binding with the C region binding to the acidic patch of the cys-rich region near L1 and the acidic patch on the other side of the hormone directed towards a small patch of basic residues (residues 307-310) on the N-terminal end of L2.

Although the structure of this fragment gives significant information about the nature of the hormone binding site, residues outside this region have also been shown to affect binding of ligand. A number of studies have implicated residues 704-715 of IR (Mynarcik, D. C et al., 1996, J. Biol. Chem. 271, 2439-2442; Kurose, T., et al., 1994, J. Biol. Chem. 269:29190-29197). These residues could contact insulin on one of the sides left open in the current structure. Using insulin labelled at the B1 residue, Fabry, M., et al., (1992, J. Biol. Chem. 267:8950-8956) cross linked insulin to the fragment 390-488, part of which is not near the site as described. The explanation for this could be either 488 reaches back to the hormone binding site, or this region could contact another hormone bound to the other half of the receptor. Further structural information is needed to establish how these other regions contact the hormone and to elucidate how binding of the hormone is communicated to the kinase inside the cell.

The structure of the L1-cys-rich-L2 domains of IGF-1R presented here represents the first structural information for the extracellular portion of a member of the insulin receptor family. The L domains display a novel fold which is common to the EGF receptor family and the modular architecture of the cys-rich domain implies that smaller building blocks should be used to describe the composition of cysteine-rich domains. This fragment contains the major specificity determinants of receptors of this class for their ligands.

It has an elongated structure with a space in the middle which could accommodate the ligand. The three sides of this site correspond to regions which have been implicated in hormone binding. Although other sites are present in the receptor ectodomain which interact with the ligand this structure gives us an initial view of how the insulin, IGF-1 and -2 might interact with their cell surface receptors to control their metabolic and mitogenic effects

Such information will provide valuable insight into the structure of the corresponding domains of the IR and insulin receptor-related receptor as well as members of the related EGFR family (Bajaj, M., et al., 1987, Biochim Biophys Acta 916:220-226; Ward, C. W. et al., 1995, Proteins: Struct Funct Genet 22:141-153).

EXAMPLE 4

Prediction of 3D Structure of the Corresponding Domains of IRR and IR Based on Structure of IGF-1R Frgament.

The sequence identities between the different members of the insulin receptor family are sufficient to allow accurate sequence alignments to facilitate 3D structure predictions by homology modelling. The alignments of the ectodomains of human IGF-1R, IR, and IRR are shown in Figure 13.

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EXAMPLE 5

25 <u>Prediction of 3D Structure of EGFR and its Family Members ERB2, ERB3</u> and ERB4.

The sequence identities between the different members of the EGFR receptor family and the insulin receptor family are sufficient to allow accurate sequence alignments to facilitate 3D structure predictions by homology modelling. The alignments of the ectodomains of human EGFR, ERB2, ERB3 and ERB4 are shown in Figure 14. The ectodomains of the EGFR family members are composed of four domains: L1 domain. cys-rich domain, L2 domain and a second cys-rich domain all of which can be modelled from the structure of the IGF-1R fragment residues 1-462.

The sequence alignment analysis and characterization of the repeat modules in the cys-rich region of IGF-1R and the homologous regions of the

IR, IRR and the first and second cys-rich regions of EGFR, ErbB2, ErbB3 and ErbB4 are shown in Figure 15. A representative of each subtype of cys repeat is found in the IGF-1R fragment 1-462 and is used to model each of these modules in the other receptors. Note the nature and order of modules in the second cys-rich repeat of the EGFR family is different to that seen in the first cys-rich region.

EXAMPLE 6

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Single-Molecule Imaging of Human Insulin Receptor Ectodomain and its **Fab Complexes**

Cloning and expression of hIR -11 ectodomain protein 10

A full length clone of the human IR exon -11 form (hIR -11) was prepared by exchanging an Aat II fragment, nucleotides 1195 to 2987, of the exon +11 clone (plasmid pET; Ellis et al., 1986; gift from Dr W. J. Rutter, UCSF) of hIR (Ebina et al., 1985, Cell 40, 747-758) with the equivalent Aat II fragment from a plasmid (pHIR/P12-1, ATCC 57493) encoding part of the extracellular domain and the entire cytoplasmic domain of hIR -11 (Ullrich et al., 1985, Nature 313, 756-761). The ectodomain fragment of hIR -11 (2901 bp, coding for the 27 residue signal sequence and residues His1-Asn914) was produced by SalI and SspI digestion and inserted into the mammalian expression vector pEE6.HCMV-GS (Celltech Limited, Slough, Berkshire, UK) into which a stop codon linker had been inserted, as described previously (Cosgrove et al., 1995, Protein Expression and Purification 6, 789-798) for the hIR exon +11 ectodomain.

The resulting recombinant plasmid pHIR II (2 µg) was transfected into glycosylation deficient Chinese hamster ovary (Lec 8) cells (Stanley, 1989, Molec. Cellul. Biol. 9, 377-383) with Lipofectin (Gibco-BRL). After transfection, the cells were maintained in glutamine-free medium GMEM (ICN Biomedicals, Australia) as described previously (Bebbington & Hentschel, 1987. In DNA Cloning (Glover, D., ectodomain.), Vol III, Academic Press, san Diego; Cosgrove et al., 1995, Protein Expression and Purification 6, 789-798). Expressing cell lines were selected for growth in GMEM with 25 μΜ methionine sulphoximine (MSX, Sigma). Transfectants were screened for protein expression using sandwich ELISA with anti-IR monoclonal antibodies 83-7 and 83-14. Metabolic labelling of cells, immunoprecipitations, insulin

binding assays and Scatchard analyses were performed as described 35

previously for the exon +11 form of hIR ectodomain (Cosgrove et al., 1995,, Protein Expression and Purification 6, 789-798).

hIR -11 ectodomain production and purification

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The selected clone (inoculum of 1.28 x 108 cells) was grown in a spinner flask packed with 10 g of Fibra-cel disc carriers (Sterilin, U.K.) in 500 ml of GMEM medium containing 10% fetal calf serum (FCS) and 25 μ M MSX. Selection pressure was maintained for the duration of the culture.

Ectodomain was recovered from harvested media by affinity chromatography on immobilized insulin and further purified by gel filtration chromatography on Superdex S200 (Pharmacia; 1 x 40 cm) in Tris-buffered saline containing 0.02% sodium azide (TBSA) as described previously (Cosgrove et al., 1995, Protein Expression and Purification 6, 789-798). Solutions of purified hIR -11 ectodomain were stored at 4° C prior to use. Production of Fab fragments and their complexes with ectodomain

Purification of Mabs 83-7, 83-14 and 18-44 from ascites fluid by affinity chromatography using Protein A-Sepharose, and the production of Fabs, were based on the methodologies described in Coligan et al.,1993, Current Protocols in Immunology, Vol 1, pp 2.7.1-2.8.9, Greene Publishing Associates & Wiley - Interscience, John Wiley and Sons. Fab was produced from monoclonal antibody by mercuripapain digestion for 1-4 h, followed by gel filtration on Superdex S200. Products were monitored by reducing and non-reducing SDS-PAGE. For 83-7 Mab, an IgG Type 1 monoclonal antibody, the bivalent (Fab)2' isolated by this method was reduced to monovalent Fab 83-7 by mild reduction with mM L-cysteine.HCl in 100 mM Tris pH 8.0 (Coligan et al., 1993, Current Protocols in Immunology, Vol 1, pp 2.7.1-2.8.9, Greene Publishing Associates & Wiley - Interscience, John Wiley and Sons).

Complexes of Fab with hIR -11 ectodomain were produced by mixing ~ 2.5 to 3.5 molar excess of Fab with hIR -11 ectodomain at ambient temperature in TBSA at pH 8.0. After 1-3 h, the complex was separated from unbound Fab by gel filtration over a Superdex S200 column in the same buffer.

Electron microscopy

Uncomplexed hIR -11 ectodomain and the Fab complexes described above were diluted in phosphate-buffered saline (PBS) to concentrations of the order of 0.01-0.03 mg/ml. Prior to dilution, 10% glutaraldehyde (Fluka) was added to the PBS to achieve a final concentration of 1% glutaraldehyde.

Droplets of ~ 3ml of this solution were applied to thin carbon film on 700mesh gold grids after glow-discharging in nitrogen for 30 s. After 1 min. the excess protein solution was drawn off and followed by application and withdrawal of 4-5 droplets of negative stain [2% uranyl acetate (Agar), 2% uranyl formate (K and K), 2% potassium phosphotungstate (Probing and Structure) adjusted to pH 6.0 with KOH, or 2% methylamine tungstate (Agar) adjusted to pH 6.8 with NH4OH]. In the case of both uranyl acetate and uranyl formate staining, an intermediate wash with 2 or 3 droplets of PBS was included prior to application of the stain. The grids were air-dried and then examined at 60kV accelerating voltage in a JEOL 100B transmission electron microscope at a magnification of 100,000x. It was found that there was a typical thickness of negative stain in which Fabs were most easily seen, hence areas for photography had to be chosen from particular zones of the grid. Electron micrographs were recorded on Kodak SO-163 film and developed in undiluted Kodak D19 developer. The electron-optical magnification was calibrated under identical imaging conditions by recording single-molecule images of the antigen-antibody complex of influenza virus neuraminidase heads and NC10 MFab (Tulloch et al., 1986, J.Mol. Biol. 190, 215-225; Malby et al., 1994, Structure, 2, 733-746).

Image processing

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Electron micrographs showing particles in a limited number of identifiable projections were chosen for digitisation. Micrographs were digitised on a Perkin-Elmer model 1010 GMS PDS flatbed scanning microdensitometer with a scanning aperture (square) size of 20 mm and stepping increment of 20 mm corresponding to a distance of 0.2 nm on the specimen. Particles were selected from the digitised micrograph using the interactive windowing facility of the SPIDER image processing system (Frank et al., 1996, *J. Struct. Biol.* 116, 190-199). Particles were scaled to an optical density range of 0.0 - 2.0 and aligned by the PSPC reference-free alignment algorithm (Marco et al., 1996, *Ultramicroscopy*, 66, 5-10). Averages were then calculated over a subset of correctly aligned particles chosen interactively as being representative of a single view of the particle. The final average image presented here is derived from a library of 94 images.

Biochemical characterization of expressed hIR -11 ectodomain

The recombinant protein examined corresponded to the the first 914 residues of the 917 residue ectodomain of the exon -11 form of the human

insulin receptor (Ullrich et al., 1986, Nature 313, 756-761). Expressed protein was shown, by SDS-PAGE and autoradiography of immunoprecipitated product from metabolically labelled cells, to exist as a homodimeric complex of -270 - 320 kDa apparent mass, which dissociated under reducing conditions into monomeric α and β ' subunits of respective apparent mass -120 kDa and -35 kDa (data not shown).

Purified hIR -11 ectodomain, expressed in Lec8 cells and purified by affinity chromatography on an insulin affinity column, ran as a symmetrical peak on a Superdex S200 gel filtration column (Figure 16). The protein eluted with an apparent mass of ~400 kDa, calculated from a standard curve generated by the elution positions of standard proteins (not shown). As expected for protein expressed in Lec 8 cells, whose glycosylation defect produces truncated oligosaccharides (Stanley, 1989, . Molec. Cellul. Biol. 9, 377-383), this value is less than the apparent mass (450 - 500 kDa) reported for hIR +11 ectodomain expressed in wild-type CHO-K1 cells (Johnson et al., 1988, Proc. Natl Acad. Sci USA 85, 7516-7520; Cosgrove et al., 1995, Protein Expression and Purification 6, 789-798).

Radioassay of insulin binding to purified ectodomain gave linear Scatchard plots and Kd values of 1.5 - 1.8 x 10-9 M, similar to the values of 2.4 - 5.0 x 10-9 M reported for the hIR -11 ectodomain (Andersen et al., 1990, Biochemistry 29, 7363-7366; Markussen et al., 1991, J. Biol. Chem. 266, 18814-18818; Schaffer, 1994, Eur. J. Biochem. 221, 1127-1132) and the values of ~1.0 - 5.0 x 10-9 M reported for the hIR +11 ectodomain (Schaefer et al., 1992, J. Biol. Chem. 267, 23393-23402; Whittaker et al., 1994, Molec.

Endocrinol. 8, 1521-1527; Cosgrove et al., 1995, Protein Expression and Purification 6, 789-798).

Expression of hIGF-1R ectodomain

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Cloning, expression and purification of this protein used elements common to those described for hIR -11 ectodomain (Cosgrove et al., 1995, Protein Expression and Purification 6, 789-798) and resulted in purified product that was recognised by receptor-specific Mabs 17-69, 24-31 and 24-60 (Soos et al., 1992. J. Biol. Chem. 267, 12955-63) and was composed of α and β ' subunits of mass similar to those of hIR ectodomain (unpublished data). Preparation of hIR -11 ectodomain/MFab complexes

A complex of hIR -11 ectodomain and Fab from antibody 83-14 eluted as a symmetrical peak of 460 -500 kDa (Figure 16), as did complexes

generated from a mixture of hIR -11 ectodomain with Fab from antibody 18-44 and a mixture of hIR -11 ectodomain with Fab 83-7 (not shown). A cocomplex of ectodomain with Fabs from antibodies 18-44 and 83-14 eluted at ~620 kDa (Figure 12), as did a co-complex with MFabs 83-14/83-7 and another with MFabs 83-7/18-44 (not shown). A complex of hIR -11 ectodomain with all three MFab derivatives, 18-44, 83-7 and 83-14, eluted at an apparent mass of ~710 kDa (Figure 16).

Electron microscopy

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Imaging of hIR -11 and hIGF-1R ectodomains

Single-molecule imaging of undecorated dimeric hIR -11 ectodomain was carried out under a variety of negative staining conditions, which emphasised different aspects of the structure of the molecular envelope. The least aggressive or penetrative stain was potassium phosphotungstate (KPT), which revealed consistent globular particles with very little internal structure other than a suggestion of a division into two parallel bars. Staining with methylamine tungstate also revealed the parallel bar images, as shown in Figure 17a.

Further investigation using progressively more penetrative, but also potentially more disruptive, stains confirmed the observations above. Staining with uranyl acetate and uranyl formate showed the separation of the parallel bars most clearly (Figure 17b), but uranyl acetate showed evidence of disrupting the structure of the particles, i.e. a decrease in the consistency of the particle shape and a tendency for particles to look unravelled or denatured despite having been subjected to chemical cross-linking prior to staining. In areas of thicker stain, parallel bars predominated (Figure 17b), whereas in more thinly stained regions, U-shaped particles could be identified, sometimes outnumbering the parallel-bar structures (Figure 18a). An averaged image of the parallel bars seen by staining hIR -11 ectodomain with uranyl formate is shown as an insert in Figure 17b.

In Figures 17c and 18b, images of hIGF-1R ectodomain are shown for comparison with Figure 17b and 18a, respectively, under similar staining conditions.

Imaging of hIR -11 ectodomain complexed with 83-7 MFab

This complex was particularly noteworthy for the consistency of the form of the particles, especially under the gentler staining conditions afforded by stains such as KPT and methylamine tungstate. The particles

were interpreted as having been restricted in the views they presented, after air-drying on the carbon support film, by the almost diametrically opposite binding of the two Fab arms to the antigen to form a highly elongated complex structure. Under these conditions three distinct views could be recognised as shown in Figure 19. Two views (interpreted as top-down/bottom-up) show the Fab arms displaced clockwise or anti-clockwise as extensions of the parallel plates with two-fold symmetry. The third view shows an image with the two Fab arms in line roughly through the centre of the receptor on its opposite sides, interpreted as a side projection of binding half-way up the plates (Figure 19).

Figure 20 shows a field of particles of hIR -11 ectodomain complexed with 83-7 MFab, stained with uranyl formate. The use of the more aggressive uranyl stains operating at lower pHs revealed internal structure of the molecular envelope at the expense of consistency of the particle morphology. For example, staining with uranyl acetate or uranyl formate showed that parallel bars can be seen in particles in which the Fab arms are displaced either clockwise or anticlockwise but not where the intermediate central or axial position of the two Fab arms is presented in projection. These observations show 83-7 MFab binding roughly half-way up the side-edge of each hIR -11 ectodomain plate. The epitope recognised by Mab 83-7 has been mapped to the cys-rich region, residues 191-297, by analysis of chimeric receptors (Zhang and Roth, 1991, *Proc. Natl. Acad. Sci. USA* 88, 9858-9862).

25 Imaging of hIR -11 ectodomain complexed with either 83-14 MFab or 18-44 MFab

Figure 21a shows the complexes formed with Fabs from the most insulin-mimetic antibody Mab 83-14. Projections showing the Fab arms bound to and extending out from near the base of the U-shaped particles can be identified. A second field of particles (Figure 21b) shows objects composed of two parallel bars as observed for the undecorated ectodomain, with Fab arms projecting obliquely from diametrically opposite extremities. Similar but less definitive images were also seen when MFab 18-44 was bound to hIR -11 ectodomain (not shown). The epitope for Mab 83-14 is between residues 469-592 (Prigent et al., 1990) in the connecting domain. This domain contains one of the disulphide bonds (Cys524-Cys524) between

the two monomers in the IR dimer (Schaffer and Ljungqvist, 1992, Biochem. Biophys. Res. Commun. 189, 650-653). The epitope for Mab 18-44 is a linear epitope, residues 765-770 (Prigent et al., 1990, . J. Biol. Chem. 265, 9970-9977) in the β-chain, near the end of the insert domain (O'Bryan et al., 1991, Mol. Cell. Biol. 11, 5016-5031). The insert domain contains the second disulphide bond connecting the two monomers in the IR dimer (Sparrow et al., 1997, J. Biol. Chem., 272, 29460-29467).

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Imaging of hIR -11 ectodomain co-complexed with two different MFabs per monomer

The double complex of hIR -11 ectodomain with MFabs 83-7 and 18-44 was stained with 2% KPT at pH 6.0, and revealed the molecular envelopes shown in Figure 22. The particle appears complex in shape and can assume a number of different orientations on the carbon support film, giving rise to a number of different projections in the micrograph. The predominant view is of an asymmetric X-shape (some examples circled). It shows the 83-7 MFab arms bound at opposite ends of the parallel bars with the two 18-44 MFabs appearing as shorter projections extending out from either side of each ectodomain.

Images of the double complex of hIR -11 ectodomain with 83-7 and 83-14 MFabs gave X-shaped images similar to those seen with the 83-7/18-44 double complex (not shown). In contrast the double complex of hIR -11 ectodomain with 18-44 and 83-14 MFabs did not present the characteristic asymmetric X-shapes described above (images not shown). Instead, the molecular envelope appeared to be elongated in many views, with only an occasional X-shaped projection. While a detailed interpretation of these images would be premature, it is clear that MFabs 18-44 and 83-14, two of the more potent insulin mimetic antibodies (Prigent et al., 1990, J. Biol. Chem. 265, 9970-9977), can bind simultaneously to the receptor.

Imaging of hIR -11 ectodomain co-complexed with three different MFabs per monomer

Figure 23 shows a field of particles from a micrograph of hIR -11 ectodomain complexed simultaneously with MFabs 83-7, 83-14 and 18-44. In the thicker stain regions the molecular envelope is X-shaped, and looks very similar to that of the double complexes of hIR -11 ectodomain with either 83-7 and 18-44 or 83-7 and 83-14. However, in the more thinly stained regions, particles of greater complexity are visible and it is possible occasionally to

identify that there are in fact more than four MFabs bound to the ectodomain dimer.

The single-molecule imaging of hIR -11 ectodomain presented here suggests a molecular envelope for this dimeric species significantly different from that of any previously published study. However, an unequivocal determination of the molecular envelope even from the present study is not entirely straightforward. A major complicating factor here has been the relative fragility of the expressed ectodomain when exposed to the rigors of electron microscope preparation by negative staining. For example, staining with potassium phosphotungstate (KPT, pH 6.0-7.0) frequently suggested a denaturation of the dimeric molecules, but when appropriate conditions were satisfied, good seemingly interpretable molecular envelope images were achieved; staining with methylamine tungstate (pH ~7.0) supported the best KPT molecular envelope images, but had the suggestion of a swelling of the molecular structure at neutral pH; and the acid-pH stains of uranyl acetate (pH \sim 4.2) and uranyl formate (pH \sim 3.0), with their ability to penetrate the ectodomain structure, appeared to illuminate not so much the molecular envelope as the zones of high projected protein density within the dimer.

An amalgam of impressions from these various staining regimens has led to the following interpretation of single-molecule images of these undecorated, or naked, dimers: the predominant dimeric molecular image encountered here has been that of 'parallel bars' of projected protein density. This view is so predominant, indeed, that it suggests there is either a single preferred orientation of the molecules on the glow-discharged carbon support film, or that this impression of parallel bars of density may represent a mixture of superficially similar structure projections, with the subtleties of these different projections being masked by the relatively coarse resolution of this single-molecule direct imaging. The impression of parallel bars of projected protein density is particularly predominant in regions of thicker negative stain. A second view of the molecular envelope, appreciably less well represented in regions of thicker stain but predominant in regions of thin staining, is that of 'open' U's, or V's. These two views of hIR -11 ectodomain were supported by the single-molecule imaging of hIGF-1R ectodomain under comparable conditions of negative staining.

If the assumption is made that these two recognisable projected views, that of parallel bars and of open U's/V's, are different views of the

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same dimeric molecule, an assumption strongly supported by the MFab complex imaging, a coarse model of the molecular envelope can be rationalized as in the schematic Figure 24. The model structure is roughly that of a cube, composed of two almost-parallel plates of high protein density, separated by a deep cleft of low protein main-chain and side-chain density able to be penetrated by stain, and connected by intermediate stain-excluding density near what is assumed here to be their base (that is, nearest the membrane-anchoring region). The width of the low-density cleft appears to be of the order of 30-35Å, sufficient to accommodate the binding of the insulin molecule of diameter ca. 30Å, although we have no electron microscopical evidence to support insulin-binding in this cleft at this stage.

It has been established through imaging of bound 83-7 MFab that there is a dimeric two-fold axis normal to the membrane surface between these plates of density. Occasionally, dimer images display a relative displacement of the bars of density, interpreted here as a limited capacity for a shearing of the interconnecting zone between the two plates along their horizontal axis parallel to the membrane; other images show bars skewed from parallel, implying a limited capacity for the plates to rotate independently around the two-fold axis, again via this interconnecting zone. These two observations each suggest a relatively flexible connectivity between the dimer plates in the membrane-proximal region of intermediate protein density, which could possibly contribute to the transmembrane signalling process.

The approximate overall measured dimensions of the ectodomain dimer depicted in Figure 24 are 110 x 90 x 120Å, calibrated against the dimensions of imaged influenza neuraminidase heads, known from the solved X-ray structure (Varghese et al., 1983, Nature 303, 35-40). It can be noted that there is a compatibility here between the molecular weights and molecular dimensions of these two molecular species: the compact tetrameric influenza neuraminidase heads of Mr $\sim\!200$ kDa occupy a volume almost 100 x 100 x 60 Å; the more open dimeric insulin receptor ectodomains of similar Mr $\sim\!240$ kDa imaged here occupy a volume approximately 110 x 90 x 120 Å . roughly twice that of the neuraminidase heads, accommodating the slightly higher molecular weight and substantial central low-density cleft.

The low-resolution roughly cubic compact structure proposed here differs substantially from the T-shaped model proposed by Christiansen et al.

(1991, Proc. Natl. Acad. Sci. U. S. A. 88, 249-252) and Tranum-Jensen et al., (1994, J. Membrane Biol. 140, 215-223) for the whole receptor and the elongated model proposed by Schaefer et al. (1992, J. Biol. Chem. 267, 23393-23402) for soluble ectodomain. Significantly, those previous studies did not provide any convincing independent electron microscopical evidence that their imaged objects were in fact insulin receptor.

In the present study, the identity of the imaged molecules as hIR -11 ectodomain has been confirmed by imaging complexes of the dimer with Fabs of the three well-established conformational Mabs against native hIR, 83-7, 83-14 and 18-44 (Soos et al.,1986, Biochem. J. 235, 199-208; 1989, Proc. Natl Acad. Sci. USA 86, 5217-5221), bound singly and in combination. In all these instances, virtually every particle in the field of view exhibited MFab decoration through binding to conformational epitopes, establishing not only the identity of the imaged particles but also the conformational integrity of the expressed ectodomains. Furthermore, the cleanliness and uniformity of these hIR -11 ectodomain preparations, both naked and decorated, visualised here by electron microscopy demonstrate their high suitability for X-ray crystallization trials.

The known flexibility of the Fab arms exacerbates image-to-image variability beyond the limited extent already described for the undecorated dimeric ectodomains, complicating any precise interpretation of these antigen-antibody complexes. Such molecular flexibility also renders largely impractical any single-molecule computer image averaging to facilitate image interpretation, progressively more so with the higher order antigen-antibody complexes studied here.

The most readily interpretable of these images, showing least image-to-image variability, are those of 83-7 MFab bound to dimers where, fortuitously, the antigen-antibody complex is constrained in its degrees of rotational freedom on the carbon support film. Many projected images show the two Fab arms in line roughly through the centre of the antigen on its opposite sides (Figure 19, arrowed examples), interpreted as a side projection of binding half-way up the plates from their membrane-proximal base. Other sub-sets of images (Figure 19, circled examples) show the two Fab arms still parallel but displaced clockwise or anticlockwise with 2-fold symmetry, each Fab approximating an extension of one of the parallel bars of antigen density, interpreted here as representing top or bottom projections

along the 2-fold axis. The third projection, along the axis of the Fab arms, could not be sampled here because of the constraining geometry of this molecular complex. These observations suggest binding of 83-7 MFab roughly half-way up the side-edge of the hIR -11 ectodomain plate. This then allows an initial attempt at spatially mapping the 83-7 MFab epitope, which has been sequence-mapped to residues 191-297 in the cys-rich region of the insulin receptor (Zhang and Roth, 1991, *Proc. Natl. Acad. Sci. USA* 88, 9858-9862). The spatial separation and relative orientations of the two binding epitopes of Mab 83-7 on the hIR -11 ectodomain dimer as indicated here appear inconsistent with the proposal that Mab 83-7 could bind intramolecularly to hIR (O'Brien et al., 1987, *Biochem J.* 6, 4003-4010).

Decoration of the ectodomain dimer with 83-7 MFab established that the two plates of high protein-density are arranged with 2-fold symmetry. Decoration with either 83-14 or 18-44 MFab, on the other hand, allowed sampling of the third projection of the ectodomain dimer precluded by 83-7 MFab binding. Significantly, this third view established unequivocally the U-shaped projection of the hIR -11 ectodomain dimer, something which was only able to be assumed with the undecorated ectodomain images. Further, this projection has allowed a rough spatial mapping close to the base of the U-shaped dimer for the epitopes recognised by 83-14 MFab (residues 469-592, connecting domain) and 18-44 MFab (residues 765-770, b-chain insert domain; exon 11 plus numbering, Prigent et al., 1990, J. Biol. Chem. 265, 9970-9977).

Inherent in the model structure presented in Figure 20 is the implication that, with the two-fold axis aligned normal to the membrane surface, the mouth of the low-density cleft where insulin binding may occur would lie most distant from the transmembrane anchor, whilst the zone of intermediate density connecting the two high-density plates would be in close proximity to the membrane. It follows, in this model, that the L1/cysrich/L2 domains(Bajaj et al., 1997, Biochim. Biophys. Acta 916, 220-226; Ward et al., 1995, Proteins: Struct., Funct., Genet. 22, 141-153), which comprise much of the insulin-binding region (see Mynarcik et al., 1997, . J. Biol. Chem. 272, 2077-2081). most probably lie in the membrane-distal upper halves of the two plates, whilst the membrane-proximal lower halves contain the connecting domains, the fibronectin-type domains, the insert domains and the interchain disulphide bonds (Schaffer and Ljungqvist, 1992, Biochem.

Biophys. Res. Commun. 189, 650-653; Sparrow et al., 1997, J. Biol. Chem., 272, 29460-29467). Such a disposition of domains is supported by the images seen with the single MFab decoration, the 83-7 MFab epitope in the cys-rich region being spatially mapped roughly half-way up the side-edge of the ectodomain plates, and the 83-14 and 18-44 MFab epitopes (connecting domain and β -chain insert domain, respectively) being mapped near the base of the plates. Our preference is for a single a-b¢ monomer to occupy a single plate, although the possibility of a single monomer straddling the two plates of protein density cannot be discounted.

The more complex images involving co-binding of two, and even more so of all three, MFabs to each monomer of the ectodomain dimer (Figures 22 and 23) are not easily interpretable with respect to relative domain arrangements within the monomer at present, not least of all because of the difficulty of finding conditions of negative staining that will simultaneously maintain the integrity of the Fab binding while highlighting recognisable and reproducible details of the internal structure of the dimeric IR ectodomain.

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The data presented here demonstrate the ability of single-molecule imaging to give an initial insight into the topology of multidomain structures such as the ectodomain of hIR, and the value of combining this technique with that of either single or multiple monoclonal Fab attachment per monomer as a potential means of epitope (and domain) mapping of the structure. By imaging Fab complexes of other members of the family (such as hIGF-1R ectodomain) and combining available sequence-mapped epitope information with that presented here, a more comprehensive understanding of domain arrangements within the IR family ectodomains should be forthcoming.

It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive

Dated this twenty-fourth day of March 1998

COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION Patent Attorneys for the Applicant:

F.B. RICE & CO.

Figure 1

ATOH	1 08	GLU	1	55.907	11.986	66.300	1.00 59.11	AAAA C
ATOH	2 06	GLU	1	56.138	11.019	65.162	1.00 78.17	AAAA C
ATOH	3 00	GLU	1	57.382	11.319	64.321	1.00 85.10	AAAA C
ATOH	4 OE1	GLU	1	58.404	10.754	64.796	1.00 86.18	AAAA O
ATOI!		GLU	ī	57.424	12.013	63.270	1.00 78.70	AAAA O
ATOH	6 2	GLU	i	53.508	12.557	66.350	1.00 48.46	AAAA C
HOTA	7 0	GLU	1	52.685	11.863	65.784	1.00 51.27	AAAA O
ATOH	10 11	SLU	1	54.25 6	10.339	67.159	1.00 61.64	AAAA H
ATOH	12 CA	GLU	1	54.602	11.778	67.081	1.00 54.77	AAAA C
ATOR	13 11	ILE	2	53.608	13.860	66.375	1.00 37.66	II AAAA II
ATOH	15 CA	ILE	2	52.768	14.699	65.604	1.00 40.87	AAAA C
ATOH	16 CB	ILE	2	52.925	16.122	66.160	1.00 41.97	AAAA C
ATOH	_	ILE	2	52.036	17.122	65.484	1.00 38.50	AAAA C
ATOH	18 CG1	ILE	2	52.560	16.006	67.663	1.00 46.58	AAAA C
ATOH.	19 CD1	ILE	2	53.150	17.176	68.498	1.00 32.29	AAAA C
ATOH	20 C	ILE	2	53.122	14.711	64.139	1.00 46.47	AAAA C
ATOH	21 0	ILE	2	54.258	15.029	63.852	1.00 51.66	AAAA O
		CYS	3	52.235	14.409	63.196	1.00 49.61	AAAA N
ATOH	22 11							
ATOH	24 CA	CYS	3	52.435	14.677	61.773	1.00 38.93	аааа с
ATOH	25 C	cis	3	51.429	15.708	61.302	1.00 42.06	AAAA C
ATOH	26 O	CYS	3	50.290	15.521	61.690	1.00 42.37	AAAA O
ATOH	27 CB	CYS	3	52.159	13.415	60.999	1.00 35.66	AAAA C
ATOH	28 SG	CYS	3	53.019	12.004	61.674	1.00 36.98	AAAA S
ATOH	29 11	GLY	4	51.851	16.709	60.580	1.00 42.39	II AAAA
					17.718	60.003		
ATOH	31 CA	GLY	4	50.973			1.00 47.71	AAAA C
ATON	32 C	GLY	4	51.703	18.407	58.869	1.00 48.23	AAAA C
ATOH	33 O	GLY	4	52.916	18.345	58.884	1.00 55.36	AAAA O
ATOH	34 11	PRO	5	51.056	19.212	58.048	1.00 49.63	AAAA N
ATOH	35 CD	FRO	5	51.637	19.947	56.860	1.00 45.28	AAAA C
HOTA	36 CA	FRO	. 5	49.605	19.341	58.083	1.00 41.57	AAAA C
		PRO	5		20.703	57.474	1.00 44.30	
ATOH				49.397				AAAA C
ATOH	38 CG	PRO	5	50.632	21.036	56.683	1.00 46.43	AAAA C
ATO:	39 C	PRO	5	48.932	19.217	57.354	1.00 36.40	AAAA C
ATOH	40 0	PRO	5	49.403	17.094	57.396	1.00 43.35	O AAAA
ATOM:	41 #	BLY	5	47.787	18.439	56.795	1.00 39.15	H AAAA H
ATOH!	43 CA	3LY	6	46.996	17.336	56.350	1.00 39.24	AAAA C
ATOL	44 6	GLY	-	47.710	16.365	55.529	1.00 33.68	AAAA C
				48.510				
ATOM	45 0	GLY	6		16.863	54.753	1.00 36.00	AAAA O
ATCH!	46 11	ÏLΞ	7	47.596	15.111	55.788	1.00 35.70	aaaa n
ATOH	48 CA	ILE	7	48.307	14.053	55.141	1.00 37.65	AAAA C
ATON	49 CB	ILE	7	48.556	12.797	55.933	1.00 36.31	AAAA C
ATOH	80 090	ILE	7	49.043	11.700	54.988	1.00 34.67	AAAA C
HOTA	51 C 31	ILE	7	49.561	12.857	57.067	1.00 39.34	AAAA C
	52 CD1	ILE	7	49.678	14.249	57.669	1.00 40.22	AAAA C
ATOH								
ATON	53 C	ILE	7	47.339	13.762	53.977	1.00 45.00	AAAA C
ATON:	54 O	ILE	7	46.150	13.643	54.195	1.00 51.52	O AAAA
ATOH	55 11	ASP	8	47.767	13.631	52.751	1.00 45.60	H AAAA H
ATON	57 CA	ASP	8	46.938	13.293	51.631	1.00 44.05	AAAA C
ATCH.	59 CB	ASP	8	47.003	14.469	50.651	1.00 44.21	AAAA C
ATOH	59 CG	ASP	8	45.909	14.379	49.600	1.00 43.49	AAAA C
HOTA		ASP	B	45.660	13.262	49.096	1.00 51.77	AAAA O
ATOH		ASP	8	45.253	15.374	49.251	1.00 46.94	AAAA O
ATOH	62 C	ASP	8	47.428	12.000	50.992	1.00 42.16	аааа с
ATOH	63 O	ASP	8	48.423	12.143	50.330	1.00 48.50	аааа о
ATOH	64 11	ILE	9	47.096	10.817	51.321	1.00 42.76	AAAA N
ATOH	66 CA	ILE	9	47.441	9.505	50.939	1.00 44.05	AAAA C
HOTA	67 CB	ILE	9	47.212	8.483	52.077	1.00 40.82	AAAA C
ATOH	69 CG2		9	47.669	7.085	51.653	1.00 36.35	AAAA C
HOTA	69 CG1		9	47.888	8.917	53.364	1.00 41.17	AAAA C
						53.286		AAAA C
ATOH	70 CD1		9	49.376	9.947		1.00 43.78	
ATOH	71 C	ILE	9	46.530	9.137	49.794	1.00 51.49	AAAA C
ATOM	72 0	ILE	9	45.338	9.420	49.832	1.00 63.05	AAAA O
ATOH	73 N	ARG	10	47.004	8.417	48.812	1.00 54.87	II AAAA II
ATOH	75 CA	ARG	10	46.283	8.089	47.600	1.00 54.17	AAAA C
HOTA	76 CB	ARG	10	45.703	9.358	47.023	1.00 48.54	AAAA C
ATOH	77 CG	ARG	10	46.361	10.169	45.952	1.00 46.55	AAAA C
ATOH	78 CD	ARG	10	46.002	11.635	46.264	1.00 52.63	AAAA C
HOTA	79 NE	ARG	10	45.082	12.226	45.284	1.00 59.27	AAAA H
ATOH	81 CS	ARG	10	44.269	13.262	45.498	1.00 56.22	AAAA C
ATOH	82 NH1		10	44.153	13.891	46.666	1.00 55.14	II AAAA II
ATOH	95 NH2	ARG	10	43.455	13.803	44.602	1.00 52.29	H AAAA H
ATOH	98 €	ARG	10	47.019	7.373	46.492	1.00 57.23	AAAA C
ATOH	89 0	ARG	10	48.240	7.288	46.281	1.00 56.32	AAAA O
ATCH	14 09	ASN	11	46.248	6.654	45.629	1.00 57.23	AAAA N
ATOH	92 CA	ASH	11	46.800	5.917	44.494	1.00 50.73	AAAA C
ATON	93 CB	ASN	11	47.704	6.798	43.671	1.00 44.65	AAAA C
ATOH	64 CC	ASN	11	46.878	7.732	42.829	1.00 50.72	AAAA C
ATOH	95 OD1	ASN	11	45.749	7.451	42.403	1.00 72.59	AAAA O
ATOH	96 ND2	ASH	11	47.499	8.869	42.587	1.00 54.38	H AAAA H
ATOH		ASII	11	47.635	4.736	44.915	1.00 53.07	AAAA C
ATOH		ASN	11	47.303	3.701	44.347	1.00 51.95	. AAAA O
				48.566	4.822		1.00 50.96	
ATOH		ASF	12			45.878		AAAA II
ATOH	103 CA	ASP	12	49.204	3.570	46.263	1.00 55.44	AAAA C

ATCH	104 CB ASP	12	50.568 3.568	45.758	1.00 66.47	aaaa c	
		12	50.879 4.026		1.00 68.25	AAAA C	
ATOH	105 00 ASP				1.00 58.31	AAAA O	
ATOH	106 OD1 ASP	12	50.441 3.185				
ATOH	197 ODC ASP	12	51.391 5.120	43.989	1.00 70.56	AAAA O	
ATOH	108 C ASP	12	49.061 3.322	47.758	1.00 59.23	AAAA C	
		12	49.687 3.849		1.00 59.65	AAAA O	
ATOH	109 O ASP				1.00 59.64	AAAA N	
ATOM	110 N TYR	13	48.411 2.187				
ATOH	112 CA TYR	13	48.328 1.672	49.397	1.00 64.06	AAAA C	
ATOH	113 CB TYR	13	47.968 0.196	49.409	1.00 64.56	AAAA C	
		13	47.467 -0.357		1.00 69.18	AAAA C	
ATOH						AAAA C	
HOTA	115 CD1 TYR	13	46.216 -0.024		1.00 72.71		
ATOH	116 CE1 TYR	13	45.746 -0.541	52.450	1.00 71.51	AAAA C	
	117 CD2 TYR	13	48.233 -1.247	51.457	1.00 70.36	AAAA C	
ATOH			47.788 -1.778		1.00 71.64	AAAA C	
ATOH	118 CE2 TYR	13					
HOTA	119 CS TYR	13		53.160	1.00 71.31	AAAA C	
ATOII	120 OH TYR	13	46.144 -1.977	54.358	1.00 63.25	AAAA O	
	122 C TYR	13		50.198	1.00 65.99	AAAA C	
ATOH					1.00 65.01	AAAA O	
HOTA	123 O TYR	13	49.621 2.321				
ATOH:	124 II GLII	14	50.786 1.541		1.00 63.51	aaaa n	
IOTA	126 CA GLN	14	52.078 1.681	50.218	1.00 63.51	AAAA C	
	127 CB GLH	14	53.174 1.318		1.00 68.37	AAAA C	
HOTA					1.00 84.62	AAAA C	
HOTA	128 CG GLN	14	52.863 -0.078				
HOTA	129 CD GLN	14	53.990 -0.515		1.00 92.28	AAAA C	
HOTA	130 OE1 GLN	14	53.945 -0.161	46.573	1.00 94.82	AAAA O	
		14	54.920 -1.254	48.361	1.00 98.03	N AAAA	
ATOH					1.00 61.62	AAAA C	
ATCH	134 C GLN	14	52.434 3.058				
HOTA	135 O GLN	14	53.266 3.292		1.00 62.09	AAAA O	
HOTA	136 II GLII	15	51.628 4.038	50.349	1.00 57.02	AAAA II	
		15	51.724 5.399		1.00 51.71	AAAA C	
ATO:					1.00 43.75	AAAA C	
ATOI:	139 CB GLII	15	50.861 6.220				
ATON	140 CG GLH	15	51.566 6.605	48.648	1.00 59.65	AAAA C	
ATOH	141 CD GLN	15	51.554 8.105	48.428	1.00 72.96	AAAA C	
			51.168 9.005		1.00 80.58	AAAA O	
ATO! I	142 OE1 GLH	15				AAAA N	
ATOH	143 NE2 GLN	15	52.016 8.378		1.00 74.17		
HOTA	146 C GLN	15	51.219 5.530	52.258	1.00 50.15	AAAA C	
	147 O GLN	15	51.576 6.500	52.940	1.00 48.04	AAAA O	
HOTA	_		50.440 4.535		1.00 46.22	AAAA D	
ATOH	142 H LEU	16				AAAA C	
ATOH	150 CA LEV	16	49.913 4.449				
ATO!!	151 CB 180	15	48.950 3.295	54.159	1.00 37.73	AAAA C	
	150 OG LEV	16	47.502 3.425	53.707	1.05 41.40	AAAA C	
ATCI:			46.837 2.063			AAAA C	
ATOH	153 CO1 LEU	16					
ATOH	154 CDZ LEU	16	46.687 4.424	54.545	1.00 35.93	AAAA C	
HOTA	185 C LEU	16	51.042 4.280	55.039	1.00 51.52	AAAA C	
		16	50.913 4.601		1.00 52.53	AAAA O	
ATO:1					1.00 51.01	AAAA N	
ATOH	157 H LYS	17	52.252 3.936				
ATON	159 CA LY <i>s</i>	17	53.422 3.914		1.00 50.73	AAAA T	
ATOH	160 CB LYS	17	54.609 3.252	54.737	1.00 56.10	aaaa t	
		17	54.539 1.733		1.00 62.40	AAAA C	
ATO!!	161 C3 LYS				1.00 63.95	AAAA C	
AT OH	162 CD LYS	17	54.769 1.278				
HOTA	163 CE LYS	17	55.316 -0.141	53.426	1.00 68.40	aaaa d	
ATOH	164 NG LYS	17	56.537 -0.225	52.554	1.00 73.83	AAAA ::	
		17	53.944 E.270		1.00 44.78	AAAA C	
ATCH	168 C LYS				1.00 39.39	AAAA O	
1!OTA	169 O LYS	17	54.492 5.262				
HOTA	170 N ARG	18		55.201	1.00 41.15	AAAA II	
11OTA	172 CA ARG	18	53.827 7.673	55.676	1.00 43.01	AAAA C	
	173 CB ARG	18	53.250 8.702	54.704	1.00 43.97	AAAA C	
ATOH					1.00 53.60	AAAA C	
ATO14	174 CG ARG	18					
HOTA	175 CD ARG	18	52.964 9.362		1.00 60.34	AAAA C	
ATOM	176 NE ARG	18	52.528 10.703	52.650	1.00 50.00	II AAAA	
HOTA	178 CS ARG	18	51.628 11.444	52.021	1.00 48.86	aaaa c	
	_		51.068 10.941	50.943	1.00 47.96	II AAAA	
ATOI-I	179 NH1 ARG	18			1.00 43.72	AAAA !!	
ATO!	182 NH2 ARG	18	51.377 12.656		-		
ATO:1	185 C ARG	18	53.268 7.924		1.00 44.03	AAAA C	
HOTA	186 O ARG	18	53.402 9.010	57.644	1.00 45.53	AAAA O	
	187 N LEU	19	52.445 7.069		1.00 46.36	II AAAA	
HOTA					1.00 50.25	AAAA C	
ATO14	189 CA LEU	19	51.653 7.282				
ATOH	190 CB LEU	19	50.186 6.924		1.00 50.83	AAAA C	
ATOH	191 CG LEU	19	49.202 7.371	57.608	1.00 46.43	AAAA C	
		19	47.846 6.743		1.00 22.57	AAAA C	
ATOH					1.00 45.88	AAAA C	
ATOH	193 CD2 LEU	19	49.018 8.866				
ATOH	194 C LEU	19	52.210 6.428	59.912	1.00 49.87	AAAA C	
ATOH	195 O LEU	19	51.870 6.810	61.030	1.00 51.54	AAAA O	
		20	53.270 5.708		1.00 49.35	AAAA II	
HOTA	196 N GLU					AAAA C	
11OTA	198 CA GLU	20	53.919 4.933		1.00 49.60		
ATCH	199 CB GLU	29	54.876 3.960		1.00 57.91	AAAA C	
ATOII	200 CG GLU	20	55.893 4.940	59.272	1.00 70.16	AAAA C	
	•	20	57.095 4.077	58.757	1.00 69.35	AAAA I	
ATOH	_					AAAA O	
ATOH	202 OE1 GLU	20	58.123 4.795		1.00 71.39		
ATCH	203 OE2 GLU	20	56.993 2.885	58.420	1.00 72.84	AAAA O	
HOTA	204 C GLU	20	54.310 5.417	61.989	1.00 43.55	AAAA C	
		20	54.301 4.652		1.00 40.01	AAAA O	
HOTA						AAAA II	
ATOH	206 H ASH	21	54.633 6.659		1.00 41.06		
ATOH	208 CA ASII	21	55.054 7.204	63.454	1.00 47.17	aaaa c	
ATÓH	209 C ASN	21	54.066 8.141	64.108	1.00 49.76	AAAA I	
ALOH)							
2011	****	21	54 220 0 156	65.303	1.00 48.10	AAAA 🗘	
ATOH	210 O ASH	21	54.228 9.456	65.303	1.00 48.10	AAAA ©	

ATCU	211	CP.	AGH	21	56.379	E.003	63.290	1 00	59.11	AAAA C
									_	
FRITA	212	3.2	ASII	21	57.413	7.051	62.796		60.38	AAAA C
ATCH	213	OD1	LASH	21	57.499	5.855	63.122	1.00	58.51	AAAA O
ATOH	214	HD2	IIZA :	21	58.348	7.469	61.890	1.00	77.90	N AAAA N
ATOH	216	11	CIS	22	53.129	8.711	63.351	_	47.44	AAAA II
ATOH	218	CA	CIS	22	52.107	9.614	63.879	1.00	42.99	AAAA C
A'TOH	219	Ĉ	CYS	22	51.215	9.089	65.021	1.00	40.43	AAAA C
ATOH	220	O	CYS	22	50.750	7.923	65.069	1 00	36.07	AAAA O
ATOH	221	CB	CYS	22	51.182	9.921	62.690		44.82	AAAA C
ATOH	222	SG	CYS	22	52.076	19.328	61.148	1.00	39.51	AAAA S
ATOH	223	11	THR	23	51.287	9.801	66.137		36.24	II AAAA
ATOH	225	CA	THR	23	50.339	9.482	67.204		43.51	AAAA C
ATOH	226	CB	THR	23	50.944	9.481	68.593	1.00	41.38	AAAA C
INTA	227	051	THR	23	51.410	19.843	68.822	1.00	51.21	AAAA O
		030		23	52.110	8.571	68.838		33.83	AAAA C
ATOH	229									
ATOH	230	C	THR	23	49.250	10.599	67.116	1.00	44.55	AAAA C
ATOH:	231	0	THR	23	48.085	10.414	67.481	1.00	45.95	AAAA O
ATOH	232	11	VAL	24	49.646	11.797	66.689		33.03	AAAA II
HOTA	234	CA	VAL	24	48.732	12.855	66.442	1.00	35.29	AAAA C
HOTA	235	CB	VAL	24	48.925	13.979	67.456	1.00	30.60	AAAA C
ATOH	236	CGI	VAL	24	48.056	15.157	67.082	1.00	27.21	AAAA C
ATOH	237		VAL	24	48.656	13.566	68.886		25.37	AAAA C
HOTA	238	Ξ.	VAL	24	48.895	13.447	65.043	1.00	41.52	AAAA C
HOTA	239	0	VAL	24	49.987	13.963	64.791	1.00	44.40	AAAA O
			ILE		47.855					
ATOH	240	} }		25		13.450	64.203		40.13	AAAA N
ATC#1	242	CA	ILE	25	47.908	14.094	62.882	1.00	32.05	AAAA C
ATOH	243	CB	ILE	25	47.113	13.299	61.853	1.00	25.85	AAAA C
HOTA	244		ILE	25	47.027	14.039	60.542		18.73	AAAA C
ATOH	245	CGI	ILE	25	47.677	11.896	61.705	1.00	29.80	AAAA C
HOTA	246	CD1	ILE	25	47.169	11.155	60.471	1.00	27.41	AAAA C
ATOH	247	C	ILE	25	47.397	15.490	62.941		32.92	AAAA C
ATOH	248	၁	ILE	_. 25	46.223	15.776	63.213		40.91	O AAAA
ATO!!	249	Ţ,	GLU	26	48.264	15.472	63.042	1.00	36.50	II AAAA
ATOH	251	CA	GLU	26	47.832	17.847	63.226	1.00	29.24	AAAA C
ATOH	252	23	GLU	26	48.875	18.703	53.856		29.92	AAAA C
ATOH:	253	2/3	GLU	25	49.490	20.144	54.116	1.00	38.06	AAAA C
HOTA	254	CD	GLU	26	49.561	20.762	65.013	1.00	37.39	aaaa c
HOTA	255	OEL		26	50.654	20.937	54.489		41.56	C EEEA
aton!	256	350		26	49.571	21.175	66.182		49.16	AAAA O
ATOH	257	•	GLU	26	47.413	18.376	51.869	1.00	37.79	AAAA C
ATOH	259	C	GLU	26	48.161	19.069	51.191	1.00	39.59	AAAA O
		::	GLY							
ATON	259			27	45.117	19.104	61.582		37.29	AAAA H
ATON!	261	CA	GLY	27	45.498	18.503	60.320	1.00	31.17	AAAA C
ATOH	262	Ç	GLY	27	44.531	17.400	59.893	1.00	33.72	AAAA C
ATOH	263	ō	GLY	27	43.988	15.715	60.775		33.29	AAAA O
ATOH	5.54	!;	TYR	28	44.304	17.209	53.604	1.00	29.24	AAAA II
ATOH	266	CA	TYR	29	43.319	16.189	59.253	1.00	28.93	AAAA C
ATOH:	267	CE.	TYR	29	42.403	16.794	57.217	3 00	31.53	AAAA C
										7.7.7.
ATC:	268	23	TYR	28	43.058	17.256	55.962		31.78	AAAA C
ATOH:	269	251	TIR	29	43.704	16.355	55.116	1.00	36.07	AAAA C
ATOH	270	CEL	TYR	29	44.361	16.706	53.967	1.00	29.91	AAAA C
ATOH:	271	702	TYR	28	43.130	19.572	\$5.606		30.99	AAAA C
ATOH	272	CE2		28	43.769	18.972	54.428		28.77	ала с
ATOH	273	CS	TYR	28	44.367	18.021	53.652	1.00	31.53	АААА С
ATOH:	274	ОН	TYR	28	44.971	18.425	52.464	1.00	44.74	O AAAA
ATOI1	276	C	TYR	28	43.953	14.946	57.697	_	29.23	AAAA C
ATON:	277	0	TYR	28	45.119	15.147	57.383		35.58	AAAA O
ATOH:	278	11	LEU	29	43.250	13.900	57.445	1.00	26.63	и аааа
HOTA	280	ÇA	LEU	29	43.764	12.730	56.803	1.00	29.83	AAAA C
ATOH	281	CB	LEU	29	43.830	11.611	57.856		27.09	AAAA C
ATOH	282	CG	LEU	29	44.212	10.258	57.242		31.90	AAAA C
ATOH	283	CD1	LEU	29	45.538	10.396	56.469	1.00	35.C3	AAAA C
ATOM	294	CD2	LEU	29	44.551	9.203	58.290	1.00	25.05	AAAA C
	285		LEU	29					33.84	
ATOH		c			42.897	12.342	55.616			AAAA C
ATOH	296	0	LEU	29	41.689	12.165	55.806	1.00	43.29	O KAAA
ATOH	287	11	HIS	30	43.389	12.285	54.395	1.00	35.95	II AAAA II
ATOH	289	CA	HIS	30	42.681	11.891	53.197		34.92	AAAA C
ATOH	290	CB	HIS	30	42.893	12.801	52.027		32.85	AAAA C
HOTA	291	CG	HIS	30	42.372	14.155	52.046	1.00	25.08	AAAA C
HOTA	292	CD2	HIS	30	41.519	14.753	52.907		.40.88	AAAA C
	293		HIS	30	42.717				33.66	
ATOI!						15.120	51.128			AAAA II
ATOH1	295		HIS	30	42.080	16.281	51.444		31.33	AAAA C
ATOH	296	HE2	HIS	30	41.329	16.093	52.539	1.00	37.27	II AAAA II
ATOH	298	c	HIS	30	43.173	10.538	52.714		37.63	AAAA C
ATOH	565	0	HIS	30	44.357	10.388	52.541		38.70	AAAA O
ATOH:	300	11	ILE	31	42.308	9.542	52.584	1.00	40.02	AAAA 11
ATOH	302	CA	ILE	31	42.750	8.271	51.992		39.47	AAAA C
ATOH	303	CB	ILE	31	42.668	7.204	53.063		37.95	AAAA C
ATO:1	304	CG2	ILE	31	43.161	5.830	52.651	1.00	23.86	AAAA C
ATOM	305	CG1	ILE	31	43.481	7.555	54.335	1.00	41.66	AAAA C
	306	CDI		31	43.170	6.575	55.473		28.22	
ATOH										AAAA C
ATOH	307	Ç	ILE	31	41.884	8.044	50.755		46.52	AAAA C
ATOH	308	0	ILE	31	40.753	7.589	50.827	1.00	43.56	AAAA O
ATOH	309	11	LEU	32	42.314	9.489	49.556		49.89	AAAA II
		CA	LEU	32			48.380			
ATOH	311	-		ت د	41.484	8.235	10.300	1.90	49.77	AAAA C

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ATON	310 OB LEU	32	41.127	9.515	47.60.	3 1.00 47.48	AAAA C
ATOR	313 OG LEU	32	42.091	10.688	17.56		AAAA C
ATOU	314 CD1 LEU	32	41.517	11.813			AAAA C
ATOH	315 CD2 LEU	32	42.371	11.229			AAAA C
HOTA	316 C LEU	32	42.136	7.296			AAAA C
ATOH	317 O LEU	32	43.338	7.370			AAAA O
ATOH	318 II LEU	33	41.270	6.722			
ATOH	320 CA LEU	33	41.602	6.175			II AAAA
ATOH	321 CB LEU	33	42.091	7.262			AAAA C
ATON	322 CG LEU	33					AAAA C
			41.233	8.537			AAAA C
IOTA	323 CD1 LEU	33	41.892	9.587			AAAA C
ATOH	324 CD2 LEU	33	39.823	8.313			AAAA C
ATOH	325 C LEU	33	42.618	5.073		1.00 48.35	AAAA C
ATOH	326 O LEU	33	43.580	5.077	44.538	1.00 54.14	AAAA O
ATOH	327 II ILE	34	42.543	4.213	46.254	1.00 47.61	AAAA N
ATOH	329 CA ILE	34	43.523	3.194	46.540	1.00 51.70	AAAA C
ATOH	330 CB ILE	34	44.101	3.346	47.963	1.00 57.98	AAAA C
ATOH	331 CG2 ILE	34	44.538	2.043	48.600		AAAA C
ATCH	332 CG1 ILE	34	45.267	4.371	47.967		AAAA C
ATO!!	333 CD1 ILE	34	45.561	4.704	49.439		AAAA C
ATOH	334 C ILE	34	42.829	1.844	16.408		AAAA C
HOTA	335 O ILE	34	41.726	1.531	46.856		
ATOH	336 II SER	35	43.622	0.833			AAAA O
ATOH	338 CA SER	35			46.013		AAAA N
	339 CB SER	35	43.048	-0.511	45.922		AAAA C
ATOH			42.767	-0.882	44.469		AAAA C
ATO11	340 OG SER	35	41.731	-1.846	44.498		AAAA O
ATOH	342 C SER	35	43.928	-1.564	46.537		AAAA C
ATOM	343 O SER	35	44.885	-1.954	45.909		AAAA O
ATOH	344 H LYS	36	43.687	-2.017	47.740	1.00 74.75	AAAA N
ATOM	346 CA LYS	36	44.465	-3.014	48.421	1.00 76.09	аааа с
HOTA	347 CB LYS	36	44.046	-3.131	49.885	1.00 81.22	AAAA C
ATOH	348 CG LYS	36	45.147	-3.654	50.775	1.00 78.87	AAAA C
ATON	349 CD LYS	36	44.693	-4.575	51.887	1.00 81.39	AAAA C
ATOH	350 CE LYS	36	44.890	-6.025	51.492	1.00 89.38	AAAA C
ATOH	351 NO LYS	36	44.371	-6.989	52.506	1.00 91.63	II AAAA
ATOH	355 C LYS	36	44.252	-4.362	47.753	1.00 81.41	AAAA C
ATOH:	356 O LYS	36	43.145	-4.772	47.451	1.00 78.20	AAAA O
ATOL	357 % ALA	37	45.371	-5.080	47.615	1.00 88.27	
ATON:	359 CA ALA	37	45.361				AAAA II
ATOL:	360 CB ALA	37		-6.396	46.986	1.00 90.10	. AAAA C
			46.700	-6.655	46.327	1.00 95.49	AAAA C
ATOH:	361 C ALA	37 37	45.011	-7.473	47.995	1.00 92.36	AAAA C
ATO!!	362 0 ALA	37	45.668	-7.627	19.012	1.00 92.35	AAAA O
ATOH	363 H SER	38	44.931	-9.301	47.622	1.00 94.31	AAAA H
ATOR	365 CA SER	38	43.528	-9.352	49.484	1.00 95.70	AAAA C
ATOH	366 CB SER	38	42.405 -		.7.858	1.00 97.44	AAAA C
ATON	367 OG SER	38	42.061 -		49.814	1.00103.48	AAAA O
Armi	369 C SER	39	44.702 -	10.263	48.821	1.00 96.87	AAAA C
ATOM	370 0 SER	38	44.761 -	10.778	49.924	1.00 98.06	AAAA O
ATCH:	371 N ASP	39	45.384 -	10.415	47.852	1.00 97.99	AAAA II
ATO! I	373 CA ASS	39	46.821 -	11.142	47.990	1.00 99.19	, AAAA C
ATO!!	374 CB ASP	39	47.579 -		46.652	1.00102.13	AAAA C
ATO:	378 C3 ASP	39	47.696 -		45.948	0.01101.22	AAAA C
ATOH	376 OD1 ASP	39	46.544 -		45.623	0.01101.42	AAAA O
ATOH	377 OD2 ASP	39	49.933 -				AAAA O
HOTA	378 C ASP	39	47.560 -		49.105	1.00 99.40	AAAA C
ATOH	379 O ASP	39	47.592 -		50.224	1.00 99.15	AAAA O
HOTA	380 N TYR	40		-9.479	49.818	1.00100.96	AAAA N
HCTA	382 CA TYR	40		-9.706	49.802	1.00101.16	AAAA C
ATOH	383 CB TYR	40		-7. 3 93	49.130	1.00103.67	
HOTA	384 CG TYR	40	_				AAAA C
HOTA	385 CD1 TYR	40		-6.281	49.887	1.00107.81	AAAA C
HOTA	386 CE1 TYR	40		-5.325	49.228	1.00109.56	AAAA C
ATOIL	387 CD2 TYR			-1.280	49.910	1.00109.67	AAAA C
		40		-6.115	51.254	1.00109.28	AAAA C
HOTA	388 CE2 TYR	10		-5.102	51.976	1.00109.83	AAAA C
ATOH	389 CC TYR	40		-4.191	51.276	1.00110.16	АААА С
ATOH	390 OH TYR	40		-3.127	51.893	1.00109.84	AAAA O
ATOI1	392 C TYR	10		-8.529	51.100	1.00 99.10	AAAA C
HOTA	393 O TYR	40	47.168 -	-8.182	51.183	1.00 99.05	AAAA O
HOTA	394 N LYS	41		-8.653	52.218	1.00 98.62	II AAAA
ATOH	396 CA LYS	41		-8.549	53.546	1.00100.30	AAAA C
HOTA	397 CB LYS	41		9.160	54.599	1.00104.42	AAAA C
ATOH	398 CG LYS	41	19.218 -1		54.814	0.01101.06	AAAA C
ATOH	399 CD LYS	41	47.776 -1		54.919	0.01100.66	AAAA C
ATOH	400 CE LYS	41	47.205 -1		56.308	0.01 99.86	AAAA C
ATOH	401 HE LYS	41	47.982 -1		57.328	0.01 99.62	AAAA II
ATOI1	405 C LYS	41			53.947	1.00 98.99	AAAA C
HOTA	406 O LYS	41			53.057	1.00103.33	AAAA O
ATOH	407 II SER	42			55.221	1.00 91.75	AAAA U
ATOH	409 CA SER	42					
ATOH	410 CB SER	42			55.604	1.00 85.06	AAAA C
ATOM	411 OG SER	45			56.147	1.00 95.33	AAAA C
ATOH					57.426	1.00104.63	AAAA O
		42			56.687	1.00 80.78	AAAA C
ATOH	414 O SER	42			57.538	1.00 91.03	AAAA O
ATOH	415 U TYR	43			56.676	1.00 73.03	AAAA II
HOTA	417 CA TYR	13	49.069 -	2.498	57.635	1.00 67.25	AAAA c

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ATME	419 CB TYR	43	49.086	-1.119	56.965	1.00 65.37	AAAA C
ATORE	419 CG TYR	43	49.953				AAAA C
ATOL	420 CD1 TYR	43	50.931				AAAA C
ATOH	421 CEL TYR	43	51.698				AAAA C
ATOH	422 CD2 TYR	43	49.770				
							AAAA C
ATOH		43	50.536				AAAA C
ATOH	424 CS TYR	43	51.508			1.00 66.94	AAAA C
ATOII	425 OH TYR	43	52.262		. 52.305		AAAA O
ATOH	427 C TYR	43	48.248			1.00 64.88	AAAA C
ATOH	428 O TYR	43	47.088				аааа о
ATOH	429 II ARG	44	48.782			1.00 57.88	aaaa n
HOTA	431 CA ARG	44	48.019	-1.285	61.039	1.00 56.45	AAAA C
ATOH	432 CB ARG	4 4	47.840	-2.611	61.760	1.00 46.51	AAAA C
ATOH	433 CG ARG	44	47.815	-2.375	63.244	1.00 54.66	AAAA C
ATOH	434 CD ARG	44	46.985	-3.327	63.986	1.00 58.54	AAAA C
ATOH	435 HE ARG	44	47.090	-2.927	65.403	1.00 69.56	AAAA N
ATOH	437 CE ARG	44	46.464			1.00 64.82	AAAA C
ATOH	438 UH1 ARG	44	45.644	-4.529		1.00 61.63	AAAA N
ATOH	441 HH2 ARG	44	46.674	-3.139		1.00 66.03	AAAA N
ATOH	444 C ARG	44	48.811	-0.285		1.00 55.59	AAAA C
		44					
ATOH			49.916			1.00 58.43	AAAA O
ATOH	446 II PHE	45	48.276	0.866		1.00 51.13	AAAA N
ATOH	448 CA PHE	45	48.865	1.944		1.00 45.94	AAAA C
ATOH	449 CB FHE	45	48.774	3.249		1.00 35.89	AAAA C
ATOH	450 CG PHE	45	49.106	2.937		1.00 30.29	AAAA C
ATOH	451 CD1 PHE	45	50.373	3.051	59.998	1.00 45.72	аааа с
ATOH!	452 CD2 PHE	45	48.127	2.428	59.728	1.00 35.95	AAAA C
ATOH	453 CE1 PHE	45	50.653	2.715	58.672	1.00 47.76	AAAA C
HOTA	454 CE2 FHE	45	48.358	2.096	58.406	1.00 39.92	AAAA C
ATO!	455 C2 PHE	45	49.612	2.244	57.867	1.00 46.44	AAAA C
ATCH	456 C PHE	45	48.181	2.123	64.203	1.00 41.65	аааа с
ATOH	457 O FHE	45	47.708	3.223		1.00 40.99	AAAA O
ATOH	459 11 280	4.6	48.494	1.338	65.212	1.00 43.20	II AAAA
ATO:	459 CD FRO	45	49.300	0.097		1.00 47.74	AAAA C
ATO:	450 CA PRO	46	49.032	1.530		1.00 43.34	AAAA C
ATC	461 CB FRO	46	48.514	0.319		1.00 44.92	AAAA C
		46					
ATC::			49.404	-0.464		1.00 45.48	AAAA C
ATO::	465 C FRO	4.5	49.558	2.768	67.233	1.00 41.30	AAAA C
ATO:	464 0 FRO	46	49.329	2.930	68.443	1.00 44.57	O AAAA
ATOL	465 H LYS	47	49.450	3.533		1.00 39.33	II AAAA II
AT 31	467 CA LYS	÷ 7	49.991	4.679		1.00 38.10	AAAA C
ATO:	469 CB LYS	47	51.379	4.981	66.852	1.00 49.07	AAAA C
ATC:	469 CG LYS	47	52.032	3.995	65.902	1.00 67.95	AAAA C
ATC::	469 C3 LYS 470 CD LYS	47	53.563	3.976	65.891	1.00 61.33	AAAA C
ATC: i	471 CE LYS	47	54.115	4.549	67.147	1.00 72.19	AAAA C
ATO::	472 NO LYS 476 O LYS	47	54.024	6.132	66.874	1.00 79.29	H AAAA N
ATO::	#76 C LYS	4.7	49.014	5.849	67.195	1.00 39.76	AAAA C
ATO:	477 0 EYS	47	49.189	6.827	67.952	1.00 35.45	AAAA O
ATO:	478 N LEU	49	49.300	5.986	66.053	1.00 36.45	II AAAA
ATON	450 CA LEV	19	47.370	7.004	65.800	1.00 49.40	AAAA C
ATC::	481 GB LEV	49	46.923	5.919	64.389	1.00 28.59	AAAA C
ATGI	490 GG LEU	49	45.947	7.967	63.787	1.00 31.04	AAAA C
ATON	493 CD1 LEU	48	46.637	9.310	63.878	1.00 36.96	AAAA C
ATON	494 CD2 LEU	48	45.591		62.294		AAAA C
		48					
:ICTA			46.186	7.022	66.807	1.00 42.21	AAAA C
ATO:	496 O LEU	48	45.271	6.187		1.00 36.48	AAAA O
ATO! 1	487 N THR	49	46.138	8.041	67.673	1.00 38.95	n aaaa
ATO:	499 CA THR	49	45.045	8.151	68.574	1.00 37.96	AAAA C
ATOL	490 CB THR	49	45.548	8.207	70.034	1.00 48.69	аааа с
IDTA	491 OG1 THR	49	46.396	9.340	70.225	1.00 35.90	AAAA O
ATOH	493 CG2 THR	49	46.230	6.957	70.529	1.00 31.99	AAAA C
ATC:	494 C THR	49	44.230	9.425	68.321	1.00 39.48	аааа с
HOTA	195 O THR	49	43.111	9.451	68.837	1.00 34.49	AAAA O
ATC:	496 N VAL	50	44.735	10.415	67.605	1.00 37.32	AAAA N
ATCH	498 CA VAL	50	43.995	11.664	67.418	1.00 38.72	AAAA C
HOTA	499 CB VAL	50	44.293	12.708	68.503	1.00 37.24	AAAA C
ATOI:	500 CG1 VAL	50	43.630	14.066	68.208	1.00 29.96	AAAA C
ATOH	501 CG2 VAL	50	43.884	12.311	69.913	1.00 32.52	AAAA C
ATOH	502 C VAL	50	44.271	12.305	66.048	1.00 37.03	AAAA C
ATO:	503 O VAL	50	45.195	11.863	65.431	1.00 37.96	AAAA O
ATOH	504 N ILE	51	43.319	12.939	65.415	1.00 37.49	M AAAA
ATOH	506 CA ILE	51					
			43.301	13.575	64.133		AAAA C
IICTA	507 CB ILE	51		12.864	63.152	1.00 34.51	AAAA C
HCTA	508 CGC ILE	51	41.995	13.802	61.978	1.00 32.31	AAAA C
ATCH	509 CG1 ILE	51	43.026	11.611	62.671	1.00 30.78	AAAA C
ATOH	510 CD1 ILE	51	42.358	10.559		1.00 19.69	AAAA C
HOTA	511 C ILE	51	42.659	14.939	64.431	1.00 34.14	AAAA C
ATOH	512 O ILE	51	41.546	14.830	64.923		AAAA O
ATOH	513 N THR	52	43.342	16.058	64.238	1.00 33.93	N AAAA
ATCH	515 CA THR	52	42.806	17.305	64.719		AAAA C
ATOH	516 CB THR	52	43.961	18.338	64.939	1.00 35.39	AAAA C
ATOU	517 OG1 THR	52	44.726	18.567	63.781	1.00 41.28	AAAA O
HOTA	519 CG2 THR	52	44.775	17.926	66.134	1.00 22.01	AAAA C
ATOI:	520 C THR	52	41.741	17.961		1.00 39.02	AAAA C
ATOI:	521 O THR	52	41.202	19.030		1.00 38.88	AAAA O
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ATM	900 H GLU	53	41.504	17.477	62,639	1.00 36.93	AAAA N		
ATON	524 CA GLU	53	40.434			1.00 38.38	AAAA C		
ATSH	505 CB GLU	53	41.064			1.00 29.76	AAAA C		
ATOH	526 OG GLU	53	42.061	19.552		1.00 30.48	AAAA C		
ATOH	527 CD GLU	53	42.517			1.00 40.82	AAAA C		
ATOH	528 OE1 GLU	53	42.638		58.556	1.00 57.56	AAAA O		
ATCH	529 OE2 GLU	53	42.799			1.00 35.74	AAAA O		
ATOH	530 C GLU	53	39.506		61.388	1.00 39.19	AAAA C		
ATOH	531 O GLU	53	38.922	16.311	62.386	1.00 38.95	AAAA O		
ATOH	532 H TYR	54	39.639		60.102	1.00 30.60	AAAA N		
ATOH	534 CA TYR	54	38.666		59.713	1.00 35.96	AAAA C		
ATOH	535 CB TYR	54	37.654	15.602		1.00 30.71	AAAA C		
ATOH	536 CG TYR	54	38.247	16.476		1.00 21.18	AAAA C	•	
ATO!1	537 CD1 TYR	54	38.487	15.733	56.305	1.00 20.22	AAAA C		
INTA	538 CEL TYR	54	38.980	16.243	55.086	1.00 21.04	AAAA C		
ATOH	539 CD2 TYR	54	38.577	17.944	57.307	1.00 23.97	AAAA C		
ATOH	540 CE2 TYR	54	39.049	18.394	56.124	1.00 24.69	AAAA C		
ATOH	541 CZ TYR	54	39.263	17.569	55.032	1.00 26.72	AAAA C		
ATOH	542 OH TYR	54	39.763	18.047	53.847	1.00 37.55	AAAA O		
ATOH	544 C TYR	54	39.405	14.115	59.142	1.00 33.87	AAAA C		
HOTA	545 O TYR	54	40.513	14.360	58.678	1.00 30.40	AAAA O		
ATOH	546 N LEU	55	38.683	13.001	59.004	1.00 23.24	AAAA II		
ATOH	548 CA LEU	55	39.111	11.612	58.454	1.00 30.08	AAAA C		
ATOH	549 CB LEU	55	39.011	10.663	59.510	1.00 14.78	AAAA C		
ATOH	550 CG LEU	55	39.349	9.314	58.818	1.00 26.98	аааа с		
HOTA	551 CD1 LEU	55	40.668	9.477	58.040	1.00 26.66	аааа с		
HOTA	552 CD2 LEU	55	39.496	8.093	59.705	1.00 14.45	AAAA C		
HOTA	553 C LEU	55	38.201	11.548	57.238	1.00 37.43	AAAA C		
HOTA	554 O LEU	55	36.995	11.632	57.427	1.00 39.55	AAAA O		
ATOH	555 H LEU	56	38.700	11.348	56.035	1.00 41.83	aaaa n		
ATOH	557 CA LEU	56	37.955	11.201	54.799	1.00 36.98	AAAA C		
ATOH	558 CB LEU	56	37.998	12.446	53.949	1.00 33.29	AAAA C		
ATO!	559 CG LEU	56	37.984	12.514	52.416	1.00 30.35	AAAA C		
ATOI:	560 CD1 LEU	56	37.076	11.460	51.821	1.00 47.95	AAAA C		
HOTA	561 CD2 LEV	56	37.286	13.807	51.985	1.00 33.47	AAAA C .		
ATOH	562 C LEV	56	38.595	19.947	54.008	1.00 39.75	AAAA C		
ATOH	S63 O LEU	56	39.714	10.205	53.547	1.00 44.38	AAAA O		
ATCH	564 N LEU	57	37.846	9.008	53.800	1.00 36.68	AAAA N		
ATOH	BAA CA LEU	57	39.133	7.932	53.034	1.00 41.53	AAAA C		
ATOH	567 CP LEV	57	37.944	6.568	53.916	1.00 37.00	AAAA C		
ATO:	568 CG LEU	57	39.064	6.534	55.025	1.00 36.13 1.00 33.26	AAAA C		
ATOH	569 CD1 LEU 570 CD2 LEU	57 57	38.513 39.630	6.930 5.160	56.417 55.039	1.00 33.20	AAAA C AAAA C		
ATCH		57	37.203	7.925	51.838	1.00 46.03	AAAA C		
ATOH ATOH	571 C 15U 572 O 15U	57	35.985	7,993	51.969	1.00 44.78	AAAA O		
ATCH	573 N FHE	59	37.792	7.928	50.642	1.00 47.07	AAAA N		
ATOH	575 CA PHE	58	36.995	2.112	49.467	1.00 49.75	AAAA C		
ATOLL	576 CB RHE	58	36.704	6.446	49.102	1.00 46.57	AAAA C		
ATOH	577 C3 PHE	59	36.447	9.815	47.692	1.00 54.66	AAAA C		
ATOH:	578 CC1 PHE	59	37.413	9.706	46.697	1.00 55.19	AAAA C		
ATOH:	579 CDD PHE	58		10.301	47.326	1.00 53.96	AAAA C		
ATOH	590 CE1 PHE	58	37.124	10.163	45.396	1.00 50.36	AAAA C		
ATO:	581 CE2 PHE	58	34.985	10.655	46.011	1.00 41.84	AAAA C		
ATOH	582 CC PHE	58	35.877	10.521	45.037	1.00 46.50	AAAA C		
ATO!!	593 C PHE	58	37.351	7.052	48.379	1.00 49.71	AAAA C		
HOTA	594 O PHE	58	38.487	7.073		1.00 52.16	AAAA O		
HOTA	585 N ARG	59	36.471	6.118		1.00 44.26	и алал		
HOTA	587 CA ARG	59	36.753	5.291		1.00 40.80	аааа с		
ATOH	588 CB ARG	59	36.911	5.993		1.00 23.79	AAAA C		
HOTA	589 CG ARG	59	35.869	7.020		1.00 46.53	AAAA C		
ATOH:	590 CD ARG	59	35.921	7.562		1.00 37.64	AAAA C		
ATOH.	591 NE ARG	59	35.822	6.422		1.00 49.23	AAAA N		
ATOH	593 CC ARG	59	34.950	5.932		1.00 41.36	AAAA C		
ATOH	594 HH1 ARG	59	33.702	6.277	41.931	1.00 47.00	AAAA N		
INTA	597 NHC ARG	59	35.237	4.729		1.00 42.58	AAAA II		
ATOH	600 C ARG	59	38.037	4.494		1.00 42.25	AAAA C AAAA O		
ATOH	601 O ARG 602 N VAL	59 60	38.981 38.001	4.513 3.625	46.232 48.023	1.00 44.11	AAAA II		
ATOH	602 N VAL 604 CA VAL	60	39.101	2.743		1.00 39.14	AAAA C		
HOTA	605 CB VAL	60	39.624	3.066		1.00 40.12	AAAA C		
ATOH ATOH	606 CG1 VAL	60	40.407	1.872		1.00 35.05	AAAA C		
ATOH	607 CG2 VAL	60	40.425	4.352		1.00 28.86	AAAA C		
ATOH	608 C VAL	60	38.539	1.337		1.00 43.56	AAAA C		
ATCI1	609 O VAL	60	37.535	1.224		1.00 47.66	AAAA O		
ATOL	610 H ALA	61	39.094	0.371		1.00 41.92	AAAA II		
ATOH	612 CA ALA	61	38.617	-0.992		1.00 42.05	AAAA C		
ATOI1	613 CB ALA	61	38.302	-1.483		1.00 52.40	AAAA C		
ATOH:	614 C ALA	61	39.613	-1.934		1.00 43.08	AAAA C		
ATOH	615 O ALA	61	40.757	-1.602		1.00 50.59	AAAA O		
ATOI1	616 N GLY	62	39.200	-3.105		1.00 45.71	AAAA II		
ATOH	618 CA GLY	62	40.136	-4.079		1.00 45.39	AAAA C		
ATOH	619 C GLY	62	40.262	-3.902		1.00 48.04	AAAA C		
ATOH:	620 O GLY	62	40.587	-4.835		1.00 52.34	AAAA O		
ATOH	621 H LEU	63	39.985		-	1.00 46.90	AAAA II		
ATOH	623 CA LEU	63	40.003	-2.443	52.805	1.00 49.11	AAAA C		

.

ATFE	614 CB LEV	53	40.274	-0.953	3 53.027	1.00 41.41	AAAA C
ATGG	605 OG LEU	63	40.265	-0.423	3 54.443	3 1.00 53.41	AAAA C
ATOH	636 CDI LEU	63	41.172	-1.164			AAAA C
ATOL	607 CDC LEV	63					
			40.637	1.047			AAAA C
ATOH	ess c ren	63	38.643	-2.881	53.323	1.00 54.20	AAAA C
ATO:	629 O LEU	63	37.587	-2.430	52.837	1.00 57.73	AAAA O
ATO(1	630 H GLU	64	38.658	-3.862			II AAAA
ATOH		64	37.462	-4.448			AAAA C
ATOH	633 CB GLU	64	37.689	-5.956	54.734	1.00 65.33	AAAA C
ATOH	634 CG GLU	64	37.832	-6.484	53.293		AAAA C
ATOH	635 CD GLU	64	37.404	-7.940	_		
							AAAA C
ATOH	636 OE1 GLU	64	37.424	-8.698			AAAA O
ATOH	637 OEC GLU	64	37.036	-0.320	51.978	1.00 88,77	AAAA O
ATOH	638 C GLU	64	37.096	-4.007			AAAA C
	639 O GLU	64					
ATOH			35.986	-4.332			AAAA O
ATON	640 II SER	65	37.766	-3.042	56.761	1.00 50.64	AAAA II
ATOH	642 CA SER	65	37.539	-2.523	58.060	1.00 47.19	AAAA C
ATOH	643 CB SER	65	37.743	-3.596			AAAA C
ATOH	614 OG SER	65	37.501	-2.971			AAAA O
HOTA	646 C SER	65	38.516	-1.405	58.432	1.00 48.35	AAAA C
ATOH	647 O SER	65	39.716	-1.692	58.374		AAAA O
HOTA	649 II LEU	66					
			38.054	-0.289			II AAAA II
ATOH	650 CA LEU	66	38.956	0.758	59.405	1.00 41.94	AAAA C
ATO!!	651 CB LEU	66	38.247	2.093	59.498	1.00 25.25	AAAA C
HOTA	652 CG LEU	66	37.283	2.476			AAAA C
ATOH	653 CD1 LEU	66	36.974	3.951		1.00 30.81	AAAA C
ATOH	654 CD2 LEU	66	37.767	2.200	56.994	1.00 34.34	AAAA C
HOTA	655 C LEU	66	39.646	0.462	60.734	1.00 45.39	AAAA C
ATOI1	656 O LEU	66	40.762	0.947	60.927	1.00 41.05	AAAA O
ATOH:	657 N GLY	67	39.000	-0.346	61.583	1.00 45.21	AAAA N
HOTA	659 CA GLY	67	39.773	-0.672	62.799		AAAA C
ATOH							
		67	40.998	-1.508	62.445	1.00 44.51	AAAA C
HOTA	661 O GLY	· 67	41.855	-1.724	63.287	1.00 45.42	аааа о
ATOH	662 N ASP	68	41.013	-2.189	61.309	1.00 47.60	AAAA II
ATOI:	664 CA ASP	68	42.194	-2.834	60.738		
						1.00 50.99	AAAA C
ATOH	665 CB ASP	68	42.012	-3.417	59.361	1.00 39.43	AAAA C
ATCH	666 CG ASP	5 8	41.205	-4.679	59.311	1.00 45.82	AAAA C
ATOH	667 OD1 ASF	-68	40.912	-5.341	60.320	1.00 44.69	AAAA O
ATOI:	669 OD2 ASP	69	40.819	-5.065	58.187	1.00 47.23	
							AAAA O
ATOH	669 C ASP	69	43.363	-1.937	60.596	1.00 45.89	AAAA C
ATO!!	670 C ASP	68	44.436	-2.269	60.903	1.00 44.84	AAAA O
ATO::	571 H LEU	59	43.145	-0.609	60.247	1.00 42.49	AAAA H
ATOH	673 CA LEU	69	44.175	0.352	60.048	1.00 45.90	
							AAAA C
HOTA	674 CB LEU	69	43.920	1.393	58.945	1.00 45.25	AAAA C
ATQ!1	675 GG LEU	59	43.902	0.882	57.494	1.00 54.25	AAAA C
ATOH	676 CE1 LEU	69	43.541	2.037	56.565	1.00 47.26	AAAA C
ATOH	677 CD2 LEU	69					
			45.211	0.200	57.113	1.00 50.76	AAAA C
ATOH:	678 C LEU	ē 3	44.347	1.107	61.350	1.00 49.50	AAAA C
ATOH	679 O LEU	59	45.470	1.210	61.851	1.00 54.51	AAAA O
ATOH	580 H PHE	7 Q	43.296	1.737	61.869	1.00 44.60	AAAA II
ATCH	692 CA PHE	70		2.564			
			43.423		63.046	1.00 39.67	AAAA C
ATCH	683 TB PHE	70	42.997	3.973	62.700	1.00 26.08	AAAA C
ATOH	694 C3 PHE	70	43.465	4.501	61.390	1.00 45.32	AAAA C
ATOH	685 ID1 PHE	70	42.532	4.749	60.384	1.00 47.41	AAAA C
ATOH		70	44.815				
				4.767	61.130	1.00 48.77	AAAA C
ATOH	687 CE1 PHE	70	42.945	5.263	59.159	1.00 56.16	AAAA C
ATOH	698 CE2 PHE	70	45.229	5.256	59.895	1.00 47.24	AAAA C
! IOTA	689 CZ PHE	70	44.293	5.506	58.896	1.00 49.54	AAAA C
ATOH	690 C PHE	70					
			42.655	1.999	64.219	1.00 40.09	AAAA C
HOTA	691 O PHE	70	41.874	2.734	64.838	1.00 35.74	AAAA O
ATOH	692 II FRO	71	43.053	0.852	64.768	1.00 39.19	N AAAA
ATOH	693 CD PRO	71	44.269	0.058	64.411	1.00 39.94	AAAA C
ATOH	694 CA PRO	71	42.444	0.237	65.899	1.00 35.30	AAAA C
ATOH	695 CB PRO	71	43.308	-0.983	66.246	1.00 38.03	AAAA C
ATOH	696 CG PRO	71	44.669	-0.564	65.717	1.00 38.36	AAAA C
ATOH	697 C PRO	71	42.453	1.089	67.126	1.00 33.72	AAAA C
ATOI1	698 O PRO	71					
			42.005	0.630	68.159	1.00 39.32	aaaa o
ATO!!	699 N ASN	72	43.058	2.220	67.231	1.00 36.55	H AAAA H
HOTA	701 CA ASN	72	43.204	3.032	68.401	1.00 32.60	AAAA C
ATOH1	702 CB ASN	72	44.637	2.916	68.962	1.00 36.89	AAAA C
ATOH	703 CG ASN						
		72	44.735	1.638	69.761	1.00 47.03	AAAA C
ATOH	704 OD1 ASN	72	44.644	1.619	70.979	1.00 64.42	AAAA O
ATOH:	705 ND2 ASN	72	44.880	0.475	69.169	1.00 63.17	AAAA II
HOTA	708 C ASN	72	42.875	4.477	68.135	1.00 30.11	AAAA C
ATOH		72					
			43.099	5.201	69.104	1.00 36.53	AAAA O
ATOH	710 N LEU	73	42.309	4.809	66.978	1.00 27.62	II AAAA II
ATOH	712 CA LEU	73	41.940	6.207	66.730	1.00 34.07	AAAA C
ATON	713 CB LEU	73	41.476	6.373	65.292	1.00 28.37	
							AAAA C
ATOH	714 CG LEU	73	40.819	7.713	64.882	1.00 29.33	AAAA C
ATOH	715 CD1 LEU	73	41.918	8.721	64.963	1.00 31.86	AAAA C
ATOH	716 CD2 LEU	7.3	40.202	7.518	63.478	1.00 32.07	AAAA C
ATOH	717 C LEU	73	40.929				
				6.569	67.817	1.00 32.14	AAAA ¢
ATOH	718 O LEU	73	40.073	5.737	68.081	1.00 35.02	AAAA O
ATOH	719 II THR	7.4	41.081	7.585	68.582	1.00 29.47	II AAAA II
ATOH	721 CA THR	7.4	40.150	7.826	69.683	1.00 34.80	AAAA C
		•			J	2.72 34.00	~ VVV

AT 31	700 CB THE	74	41.026	7.744	70.950	1.00 46.09	
							AAAA C
5.Tr.41	703 OG1 THR	74	41.729				AAAA O
ATOH	725 092 THR	74	40.060	7.831	72.253	3 1.00 39.45	AAAA C
ATOH	726 C THR	74	39.424	9.155	69.603	1.00 35.48	AAAA C
ATOH	727 O THR	74	38.270				
							AAAA O
ATOH	728 II VAL	75	40.047	10.198	69.073		II AAAA II
ATOH	730 CA VAL	75	39.351	11.474	68.892	1.00 34.91	AAAA C
ATOH	731 CB VAL	75	39.856				AAAA C
ATOH	732 CGI VAL	75	39.173				AAAA C
ATOH	733 CG2 VAL	75	39.675	11.910	71.366	1.00 19.87	AAAA C
ATOI1	734 C VAL	75	39.613	12.045			AAAA C
ATOH	735 O VAL	75	40.724				AAAA O
ATOH	736 II ILE	76	38.600	12.555	66.796	1.00 35.91	II AAAA
ATOH:	738 CA ILE	76	38.696	13.340	65.592	1.00 31.48	AAAA C
ATOH	739 CB ILE	76	37.831				AAAA C
INTA	740 CG2 ILE	76	37.856	13.630	63.208	1.00 19.54	AAAA C
ATOH.	741 CG1 ILE	76	38.222	11.314	64.277	1.00 28.52	AAAA C
ATOH:	742 CD1 ILE	76	37.149				AAAA C
	743 C ILE	76					
IOTA			38.157				AAAA C
ATOH	744 O ILE	76	36.987	14.777	66.274	1.00 38.84	AAAA O
ATO!!	745 II ARG	77	38.906	15.733	66.230	1.00 30.32	M AAAA N
ATOH	747 CA ARG	77	38.605				
							AAAA C
ATOH	748 CB ARG	77	39.961	17.475	67.461	1.00 26.62	AAAA C
ATOH	749 CG ARG	77	39.993	18.836	68.058	1.00 52.42	AAAA C
HOTA	750 CD ARG	77	41.290				AAAA C
		77					
ATOH	751 HE ARG		41.411	17.817			AAAA II
HOTA	753 CE ARG	77	40.977	18.016	71.064	1.00 48.79	AAAA C
HOTA	754 HHI ARG	77	40.440	19.104	71.610	1.00 30.34	II AAAA II
HOTA	757 HH2 ARG	77	41.061				
				17.012			и аааа
INTA	760 C ARG	77	37.643	17.733	66.225	1.00 31.75	AAAA C
ATOH	761 O ARG	77	36.944	18.637	66.664	1.00 31.40	AAAA O
ATOH	762 II GLY	78	37.688	17.661	64.884		
							AAAA N
ATOLL	764 CA GLY	78	36.982	18.409			AAA4 C
ATOH	765 C GLY	78	37.199	19.880	64.063	1.00 31.58	AAAA C
ATOI!	755 O GLY	78	36.363	20.775	63.674	1.00 34.03	AAAA O
ATOR	767 N TRP	79	38.439	20.321	64.304	1.00 31.21	
							AAAA M
ATCH	769 CA TRP	79	38.757	21.740	64.337	1.00 30.80	AAAA C
ATC:	770 CB TRP	79	40.177	21.943	64.845	1.00 39.07	AAAA C
ATOH:	T71 CG TRP	79	40.626	23.343	65.164	1.00 36.64	AAAA C
ATCH	THE COS TRP	79					
			41.691	24.001	64.433	1.00 28.52	AAAA C
ATOH:	773 CEC TRP	79	41.926	25.288	65.002	1.00 36.49	AAAA C
ATON:	774 CE3 TRP	79	42.473	23.625	63.370	1.00 37.96	AAAA C
ATON:	775 CD1 TRP	79	40.199	24.235	66.113	1.00 29.59	AAAA C
ATOH	776 HEL TRP	79	40.917				
				25.413	66.054	1.00 27.67	AAAA H
ATOH	778 CES TRP	79	42.770	26.213	64.543	1.00 31.83	C AAAA
ATOH	779 CD3 TRP	79	43.389	24.548	62.876	1.00 46.14	AAAA C
HOTA	T90 CH2 TRP	79	43.525	25.794	63.470	1.00 35.31	AAAA C
ATON		79					
			39.605	23.418	62.986	1.00 28.75	AAAA C
ATOH	792 O TRE	7.9	30.595	23.624	62.961	1.00 23.61	AAAA C
ATON:	783 H LYS	90	38.659	21.694	61.895	1.00 31.84	AAAA H
ATOH:	785 CA LYS	80	38.305	22.153	60.573	1.00 32.78	AAAA C
ATOH	T96 CB LYS	80	39.453	22.498	59.689	1.00 41.17	
							AAAA C
ATCH!	797 OG LYS	80	39.938	23.911	59.470	1.00 34.68	AAAA C
HOTA	798 CD LYS	80	41.025	24.350	60.306	1.00 44.77	AAAA C
ATOH:	789 CE LYS	80	41.276	25.811	59.898	1.00 50.41	AAAA C
HOTA	790 NZ LYS	80	42.530	25.752	59.092	1.00 67.26	
							II AAAA II
ATOH	791 C LYS	80	37.585	20.960	59.917	1.00 34.52	AAAA C
ATOH	792 O LYS	80	37.950	19.843	60.237	1.00 37.62	aaaa o
ATOH	793 II LEU	81	36.477	21.267	59.207	1.00 31.77	N AAAA
ATOH	795 CA LEU	81	35.742	20.157	58.600	1.00 31.02	AAAA C
HOTA		81	34.290	20.315	59.092	1.00 31.20	AAAA C
HOTA	797 CG LEU	81	34.115	20.319	60.632	1.00 36.97	AAAA C
HOTA	798 CD1 LEU	81	32.832	21.080	60.954	1.00 27.98	AAAA C
ATO! 1	799 CD2 LEU	81	34.089	18.955	61.297	1.00 28.77	AAAA C
ATOH	800 C LEU	81	35.733	20.023	57.104	1.00 29.86	AAAA C
ATCH	901 O LEU	81	36.082	20.947	56.368	1.00 29.34	AAAA O
ATOH	802 N PHE	82	35.430	18.813	56.594	1.00 27.78	AAAA H
HOTA	804 CA PHE	82	35.176	19.653	55.182	1.00 28.68	AAAA C
ATO!!	805 CB PHE	82	35.513	17.226	54.795	1.00 32.78	AAAA C
HOTA	806 CG PHE	82	35.348	16.901	53.357	1.00 30.48	AAAA C
HOTA	807 CD1 PHE	82	36.378	17.130	52.447	1.00 32.86	AAAA C
ATOM	909 CD2 PHE	82	34.142	16.361	52.914		
						1.00 30.93	AAAA C
ATOH	809 CE1 PHE	82	36.217	16.769	51.104	1.00 43.27	AAAA C
ATOH	810 CE2 PHE	92	33.963	16.061	51.538	1.00 26.30	AAAA C
HOTA	911 CO PHE	82	35.005	16.238	50.672	1.00 37.73	AAAA C
ATO!1	812 C FHE	82					
			33.670	18.911	54.993	1.00 30.06	AAAA C
HOTA	813 O PHE	82	32.830	18.045	55.278	1.00 27.36	AAAA O
ATOH	814 N TYR	83	33.301	20.148	54.770	1.00 31.68	II AAAA
ATOH	815 CA TYR	83	31.911	20.605	54.633	1.00 40.76	AAAA C
ATOH	816 C TYR	83					
			31.043	19.977	55.726	1.00 44.00	AAAA C
ATOH	817 O TYR	83	30.075	19.210	55.487	1.00 50.47	AAAA O
ATOH1	818 CB TYR	83	31.359	20.199	53.269	1.00 31.55	AAAA C
HOTA	819 CG TYR	83	32.196	20.742	52.117		AAAA C
						0.01 20.00	AAAA C
HOTA	820 CD1 TYR	83	33.254	19.982	51.609	0.01 20.00	AAAA C
1 KOTA	821 CD2 TYR	83	31.906	21.998	51.575	0.01 20.00	AAAA C

							;
ATM	900 TEN TYR	و بب	34.927	20.484	50.55	6 0.01 20.00	AAAA C
ATM	#23 CEC TYR	83	32.679	22.496	6 50.52	1 0.91 20.00	AAAA C
ATOD	824 CD TYR	8.3	33.740				AAAA C
ATOR	825 OH TYR	83	34.492	22.222	2 48.98	9 0.01 20.00	AAAA O
ATOH	826 II ASII	84	31.043	20.461	l 56.92	4 1.00 40.91	AAAA N
ATOU	827 CA ASN	84	30.250		7 58.05	6 1.00 36.54	AAAA C
ATOH	928 CB ASN	84	28.763				AAAA C
ATOH	929 CG ASN	84	28.274				AAAA C
ATOH	830 OD1 ASN	84	28.319				AAAA O
ATCH	831 IID2 ASII	84	27.839				n aaaa
ATOH	832 C ASII	84	30.686				AAAA C
ATOH	833 O A5II	84	30.137				AAAA O
ATOH	934 II TYR	85	31.455				N AAAA
ATOH	936 CA TYR	85	31.617				AAAA C
ATON	837 CB TYR	85	31.473				AAAA C
ATOH	838 CG TYR	85	30.078				AAAA C
ATOH	839 CD1 TYR	85	29.868				AAAA C
ATOH	840 CEI TYR	85	28.611	16.445			AAAA C
ATOH	841 CD2 TYR	85	28.954	15.371			AAAA C
ATOH	842 CE2 TYR	85	27.661	15.533	56.705		AAAA C
ATOH	843 CS TYR	85	27.497	16.072	55.445	1.00 46.06	AAAA C
IIOTA	844 OH TYR	85	26.258	16.315	54.886	1.00 46.05	AAAA O
ATOH	846 C TYR	85	32.977	16.367		1.00 32.08	AAAA C
ATOH	847 O TYR	85	33.943	16.977			AAAA O
ATOH	848 II ALA	86	33.027	15.691		1.00 30.21	- AAAA N
ATOH	850 CA ALA	86	34.257	15.325	60.670	1.00 34.10	AAAA C
ATOH	951 CB ALA	86	33.999	15.370			AAAA C
ATOH	852 C ALA	86	34.729	13.962		1.00 32.67	AAAA C
ATOH	853 O ALA	86	35.795	13.481			AAAA O
ATON	854 II LEU	87	33.832	13.173			AAAA N
IOTA	856 CA LEU	87	34.188	11.805			AAAA C
ATOH	857 CB LEU	87	33.798	10.860			AAAA C
ATOH	858 CG LEU	. 87	33.801	9.363	60.188		аааа с
ATOH	859 CD1 LEU	87	35.140	8.915	59.571	1.00 27.21	AAAA C
ATO:	880 CDC TEN	87	33.637	8.432	61.393		AAAA C
HOTA	961 C LEU	87	33.530	11.429	58.021	1.00 35.60	AAAA C
ATON ATON	962 G LEU 963 H VAL	87	32.320	11.421	58.001	1.00 38.97	AAAA O
ATON		98 60	34.174	11.300	56.975	1.00 37.86	AAAA 11
ATON	965 CA VAL 966 CB VAL	99 99	33.438	11.032	85.628	1.00 33.32	AAAA C
ATOH	967 OG1 VAL	88	33.666 32.974	12.095	54.553	1.00 22.39	AAAA C
ATOH	968 092 VAL	88	33.165	11.675	53.261	1.00 19.24	AAAA C
ATO:	869 C VAL	89	33.899	9.684	55.042 55.114	1.90 13.27 1.90 31.79	AAAA C
ATOH:	870 0 VAL	88	35.069	9.407	55.117	1.00 31.79	AAAA C AAAA O
ATCH	971 N ILE	89	33.078	9.728	54.822	1.00 31.08	U AAAA
ATOH	era da ila	89	33.361	433	54.280	1.00 30.45	AAAA C
ATOH	874 CB ILE	8 9	32.941	5.384	55.296	1.00 30.17	AAAA C
ATOH	875 GEO ILE	8 9	32.898	4.954	54.901	1.00 37.24	AAAA C
ATC!:	876 CG1 ILE	39	33.893	5.420	56.500	1.00 24.92	AAAA C
ATOH	att col ile	99	33.424	5.613	57.675	1.00 23.96	AAAA C
ATCH	978 C ILE	39	32.509	7.206	53.027	1.00 40.64	AAAA C
ATOH	879 O ILE	99	31.330	6.991	53.205	1.00 38.69	AAAA O
ATOH	980 N SHE	9.Ū	33.982	7.464	51.845	1.00 41.45	AAAA II
ATCI:	882 CA PHE	ā 0	32.346	7.371	50.591	1.00 37.67	AAAA C
ATO!1	883 CB PHE	90	32.347	8.776	50.110	1.00 32.17	AAAA C
HOTA	884 CG PHE	90	31.581	9.081	48.865	1.00 39.77	AAAA C
HOTA	895 CD1 PHE	90	30.387	9.772	49.025	1.00 32.02	аала с
IOTA	886 CD2 PHE	90	32.052	9.721	47.620	1.00 29.28	AAAA C
HOTA	887 CE1 PHE	90	29.611	10.111	47.938	1.00 33.30	AAAA C
HOTA	888 CE2 PHE	90	31.290	9.086	46.534	1.00 43.09	AAAA C
HCTA	989 CT PHE	90	. 30.083	9.764	46.687	1.00 50.24	AAAA C
HOTA	890 C PHE 891 O PHE	90	32.856	6.384	19.557	1.00 40.72	AAAA C
ATOH	891 O PHE 892 !! GLU	90	34.027	6.296	49.203	1.00 46.15	AAAA O
ATON	894 CA GLU	91 91	32.024	5.519	49.001	1.00 39.16	AAAA II
HOTA	895 CB GLU	91	32.248	1.601	47.954	1.00 42.45	AAAA C
ATOH	896 CG GLU	91	32.479 31.136	5.231 5.865	46.583	1.00 38.08	AAAA C
ATOH	897 CD GLU	91	30.855	5.776	46.250 44.757	1.00 58.86 1.00 63.55	AAAA C
ATON	898 OE1 GLU	91	31.473	6.651	44.757	1.00 63.33	AAAA C
ATOH	899 OE2 GLU	91	30.058	4.813	44.573	1.00 63.64	AAAA O AAAA O
HOTA	900 C GLU	91	33.422	3.734	48.313	1.00 42.06	
ATOH	901 O GLU	91	34.298	3.411	47.587	1.00 42.06	AAAA C AAAA O
HOTA	902 II HET	92	33.352	3.209	49.482	1.00 46.52	AAAA N
ATOH	304 CA MET	92	34.409	2.401	50.088	1.00 42.26	AAAA C
ATON	905 CB MET	92	34.299	2.659	51.594	1.00 38.37	AAAA C
HOTA	906 CG HET	92	35.412	2.156	52.420	1.00 59.29	AAAA C
ATOM	907 SD MET	92	36.802	3.306	52.401	1.00 57.67	AAAA S
HOTA	908 CE HET	92	36.340	4.405	51.108	1.00 38.36	AAAA C
HOTA	909 C MET	92	34.012	1.005	49.745	1.00 43.37	AAAA C
ATOH	910 O HET	92	33.335	0.298	50.523	1.00 45.58	AAAA O
HOTA	911 N THR	93	34.449	0.518	48.602	1.00 47.09	AAAA 11
HOTA	913 CA THR	93		-0.900	48.273	1.00 47.32	AAAA C
ATOH	914 CB THR	93	34.666	-1.281	16.868	1.00 55.28	AAAA C
HOTA	915 OG1 THR	93	34.013	-0.488	45.892	1.00 57.81	AAAA O
ATOH	917 CGC THR	93	34.332	-2.715	46.516	1.00 44.71	AAAA C

ATCH 919 0 THR 93 ATCH 919 0 THR 93 ATCH 919 0 THR 93 ATCH 920 H ASH 94 ATCH 920 CA ASH 94 ATCH 920 CASH 94 ATCH 931 H LEU 95 ATCH 931 H LEU 95 ATCH 931 CB LEU 95 ATCH 934 CB LEU 95 ATCH 935 CG LEU 95 ATCH 936 CD LEU 95 ATCH 937 CD2 LEU 95 ATCH 938 C LEU 95 ATCH 939 C LEU 95 ATCH 940 H LVS 96 ATCH 940 H LVS 96 ATCH 940 H LVS 96 ATCH 941 CB LVS 96 ATCH 942 CA LVS 96 ATCH 943 CB LVS 96 ATCH 945 CD LVS 96 ATCH 946 CE LVS 96 ATCH 951 C LVS 96 ATCH 951 C LVS 96 ATCH 955 CA ASP 97 ATCH 956 CB ASP 97 ATCH 957 CG ASP 97 ATCH 958 ODL ASP 97 ATCH 958 ODL ASP 97 ATCH 958 CD LVS 96 ATCH 959 CD ASP 97 ATCH 950 CD ASP	36.115 -1.777	AAAAA C C C C C C C C C C C C C C C C C
ATCH 1010 H LEU 103 ATCH 1012 CA LEU 103 ATCH 1013 CB LEU 103 ATCH 1014 CG LEU 103 ATCH 1015 CD1 LEU 103	36.845 4.640 68.882 1.00 35.28 36.473 6.040 68.621 1.00 36.57 35.948 6.140 67.213 1.00 34.77 35.525 7.492 66.612 1.00 30.32	AAAA 11 AAAA C AAAA C AAAA C

ATMI 1000 CB ARG 104 ATMI 1003 CG ARG 104 ATMI 1003 CG ARG 104 ATMI 1005 HE ARG 104 ATMI 1007 CD ARG 104 ATMI 1007 CD ARG 104 ATMI 1007 CD ARG 104 ATMI 1008 HHI ARG 104 ATMI 1008 HHI ARG 104 ATMI 1008 C ARG 104 ATMI 1008 CA ASH 105 ATMI 1009 CB ILE 106	35.569	AAAA C AAAA C AAAA N AAAA N AAAA N AAAA C AAAA C
ATON 1052 CD1 ILE 106 ATON 1053 C ILE 106 ATON 1054 O ILE 106 ATON 1055 N THR 107 ATON 1057 CA THR 107 ATON 1059 CB THR 107 ATON 1059 CB THR 107 ATON 1061 CG2 THR 107 ATON 1062 C THR 107 ATON 1063 O THR 107 ATON 1064 N ARG 108 ATON 1064 CA ARG 108 ATON 1065 CA ARG 108 ATON 1066 CA ARG 108 ATON 1066 CA ARG 108 ATON 1067 CB ARG 108 ATON 1068 CD ARG 108	33.055 11.293 64.643 1.00 25.48 33.803 14.909 68.009 1.00 27.40 32.628 15.106 68.243 1.00 32.86 34.719 15.789 68.350 1.00 30.43 34.532 16.983 69.145 1.00 28.27 35.902 17.607 69.579 1.00 35.78 36.819 16.503 69.738 1.00 40.26 35.954 18.411 70.855 1.00 28.13 33.728 17.950 68.332 1.00 27.95 33.392 19.060 68.831 1.00 32.99 33.669 17.777 67.019 1.00 30.28 33.965 20.011 65.591 1.00 25.13 33.105 21.174 65.543 1.00 30.68 33.917 22.444 65.529 1.00 17.12 33.511 23.376 64.451 1.00 33.40 34.045 23.608 63.266 1.00 46.41 35.162 22.929 62.868 1.00 49.30 33.454 24.543 62.494 1.00 39.82	AAAA C
ATCH 1050 O ARG 108 ATCH 1091 H GLY 109 ATCH 1093 TA GLY 109 ATCH 1094 G GLY 109 ATCH 1095 O GLY 109 ATCH 1095 O GLY 109 ATCH 1095 CA ALA 110 ATCH 1097 CB ALA 110 ATCH 1097 C ALA 110 ATCH 1099 C ALL 111 ATCH 1095 CB ILE 111 ATCH 1096 CG2 ILE 111 ATCH 1098 CD1 ILE 111 ATCH 1098 CD1 ILE 111 ATCH 1099 C ILE 111 ATCH 1099 C ILE 111 ATCH 1100 O ILE 111 ATCH 1101 H ARG 112 ATCH 1101 H ARG 112	33.379 17.391 64.430 1.00 32.67 31.567 18.909 64.284 1.00 32.60 31.082 18.395 62.983 1.00 28.87 30.471 16.306 64.006 1.00 32.32 30.471 16.306 64.006 1.00 38.03 29.920 16.560 61.894 1.00 34.11 29.086 15.371 61.833 1.00 36.77 27.708 18.721 61.223 1.00 15.32 29.745 14.335 60.957 1.00 32.12 39.921 14.332 60.687 1.00 34.11 29.030 13.337 60.557 1.00 26.55 29.569 12.273 59.771 1.00 32.90 29.669 10.967 60.591 1.00 38.07 30.091 11.140 62.036 1.00 34.05 28.345 10.237 60.684 1.00 26.54 28.437 8.872 61.407 1.00 27.11 28.738 11.928 58.521 1.00 33.98 27.533 12.179 58.532 1.00 30.54 28.773 11.107 56.247 1.00 27.48	AAAA C
ATOH 1104 CB ARG 112 ATOH 1105 CG ARG 112 ATOH 1106 CD ARG 112 ATOH 1107 NE ARG 112 ATOH 1109 CD ARG 112 ATOH 1109 CD ARG 112 ATOH 1110 NH1 ARG 112 ATOH 1111 NH2 ARG 112 ATOH 1113 NH2 ARG 112 ATOH 1116 C ARG 112 ATOH 1117 O ARG 112 ATOH 1118 N ILE 113 ATOH 1120 CA ILE 113 ATOH 1121 CB ILE 113 ATOH 1121 CG ILE 113 ATOH 1123 CGI ILE 113 ATOH 1124 CDI ILE 113 ATOH 1125 C ILE 113 ATOH 1126 O ILE 113 ATOH 1127 N GLU 114 ATOH 1129 CA GLU 114 ATOH 1130 CB GLU 114 ATOH 1131 CG GLU 114 ATOH 1131 CG GLU 114 ATOH 1131 CG GLU 114 ATOH 1132 CD GLU 114 ATOH 1133 CEI GLU 114	29.186 12.085 55.169 1.00 26.35 28.548 11.653 53.816 1.00 25.93 28.659 12.912 52.992 1.00 32.92 27.950 12.726 51.770 1.00 50.34 27.778 13.503 50.720 1.00 47.61 28.334 14.695 50.696 1.00 44.92 27.012 12.925 49.789 1.00 46.00 29.200 9.738 55.791 1.00 29.74 30.343 9.611 55.406 1.00 36.52 28.326 9.754 55.886 1.00 33.99 28.612 7.376 55.555 1.00 36.26 28.457 6.461 56.760 1.00 33.27 28.850 5.021 56.449 1.00 15.95 29.374 7.012 57.874 1.00 31.92 29.324 6.250 59.176 1.00 42.34 27.729 6.959 54.398 1.00 39.26 26.637 </td <td>AAAA C AAAA C AAAA II AAAA II AAAA II AAAA C AAAA C</td>	AAAA C AAAA C AAAA II AAAA II AAAA II AAAA C

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							'
ATMI ATM		:14 114	25.787				AAAA O
AT 31		114	29.039 29.120				AAAA C
ATOR		115	27.191				AAAA O
ATOH		115	27.219				AAAA C
ATOH	1140 CB LYS	115	27.275				AAAA C
ATOU		115	27.019	6.19	4 47.41		AAAA C
ATOH		115	26.537				AAAA C
ATOH		115	26.751				AAAA C
HOTA HOTA		115 115	27.165				H AAAA N
ATOH		115	28.287 29.102				AAAA C
ATOH		116	28.137				O AAAA N AAAA
ATOH		116	29.022				AAAA C
ATOH	1153 CB ASN	116	29.534				AAAA C
ATOH		116	30.372	3.153	3 52.345	1.00 48.92	AAAA C
ATOH		116	31.337	3.016			AAAA O
IOTA IOTA		116 116	29.927	4.174			II AAAA
IICTA		116	28.275 28.067	0.277 -0.361			AAAA C
ATCH		117	27.989	-0.188			AAAA O AAAA N
ATOH	1163 CA ALA	117	27.195	-1.376			AAAA C
ATON	1164 CB ALA	117	27.494	-1.884			AAAA C
ATOH	1165 C ALA	117	27.294	-2.504	50.529		AAAA C
ATOH	1166 O ALA	117	26.211	-2.998			AAAA O
ATCH	1167 H ASP	118	28.484	-2.823			II AAAA 11
HOTA HOTA	1169 CA ASP 1170 CB ASP	118 118	28.559	-3.980			AAAA C
HOTA	1171 CG ASP	118	29.659 29.684	-4.945 -5.119			AAAA C
ATOH	1172 OD1 ASP	118	28.870	-5.976			AAAA C AAAA O
HOTA	1173 OD2 ASP	118	30.448	-4.447		1.00 66.73	AAAA O
HCTA	1174 C ASP	118	28.818	-3.586		1.00 37.29	AAAA C
ATOH	1175 O ASP	118	29.127	-4.536		1.00 42.89	AAAA O
ATCH	1176 N LEU	119	28.670	-2.327		1.00 36.46	II AAAA II
ATO!: ATO!:	1179 CA LEU 1179 CB LEU	119 119	28.986 29.159	-1.895		1.00 40.58	AAAA C
ATOH	1180 OG LEU	119	29.540	-0.389 0.331	55.145 56.378	1.00 34.31 1.00 36.58	AAAA C
ATCH:	1181 CD1 LEU	119	30.950	-0.101	56.948	1.00 35.37	AAAA C AAAA C
ATO:	1182 CDZ LEU	119	29.791	1.830	56.104	1.00 29.68	AAAA C
ATQU	1193 T LEU	119	27.937	-2.376	56.007	1.00 43.67	AAAA C
ATO!:	1184 O LEU	119	26.748	-2.248	55.743	1.00 45.32	AAAA O
ATOH ATOH	1195 N CYS 1197 CA CYS	120	28.361	-2.967	57.110	1.00 43.53	H AAAA H
ATO!:	1198 C CYS	120 120	27.378 27.881	-3.407	59.089	1.00 38.93	AAAA C
ATO!!	1189 O CYS	120	29.560	-2.921 -1.960	59.426 59.446	1.00 41.91 1.00 43.66	AAAA C AAAA O
ATOH	1190 CB CYS	120	27.285	-4.907	59.100	1.00 37.59	AAAA C
ATCH:	1191 SG CYS	120	26.568	-5.603	56.639	1.00 58.32	AAAA S
ATO::	1190 N TYR	121	27.328	-3.455	60.509	1.00 38.05	AAAA II
HOTA HOTA	1194 CA TYR	121	27.795	-3.010	61.927	1.00 38.58	AAAA C
ATOH	1195 CB TYR 1196 CG TYR	121 121	29.189	-3.572	62.130	1.00 34.61	AAAA C
ATO:	1197 CD1 TYR	121	28.950 29.087	-5.032 -6.045	62.519 61.582	1.00 36.52 1.00 33.58	AAAA C
ATON	1198 CEL TYR	121	28.852	-7.350	61.980	1.00 41.21	AAAA C AAAA C
ATO:	1199 CD2 TYR	121	28.560			1.00 36.31	AAAA C
HOTA	1200 CE2 TYR	121	28.287	-6.630	64.201	1.00 39.48	AAAA C
ATOH	1201 CD TYR	121	28.432	-7.641	63.270	1.00 46.07	AAAA C
HOTA HOTA	1202 OH TYR 1204 C TYR	121 121	28.161	-8.924	63.730	1.00 49.20	AAAA O
HOTA	1205 O TYR	121	27.674 28.445	-1.523 -0.778	61.789 62.369	1.00 38.83	AAAA C AAAA O
ATOH	1206 H LEU	122	26.587	-1.045	61.180	1.00 43.22	AAAA U
ATOH	1208 CA LEU	122	26.361	0.405	61.090	1.00 44.82	AAAA C
HOTA	1209 CB LEU	122	25.990	0.715	59.634	1.00 46.48	AAAA C
ATON	1210 CG LEU	122	26.497	2.014	59.108	1.00 44.44	AAAA C
HOTA HOTA	1211 CD1 LEU 1212 CD2 LEU	122 122	25.778	2.448	57.859	1.00 32.19	AAAA C
ATOH	1213 C LEU	122	26.136 25.212	3.057 0.910	60.170 61.935	1.00 47.76 1.00 44.85	AAAA C
INTA	1214 O LEU	122	25.269	1.759	62.839	1.00 47.66	AAAA C AAAA O
HOTA	1215 H SER	123	24.104	0.137	61.843	1.00 40.12	AAAA N
HOTA	1217 CA SER	123	22.949	0.435	62.703	1.00 33.98	AAAA C
ATOH	1218 CB SER	123		-0.330	62.239	1.00 19.26	AAAA C
HOTA HOTA	1219 OG SER 1221 C SER	123		-1.762	62.402	1.00 34.35	AAAA O
ATOH	1221 C SER 1222 O SER	123 123	23.165 22.326	0.060 0.280	64.159 65.025	1.00 37.43	AAAA C
ATOH	1223 N THR	124		-0.698	64.432	1.00 35.33 1.00 39.03	AAAA O AAAA II
ATOH	1225 CA THR	124		-1.165	65.753	1.00 37.78	AAAA C
ATOH	1226 CB THR	124	25.368	-2.461	65.719	1.00 42.39	AAAA C
ATOM	1227 OG1 THR	124		-2.020	64.924	1.00 47.70	AAAA O
ATOM ATOM	1229 CG2 THR 1230 C THR	124		-3.622	65.006	1.00 40.93	AAAA C
ATO4		124 124		-0.206	66.445	1.00 39.29	AAAA C
ATOH		124	25.948 · 25.737		67.499 65.985	1.00 41.41 1.00 37.80	AAAA O
ATOH		125	26.594			1.00 37.80	AAAA N AAAA C
ATOH	1235 CB VAL	125	27.683			1.00 39.50	AAAA C
ATOH		125	28.570	3.599	66.352	1.00 28.36	AAAA 🤆
ATOH	1237 GG2 VAL	125	28.693	1.565	65.110	1.00 33.07	AAAA 🔈

AT14			25.759	3.10	7 67.179	9 1.00 41.17	AAAA C
ATM	1039 O VAL	125	24.941	3.75	0 66.531	1.00 41.22	
ATO	1140 H ASP	126	26.972	3.63	6 68.367		
ATOL	1 1242 CA ASP		25.310				
ATOD			24.862				
ATOI							
			23.879				AAAA C
ATON			23.699				AAAA O
ATON	1 1246 ODC ASP	126	23.220	4.865	5 71.964	1.00 52.32	
ATOH	I 1247 C ASP	126	26.146				
ATOR			26.740				
ATON							AAAA O
			26.029			· -	II AAAA II
ATOH			26.777			1.00 33.02	AAAA C
ATOU	1252 CB TRP	127	26.568	8.296	65.930	1.00 24.89	AAAA C
ATOH	1253 CG TRP	127	27.195	7.372	64.907		AAAA C
ATON	1254 CD2 TRP	127	28.587				
ATOR		127	28.631				AAAA C
				6.186			AAAA C
ATOH		127	29.778				аааа с
ATOH		127	26.465	6.450	64.188	1.00 18.67	AAAA C
INTA	1258 HEL TRP	127	27.311	5.712	63.394	1.00 42.87	II KAAA
ATOH	1260 CZ2 TRP	127	29.792	5.783			AAAA C
ATOH	1261 CC3 TRP	127	30.972	7.445			
ATOH		127	30.937	6.405			AAAA C
ATOH							AAAA C
		127	26.558	9.010	_		AAAA C
ATOH		127	27.382	9.977		1.00 40.87	AAAA O
ATOH	1265 # SER	128	25.493	8.931	69.171	1.00 31.24	H AAAA H
HOTA	1267 CA SER	128	25.201	10.041	70.081	1.00 34.04	AAAA C
ATOR	1268 CB SER	128	23.757	10.042			
HOTA	1269 OG SER	128	23.433				AAAA C
ATOLI				8.917		1.00 28.96	AAAA O
		128	26.133	9.975		1.00 32.39	AAAA C
ATOH	1272 O SER	128	26.212	10.857	72.134	1.00 30.91	AAAA O
HOTA	1273 H LEU	129	26.662	8.792	71.549	1.00 27.18	AAAA N
HOTA	1275 CA LEU	129	27.701	8.607	72.526	1.00 36.73	AAAA C
HOTA	1276 CB LEU	129	27.920	7.132	72.741		
ATOR	1077 OG LEU	129				1.00 32.53	AAAA C
			26.795	6.324	73.371	1.00 39.28	AAAA C
ATOH	1279 CD1 LEU	129	27.292	5.024	73.975	1.00 32.54	AAAA C
ATOR	1279 CD3 LEU	129	26.237	7.117	74.560	1.00 32.12	AAAA C
ATON	1280 C LEV	129	29.054	9.226	72.113	1.00 38.04	AAAA C
ATORE	1291 O LEU	129	29.645	10.001	72.874	1.00 34.50	AAAA O
ATO!!	1292 # ILE	130	29.316	9.217	70.907	1.00 42.09	
ATO:	1284 CA ILE	130	30.490				AAAA II
				9.743	70.144	1.00 41.35	
ATON	1248 25 ITE	130	30.793	9.896	68.901	1.00 41.73	AAAA C
ATOH	1296 CG2 ILB	130	31.992	9.434	68.176	1.00 31.95	AAAA C
ATO!!	1297 TG1 ILE	130	30.969	7.413	69.347	1.00 26.54	AAAA C
ATOH	1099 CD1 ILE	130	31.053	6.457	68.165	1.00 42.63	AAAA C
ATON	1289 C ILE	130	30.305	11.178			
ATOH	1290 C ILE	130			69.679	1.00 46.43	AAAA C
			31.224	11.995	69.966	1.00 38.46	AAAA O
ATON	1091 H LEU	131	29.089	11.495	69.193	1.00 45.14	AAAA ::
ATOH	1293 CA LEU	131	29.895	12.965	68.651	1.00 41.45	AAAA C
ATG()	1294 OB LEU	131	28.499	12.516	57.259	1.00 46.51	AAAA C
ATCH	1295 GG LEU	131	29.823	12.905	65.879	1.00 36.79	AAAA
ATON	1096 CD1 LEU	131	29.128	11.405			
ATON	1297 CD2 LEU	131			65.324	1.00 30.15	ARAR C
HOTA			27.625	13.581	5 5.334	1.00 19.92	AAAA C
		131	27.551	13.525	69.295	1.00 39.19	AAAA C
ATOH	1299 O LEU	131		12.967	69.311	1.00 37.75	AAAA O
ATOH	1300 N ASP	132	27.742	14.311	69.518	1.00 33.73	AAAA II
ATOH	1302 CA ASP	132	26.610	15.542	70.003	1.00 38.20	AAAA C
ATOH	1303 CB ASP	132	27.017	16.944	70.381	1.00 43.17	AAAA C
ATOH:	1304 CG ASP	132	27.349	17.137	71.834		
HOTA	1305 OD1 ASP	132	27.536			1.00 43.29	AAAA C
ATOH				16.122	72.521	1.00 47.12	AAAA C
		132	27.413	18.331	72.208	1.00 60.58	AAAA O
ATOH	1307 C ASP	132	25.520	15.659	68.946	1.00 43.46	AAAA C
HOTA	1308 O ASP	132	24.481	15.032	68.939	1.00 49.32	AAAA O
HOTA	1309 H ALA	133	25.754	16.398	67.900	1.00 45.03	AAAA H
ATOH	1311 CA ALA	133	24.947	16.776	66.773	1.00 38.62	AAAA C
ATOH	1312 CB ALA	133	25.628	17.987	66.092	1.00 33.92	2222
ATOH.	1313 C ALA	133					S AAAA
ATOH			24.694	15.669	65.775	1.00 33.33	AAAA C
		133	24.777	15.791	64.517	1.00 33.71	C AAAA
ATOH	1315 H VAL	134	24.115	14.565	66.219	1.00 27.89	AAAA H
ATOH	1317 CA VAL	134	23.813	13.440	65.377	1.00 29.90	AAAA C
ATCH:	1318 CB VAL	134		12.241	66.120	1.00 40.63	AAAA C
ATOH:	1319 CG1 VAL	134		11.441	66.855		
ATOH	1320 GG2 VAL	134		12.701		1.00 35.20	AAAA C
ATOH	1321 C VAL	134			67.068	1.00 30.94	AAAA C
				13.732	64.353	1.00 36.98	AAAA C
ATOH	1322 O VAL	134		13.106	63.292	1.00 32.95	AAAA O
ATON	1323 II SER	135	21.920	14.777	64.626	1.00 39.65	AAAA N
ATOR	1325 CA SER	135		15.139		1.00 43.12	AAAA C
ATOH	1326 CB SER	135		16.277		1.00 45.19	AAAA C
ATOH	1327 OG SER	135		17.369		1.00 39.25	
ATOM	1329 C SER	135	_				AAAA O
ATOM				15.516		1.00 41.15	AAAA C
	1330 O SER	135		15.642		1.00 43.81	AAAA O
ATOH	1331 II ASII	136		15.911	62.165	1.00 41.11	H AAAA
ATON	1333 CA ASII	136		16.353		1.00 37.21	AAAA C
ATOH	1334 CB ASII	136		17.372		1.00 39.66	AAAA C
HOTA	1335 CG ASH	136				1.00 36.59	2247 C
ATON	1336 OD1 ASH	136					AAAA :
	1000 OFT Mail	100		19.079	61.149	1.00 50.81	AAAA O

ATTHE 133T HDD AGH 136 ATTHE 1340 C AGH 136 ATOH 1341 G AGH 136	24.379 19.44 24.031 15.23 24.535 15.48	0 60.259 1.00 35.31 4 59.194 1.00 38.70	AAAA D AAAA C AAAA O
ATOR 1342 R ASR 137 ATOR 1344 CA ASR 137 ATOR 1345 CB ASR 137	24.057 14.039 24.721 12.959 24.737 11.700	9 60.126 1.00 32.98	AAAA C AAAA II
ATOH 1346 CG ASH 137 ATOH 1347 ODI ASH 137	25.631 11.965 26.070 13.121	5 62.217 1.00 26.63 1 62.369 1.00 30.22	AAAA C AAAA O
ATON 1348 ND2 ASN 137 ATON 1351 C ASN 137 ATON 1352 O ASN 137	25.830 10.923 23.950 12.749 22.716 12.755	58.817 1.00 35.89	АААА Н АААА С АААА О
ATOH 1353 H TYR 138 ATOH 1355 CA TYR 138	24.592 12.251 24.093 11.983	57.785 1.00 32.86	AAAA C
ATOH 1356 CB TYR 138 ATOH 1357 CG TYR 138	24.682 12.861 24.018 12.741	54.079 1.00 37.89	AAAA C AAAA C
ATOH 1358 CDI TYR 138 ATOH 1359 CEI TYR 138 ATOH 1360 CD2 TYR 138	23.083 13.671 22.510 13.579 24.357 11.717	52.392 1.00 37.65	AAAA C AAAA C AAAA C
ATOH 1361 CE2 TYR 138 ATOH 1362 CE TYR 138	23.801 11.615 22.868 12.562	51.951 1.00 41.97 51.564 1.00 39.42	AAAA C AAAA C
ATON 1363 OH TYR 138 ATON 1365 C TYR 138 ATON 1366 O TYR 138	22.296 12.504 24.373 10.578 25.505 10.317	56.051 1.00 31.33	AAAA C
ATON 1367 N ILE 139 ATON 1369 CA ILE 139	23.461 9.660 23.637 8.249	56.116 1.00 35.40	AAAA O AAAA II
ATOM 1370 CB ILE 139 ATOM 1371 CG2 ILE 139 ATOM 1372 CG1 ILE 139	23.234 7.450 23.640 5.984	57.093 1.00 21.99	AAAA C AAAA C
ATON 1373 CD1 ILE 139 ATON 1374 C ILE 139	23.711 8.057 24.455 7.100 22.729 7.708	59.389 1.00 52.23	AAAA C AAAA C AAAA C
ATON 1375 O ILE 139 ATON 1376 N VAL 140	21.538 7.890 23.286 6.997	54.757 1.00 42.61	AAAA O
ATON 1378 CA VAL 140 ATON 1379 CB VAL 140 ATON 1380 C31 VAL 140	22.533 6.481 21.967 7.627 22.800 8.375	52.755 1.00 32.39 51.981 1.00 36.05 50.881 1.00 25.89	AAAA C AAAA C
ATON 1391 CG2 MAL 140 ATON 1392 C MAL 140	20.807 7.034 23.422 5.670	51.047 1.00 34.96 51.874 1.00 41.96	AAAA C AAAA C AAAA C
ATON 1383 O VAL 140 ATON 1384 N GLY 141 ATON 1396 CA GLY 141	24.537 6.172 22.899 4.562	51.637 1.00 44.03 51.402 1.00 42.66	aaaa o aaaa n
ATOM: 1387 C GLY 141 ATOM: 1388 C GLY 141	23.391 3.905 24.265 2.696 25.132 2.003	50.279 1.00 30.94 50.935 1.00 38.99 50.176 1.00 35.87	AAAA C AAAA C AAAA O
ATOM: 1399 N. ASN 142 ATOM: 1391 DA ASN 142	23.985 2.418 24.858 1.390	52.116 1.00 38.92 52.746 1.00 44.32	AAAA II. AAAA C
ATG: 1390 08 ASN 142 ATG: 1393 03 ASN 142 ATG: 1394 001 ASN 142	25.257 1.774 26.131 3.022 26.984 3.077	54.187	AAAA C AAAA C AAAA O
ATO: 1395 ::D2 ASN 140 ATO: 1398 C ASN 142	25.945 4.022 24.153 0.066	55.019 1.00 41.99 52.687 1.00 45.84	AAAA ::
ATM: 1399 0 ASH 142 ATM: 1490 H 1YS 143 ATM: 1492 DA 1YS 143	23.113 -0.015 24.674 -0.990 24.073 +2.299	52.055 1.00 49.65 53.272 1.00 45.23 53.195 1.00 49.14	AAAA O AAAA H AAAA C
ATON 1403 CB LYS 143 ATON 1404 CB LYS 143	25.166 -3.328 24.750 -4.686	53.433 1.00 41.49 53.832 1.00 44.96	AAAA C AAAA C
ATOM 1405 CD LYS 143 ATOM 1406 CE LYS 143 ATOM 1407 MZ LYS 143	25.512 -5.743 25.043 -7.131 26.080 -8.093	53.100 1.00 48.66 53.558 1.00 38.35 53.040 1.00 53.83	AAAA C AAAA C AAAA II
ATON 1411 C LYS 143 ATON 1412 O LYS 143	22.902 -2.431 22.960 -2.099	54.169 1.00 52.85 55.360 1.00 55.21	AAAA C AAAA O
ATON 1413 N PRO 144 ATON 1414 CD PRO 144 ATON 1415 CA PRO 144	21.806 -3.047 21.617 -3.469 20.559 -3.118	53.731 1.00 52.39 52.315 1.00 52.58 54.489 1.00 49.30	AAAA H AAAA C AAAA C
ATOM 1416 CB PRO 144 ATOM 1417 CG PRO 144	19.549 -3.602 20.134 -3.299	53.455 1.00 51.41 52.099 1.00 50.41	AAAA C AAAA C
ATON 1419 C PRO 144 ATON 1419 O PRO 144 ATOM 1420 N PRO 145	20.521 -4.050 29.904 -5.236 20.318 -3.533	55.659 1.00 44.65 55.501 1.00 36.84	AAAA C AAAA O
ATOM 1421 CD FRO 145 ATOM 1422 CA PRO 145	20.123 -2.054 20.448 -4.233	56.859 1.00 45.12 57.094 1.00 38.17 59.128 1.00 40.19	AAAA C AAAA C AAAA C
ATON 1423 CB PRO 145 ATON 1424 CG PRO 145 ATON 1425 C PRO 145	19.704 -3.288 20.040 -1.910 19.993 -5.655	59.099 1.00 37.08 58.602 1.00 33.65	AAAA C AAAA C
ATOM 1426 O PRO 145 ATOM 1427 W LYS 146	19.993 -5.655 20.556 -6.592 18.879 -5.924	58.155 1.00 47.17 58.768 1.00 49.05 57.499 1.00 53.72	AAAA C AAAA O AAAA II
ATON 1429 CA LYS 146 ATON 1430 CB LYS 146 ATON 1431 CG LYS 146	18.268 -7.229 16.894 -7.050	57.295 1.00 56.94 56.647 1.00 65.44	AAAA C AAAA C
ATOH 1432 CD LYS 146 ATOH 1433 CE LYS 146	14.797 -0.422 14.194 -9.717	55.982 1.00 64.32 56.451 0.01 62.75 55.934 0.01 62.14	AAAA C AAAA C AAAA C
ATOH 1434 HZ LYS 146 ATOH 1438 C LYS 146 ATOH 1439 O LYS 146	12.720 -9.610 19.138 -8.138	55.753 0.01 61.38 56.446 1.00 61.40	AAAA C
ATOH 1440 H GEU 147 ATOH 1492 CA GLU 147	19.779 -7.649	56.732 1.00 66.22 55.389 1.00 62.92 54.742 1.00 67.00	AAAA O AAAA II AAAA C
ATOH 1443 CB GLU 147		53.294 1.00 62.32	AAAA C

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ATO	: 1441 UI SW	147	19.967 -7.57			
ATO		147				AAAA C
			20.164 -7.41			AAAA C
ATM		147	21.339 -7.63			AAAA O
ATO		147	19.201 -7.05		6 1.00 87.47	AAAA O
ATON		147	22.136 -8.47	0 55.54	1 1.00 69.40	AAAA C
ATOU	1449 O GLU	147	22.883 -9.43	7 55.36		AAAA O
ATOH	1 1450 H CYS	148	22.506 -7.48			AAAA H
ATOU		148	23.693 -7.58			
ATOL		148		_		AAAA C
			23.598 -8.70			AAAA C
ATOL		148	24.473 -9.52		4 1.00 65.89	AAAA O
ATOH		148	23.952 -6.30	1 58.00	1 1.00 57.29	AAAA C
ATOR	1456 3G CYS	148	24.565 -5.09	1 56.80		AAAA S
ATON	1457 N GLY	149	22.514 -8.74			AAAA II
ATOH		149	22.387 -9.74	_		
						AAAA C
ATOG		149	23.443 -9.62			AAAA C
ATOR		149	23.925 -10.603	3 61.699	9 1.00 61.11	AAAA O
ATOH	1462 N ASP	150	23.717 -8.420	6 61.596	5 1.00 54.88	H AAAA II
ATOH	1464 CA ASP	150	24.794 -8.199			AAAA C
ATOH	1465 CB ASP	150	25.041 -6.70			AAAA C
ATOH		150				
			25.320 -6.03			аааа с
ATOH		150	25.726 -6.796			AAAA O
ATOH		150	25.102 -4.819	9 61.363	1.00 49.69	AAAA O
ATOR	1469 C ASP	150	24.519 -9.854	63.855	1.00 59.36	AAAA C
ATOH	1470 O ASP	150	23.392 -9.820			AAAA O
ATOII		151	25.532 -9.369			
ATOH		151				H AAAA
			25.314 -9.908			AAAA C
ATON		151	25.208 -11.409	65.806	1.00 58.55	AAAA C
ATON	1475 CG LEU	151	24.063 -12.101	65.092	1.00 69.45	AAAA C
ATOH	1476 CD1 LEU	151	24.515 -13.421			AAAA C
ATOH	1477 CD2 LEU	151	22.837 -12.372			
ATOH	1478 C LEU	151	_	-		AAAA C
ATON:			26.409 -9.454			AAAA C
	1479 O LEU	151	27.598 -9.734		1.00 55.59	AAAA O
ATOH	1490 N CYS	152	26.024 -8.773	57.849	1.00 48.62	II AAAA II
ATOM	1490 TA TYS	152	26.992 -9.189	68.740	1.00 56.73	AAAA C
ATC11	1493 C CYS	152	27.650 -9.325			AAAA C
ATCH:	1484 O TYS	152	27.074 -12.405			
ATC1:	1495 TB CYS	152	26.358 -7.144			AAAA O
ATO:						AAAA C
		152	25.935 -5.635		-	raar s
ATOM	1497 N PRO	153	29.825 -9.072		1.00 68.05	AAAA II
ATON	1488 TO PRO	153	29.618 -7.938	59.903	1.00 56.65	AAAA C
ATON	1489 CA PRO	153	29.497 -10.094		1.00 70.60	AAAA C
ATO:	1491 CB FRO	153	30.601 -9.323			AAAA C
ATON	1491 03 980	153				
	1471 03 750		30.961 -9.159			AAAA C
ATON	1492 C PRO	153	29.543 -10.734		1.00 69.54	AAAA C
ATOH:	1493 O FRO	153	27.859 -10.075	72.615	1.00 69.58	AAAA O
AT CH	1494 H BLY	154	28.444 -12.049	71.943	1.00 71.23	AAAA M
ATON	1496 TA BLY	154	27.610 -12.804	72.745	1.00 78.07	AAAA C
ATOH:	1497 C 31Y	154	26.245 -13.230		1.00 81.75	
ATON	1498 5 BLY	154	25.786 -14.318			AAAA C
				72.547	1.00 80.26	AAAA O
ATON		155	25.649 -12.468	71.314	1.00 84.54	AAAA ::
ATON	1501 TA THR	155	24.314 -12.683	70.828	1.00 89.38	AAAA C
ATON	1501 TB THR	155	24.016 -11.661	69.705	1.00 85.07	AAAA C
ATOH	1503 OG1 THR	155	24.063 -13.417	70.420	1.00 84.51	AAAA O
ATO:	1505 032 THR	155	22.686 -11.995		1.00 82.27	AAAA C
ATO!!	1506 C THR	155	24.960 -14.094	70.353	1.00 93.69	
HOTA	1507 O THR	155	23.905 -14.564		1.00 95.92	AAAA C
HOTA				70.617		O AAAA
		156	25.003 -14.655	69.617	1.00 97.23	AAAA N
ATOH	1510 CA MET	156	24.884 -15.973	69.024	1.00 99.05	AAAA C
ATOH	1511 CB MET	156	25.907 -15.190	67.896	1.00100.40	AAAA C
ATOH	1512 OG HET	156	25.456 -15.675	66.542	0.01 99.75	AAAA C
ATOU	1513 SD HET	156	23.637 -15.857	66.255	0.01 99.72	AAAA S
ATOH	1514 CE MET	156	23.664 -17.214	65.087	0.01 99.59	
. ATOH	1515 C MET	156				AAAA C
			25.027 -17.106	70.032	1.00100.57	AAAA C
ATOH	1516 O MET	156	24.353 -18.122	69.835	1.00101.64	AAAA O
ATOH	1517 N ALA	157	25.974 -17.057	70.967	1.00100.53	I: AAAA
ATOU	1519 CA ALA	157	26.022 -19.102	71.986	1.00101.00	AAAA C
HOTA	1520 CB ALA	157	27.317 -19.158	72.766	1.00103.42	AAAA C
ATON	1521 C ALA	157	24.856 -17.890	72.959	1.00101.10	AAAA C
ATOH	1522 O ALA	157	23.893 -18.654	72.921	1.00101.10	
ATOH						AAAA O
	1523 N GLU	158	24.984 -16.906	73.841	1.00 98.39	AAAA N
ATOH	1525 CA GLU	158	23.935 -16.629	74.781	1.00 97.43	AAAA C
ATOH	1526 CB GLU	158	23.128 -17.965	75.208	1.00105.93	AAAA C
ATOH	1527 GG GLU	158	21.687 -17.546	75.560	1.00113.87	AAAA C
HOTA	1529 OD GLU	158	21.347 -16.081	75.302	1.00119.34	AAAA C
ATON	1529 OE1 GLU	159	21.284 -15.733	74.096	1.00126.27	
ATOH	1530 CE2 GLU	158				AAAA C
			21.199 -15.317	76.282	1.00117.79	AAAA O
HOTA	1531 C GLU	158	24.434 -15.915	76.025	1.00 95.00	AAAA C
ATOH	1532 O GLU	158	23.988 -16.117	77.145	1.00 95.89	AAAA O
ATOH:	1533 N SER	159	25.276 -14.942	75.769	1.00 93.30	AAAA 11
ATOH	1535 CA SER	159	25.810 -14.119	76.848	1.00 92.28	AAAA C
ATOH		159	26.989 -14.905	77.517	1.00 97.37	
ATOH		159				AAAA C
			26.972 -14.427	78.886	1.00 98.08	AAAA C
ATOH	1539 C SER	159	26.228 -12.793	76.226	1.00 91.47	AAAA C
ATOH		159	27.368 -12.592	75.810	1.00 92.75	AAAA C
ATOH	1541 N PRO	150	25.196 -12.007	75.932	1.00 88.65	AAAA II

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APV H 1542 TO PER 160	22 780	-12.122	76.395	1.00 86.67	
					AAAA C
ATM: 1543 (A PRO 160)		-10.701		1.00 84.74	AAAA C
ATOM: 1544 TB PRO 160	24.125	-9.978	75.456	1.00 84.79	AAAA C
ATC4) 1545 00 PRO 160	23.370	-10.671	76.515	1.00 84.62	AAAA C
ATOH 1546 C PRO 160		-10.025			
					AAAA C
ATOM 1547 0 PRO 160	26.319	-9.934		1.00 79.70	AAAA O
ATON 1548 N MET 161	27.563	-9.522	75.596	1.00 74.45	AAAA N
ATOH 1550 CA MET 161	28.530	-0.735			AAAA C
ATOH 1551 CB MET 161	29.924				
		-9.178			AAAA C
ATOM 1552 CG MET 161		-10.630			AAAA C
ATON 1553 SD MET 161	30.716	-11.621	77.094	1.00 85.25	AAAA S
ATON 1554 CE NET 161	29.841	-10 905			AAAA C
	28.358	-7.234	76.189		AAAA C
ATCH 1556 O HET 161	28.788	-6.443	77.034	1.00 58.60	AAAA O
ATOH 1557 H CYS 162	27.681	-6.819	75.095	1.00 54.81	II AAAA II
ATOM 1559 CA CYS 162	27.493	-5.384	74.938		AAAA C
ATON 1560 C CYS 162	26.306	-4.777			
			75.670		AAAA C
ATON: 1561 O CYS 162	25.224	-5.324	75.928	1.00 53.89	AAAA O
ATOM 1562 CB CYS 162	27.422	-5.099	73.459	1.00 48.31	AAAA C
ATOM 1563 SG CYS 162	28.533	-6.064	72.432		AAAA S
ATOH 1564 H GLU 163	26.409	-3.522			
			76.031		N AAAA
ATON 1566 CA GLU 163	25.355	-2.675	76.538	1.00 47.19	AAAA C
ATON 1567 CB GLU 163	26.051	-1.412	77.027	1.00 49.95	AAAA C
ATON 1568 OF GLU 163	26.476	-1.364	78.465		AAAA C
ATOH 1569 CD GLU 163	25.817	-0.135	79.116	1.00 81.67	
					AAAA C
	26.470	0.473	80.016	1.00 73.22	aaaa o
ATON: 1571 OE2 GLU 163	24.646	0.208	78.721	1.00 80.93	AAAA O
ATOM: 1572 C GLU 163	24.299	-2.340	75.472	1.00 49.05	AAAA C
ATON 1573 O GLU 163	24.488	-2.423	74.234		
				1.00 45.90	AAAA O
ATOH 1574 H LYS 164	23.142	-1.815	75.880	1.00 47.43	AAAA N
ATON 1576 CA LYS 164	22.011	-1.499	75.081	1.00 43.92	AAAA C
ATON 1577 CB LYS 164	20.714	-2.244	75.450	1.00 44.48	AAAA C
ATON 1578 OG LYS 164	20.560	-3.639			
			74.870	1.00 48.65	AAAA C
ATOM 1879 CD LYS 164	19.480	-1.432	75.622	1.00 49.04	AAAA C
ATCH 1580 CE LYS 164	18.409	-5.012	74.720	1.00 49.21	AAAA C
ATON 1891 NO LYS 164	17.951	-5.372	75.134	1.00 37.67	AAAA II
ATOM 1895 C LYS 164		-0.040	75.204	1.00 45.01	
					AAAA C
	21.466	0.484	76.282	1.00 45.69	AAAA O
ATCH 1597 H THR 165	21.333	0.570	74.034	1.00 44.94	AAAA N
ATON: 1889 CA THR 165	20.775	1.943	74.077	1.00 43.13	AAAA C
ATOM: 1899 OB THR 165	21.831	2.952	73.553	1.00 47.81	AAAA C .
ATOM 1591 OG1 THR 165	22.053				
		2.689	72.127	1.00 39.13	AAAA O
ATOM 1593 032 THR 165	23.119	2.842	74.362	1.00 40.40	AAAA C
ATON 1594 C THR 165	19.532	1.881	73.189	1.00 40.92	AAAA C
ATCH 1598 0 THR 165	19.346	0.897	72.414	1.00 35.91	AAAA O
ATOM: 1896 # THR 166	19.781				
		2.985	73.173	1.00 39.18	aaaa n
ATON 1899 CA THR 166	17.689	2.991	72.182	1.00 42.97	AAAA C
ATON 1899 OF THR 166	16.297	3.096	72.833	1.00 55.99	AAAA C
ATCH: 1600 DG1 THR 166	15.562	4.385	72.819	1.00 41.42	AAAA O
ATOM: 1800 GG0 THR 166	16.157	2.740	74.313	1.00 42.93	AAAA C
ATOM: 1603 G THR 166	17.983				
		4.051	71.137	1.00 40.17	AAAA C
ATOM 1604 0 THR 166	18.219	5.206	71.509	1.00 35.72	AAAA O
ATOM 1605 W ILE 167	17.912	3.725	69.866	1.00 42.21	AAAA II
ATOM: 1607 CA ILE 167	18.182	4.672	68.777	1.00 41.05	AAAA C
ATON 1609 CB ILE 167	19.437	4.335		1.00 39.50	AAAA C
ATOH 1609 CG2 ILE 167	19.589				
		5.346		1.00 15.26	AAAA C
	20.722	4.305	68.724	1.00 36.20	аааа с
ATOM 1611 CD1 ILE 167	21.899	3.665	67.966	1.00 35.70	AAAA C
ATON 1612 C ILE 167	16.937	4.524	67.882	1.00 40.94	AAAA C
ATOM 1613 O ILE 167	16.655	3.435	67.394	1.00 35.51	. AAAA O
ATOM 1614 W ASW 168	16.318				
		5.635	67.537	1.00 42.29	AAAA N
	15.112	5.633	66.713	1.00 45.22	AAAA C
ATON 1617 CB ASN 168	15.526	5.253	65.292	1.00 45.69	AAAA C
ATON 1619 CG ASN 168	14.497	5.696	64.244	1.00 51.19	AAAA C
ATOM 1619 OD1 ASN 168	14.344	5.112	63.150	1.00 41.75	AAAA O
ATOH 1620 HD2 ASH 168	13.749				
			64.522	1.00 48.89	AAAA II
ATOM 1623 C ASN 168		4.739		1.00 46.55	AAAA C
ATOM 1624 O ASM 168	13.544	3.879	66.326	1.00 45.95	AAAA O
ATON 1625 N ASN 169			68.433	1.00 45.12	AAAA N
ATOM 1627 CA ASM 169		3.759		1.00 43.67	AAAA C
ATON 1629 CB ASN 169					
				1.00 36.84	AAAA C
ATOH 1629 CG ASH 169			69.093	1.00 42.75	AAAA C
ATOM 1630 OD1 ASM 169	10.917	5.779	70.280	1.00 36.67	AAAA O
ATON 1631 ND2 ASN 169				1.00 40.74	AAAA II
ATON 1634 C ASN 169				1.00 44.69	
ATON 1635 O ASN 169					AAAA C
				1.00 45.72	AAAA O
ATOH 1636 H GLU 170			68.862	1.00 41.64	II AAAA
ATOH 1638 CA GLU 170	14.655			1.00 45.88	AAAA C
ATOH 1639 CB GLU 170				1.00 55.92	AAAA C
ATOM 1640 CG GLU 170					
				1.00 67.08	AAAA C
ATOM 1641 CD GLU 170				1.00 74.56	AAAA C
ATON 1642 OE1 GLU 170	13.869	0.466	65.049	1.00 77.75	AAAA O
ATOH 1643 OE2 GLU 170				1.00 70.71	AAAA O
ATCH 1644 C GLU 170				1.00 47.10	AAAA C
ATON 1645 O GLU 170					
1,42 G JW 170	AV.582 .	1.172		1.00 49.92	AAAA O

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ATM	1646 1	TYF	1/1	15.344	-0.46	2 70.95	2 1.00 49.10	2232 11
ATM	1 3648 C	A TYP				_		
			_	16.231				AAAA C
AT:31	l 1649 C	B TYP	171	15.434	-9.86	1 73.35	9 1.00 49.94	AAAA C
ATOH	1650 C	G TYP	171	16.175				
ATOH	1651 C	D1 TYP	171	16.980	-0.210	0 75.23	7 1.00 46.46	AAAA C
ATOU	1652 C	E1 TYR	171	17.634	-0.469	9 76.40		
			_					
ATOH		D2 TYR		16.065	-2.429	9 75.19	4 1.00 43.62	AAAA C
ATOH	1654 C	E2 TYR	171	16.734	-2.675			
								AAAA C
ATOH	1655 C	Z TYR	171	17.516	-1.718	3 76.973	3 1.00 43.58	AAAA C
ATOH	1656 O	H TYR	171	18.174	-2.017	7 78.146	5 1.00 40.16	
								AAAA O
ATOH	1658 C	TYR	171	17.058	-1.938	71.832	2 1.00 51.41	AAAA C
ATON	1659 0	TYR	. 171	16.519	-3.024	71.889	1.00 52.59	AAAA O
ATOH	1660 II			18.331	-1.752	71.493	3 1.00 53.70	H AAAA H
ATOH	1662 C	A ASII	172	19.203	-2.898	71.193		
								AAAA C
ATOH				19.085	-3.278	69.709	1.00 55.43	AAAA C
ATOII	1664 C	G ASII	172	10.939	-4.766	69.498	1.00 61.75	AAAA C
ATOH		D1 ASN						
				19.233	-5.646	70.304	1.00 61.61	AAAA O
ATOH	1666 N	D2 ASN	172	18.449	-5.048	68.295	1.00 57.97	II AAAA II
ATOH	1669 C	ASII	172					
				20.665	-2.712			AAAA C
HOTA	1670 O	ASN	172	21.163	-1.760	72.213	1.00 39.38	AAAA O
ATOH	1671 11	TYR	173	21.373	-3.796			
								AAAA N
ATOH	1673 CA	A TYR	173	22.794	-3.929	71.698	1.00 44.76	AAAA C
ATOH	1674 CE	3 TYR	173	23.223	-5.374			
								AAAA C
ATOH	1675 CG	TYR	173	22.759	-6.274	72.630	1.00 45.18	AAAA C
ATOH	1676 CE	DI TYR	173	21.931	-7.316	72.237	1.00 46.48	
ATOH		1 TYR				_		AAAA C
			173	21.438	-8.191	73.193	1.00 51.36	AAAA C
ATOH	1678 CD	2 TYR	173	23.081	-6.132	73.978	1.00 44.85	AAAA C
ATON	1679 CE	2 TYR	173					
				22.583	-7.016	74.916	1.00 46.92	AAAA C
INTA	1680 CD	TTR	173	21.757	-8.038	74.535	1.00 50.33	AAAA C
HOTA	1681 OH		173					
				21.171	-9.006	75.328	1.00 50.64	AAAA O
ATOH	1683 C	TYR	173	23.673	-3.099	70.762	1.00 46.94	AAAA C
HOTA	1684 0	TYR	173					
				23.389	-2.983	69.567	1.00 49.76	AAAA O
HOTA	1685 N	ARG	174	24.579	-2.318	71.366	1.00 47.79	II AAAA II
ATOH	1687 CA	ARG	174					
				25.517	-1.496	70.577	1.00 49.13	AAAA C
: ICTA	1688 CB	ARG	174	25.537	-0.132	71.233	1.00 44.32	AAAA C
ATOH	1669 03	ARG	174	24.210				
					0.623	71.234	1.00 48.14	AAAA C
ATON	1690 CD	ARG	174	23.372	0.344	70.003	1.00 51.47	AAAA C
ATO::	1591 NE	ARG	174	21.974	0.760	70.039	1.00 48.35	
ATOH								AAAA N
	1693 CC		174	21.144	0.570	69.017	1.00 48.23	AAAA C
ATO:	1694 DH	1 ARG	174	21.477	0.022	67.864	1.00 38.98	II AAAA II
ATOH		2 ARG	174					
				19.909	1.922	69.197	1.00 54.65	AAAA II
ATO!:	1700 C	ARG	174	26.921	-2.094	70.461	1.00 45.98	AAAA C
ATOH:	1701 0	ARG	174					
				27.548	-2.557	71.406	1.90 44.97	AAAA O
. ATOU	1702 #	CYS	175	27.493	-2.183	69.294	1.00 46.21	AAAA II
ATOH	1704 CA	773	175	28.787	-2.758	68.997		
							1.00 45.60	AAAA C
ATOH	1705 C	CYS	175	29.407	-2.395	67.665	1.00 46.23	AAAA C
ATOH	1706 0	CYS	175	28.755	-2.018	66.665	1.00 44.79	
								AAAA C
ATOH	1707 CB	CYS	175	28.576	-4.253	69.167	1.00 35.62	AAAA C
ATCH:	1708 SG	CYS	175	27.812	-5.191	67.927	1.00 51.92	AAAA S
ATC:	1709 #	TRP	176					
		-		30.764	-2.517	67.583	1.00 48.16	II AAAA
ATOH	1711 CA	125	176	31.430	-2.091	65.325	1.00 42.49	AAAA C
ATOH	1712 CB	TRP	176	32.769				
					-1.409	66.554	1.00 36.38	AAAA C
HOTA	1713 CG	TRP	176	32.689	-0.069	67.203	1.00 25.56	AAAA C
HOTA	1714 CD3	2 TRP	176	32.588	1.186		1.00 23.71	
						66.480		AAAA C
ATOH		2 TRP	176	32.558	2.217	67.422	1.00 32.40	AAAA C
ATOH:	1716 CE3	TRP	176	32.535	1.520	65.141	1.00 24.31	AAAA C
ATOH								
		TRP	176	32.730	0.257	68.525	1.00 28.37	AAAA C
HOTA	1718 NE1	TRP	176	32.636	1.636	68.678	1.00 37.21	AAAA 11
ATOH		TRP	176					
				32.441	3.565	67.088	1.00 28.51	AAAA C
ATOH	1721 CD3	TRP	176	32.447	2.822	64.789	1.00 22.23	AAAA C
HOTA	1722 CH2	TRP	176	32.406	3.817	65.745	1.00 29.51	AAAA C
HOTE	1723 ¢	TRP	176	31.631	-3.268	65.408	1.00 39.30	AAAA C
ATOH	1724 0	TRP	176	31.703	-3.121	64.199	1.00 39.15	AAAA O
ATOH								
		THR	177		-4.460	66.005	1.00 41.33	AAAA II
ATOH	1727 CA	THR	177	31.964	-5.644	65.161	1.00 49.28	AAAA C
HOTA	1708 CB	THR	177					
					-6.062	65.162	1.00 43.66	AAAA C
ATOH	1729 OG1	THR	177	34.309	-5.025	64.613	1.00 47.85	AAAA O
ATOH	1731 CG2	THR	177					
					-7.271	61.283	1.00 58.51	AAAA C
ATOH	1732 C	THR	177	31.290	-6.814	65.858	1.00 48.76	AAAA C
HOTA	1733 0	THR	177					
					-6.539	67.001	1.00 51.53	AAAA O
ATOH	1734 H	THR	178	31.269	-8.000	65.331	1.00 51.96	II AAAA
ATOM	1736 CA	THR	178		-9.236			
						65.946	1.00 58.95	AAAA C
ATOH	1737 CB	THR	178	31.253 -	10.500	65.082	1.00 66.55	AAAA C
ATOH	1738 OG1	THR	179	31.505 -		63.734	1.00 75.70	
								AAAA O
ATOH		THR	178	30.104 -	11.499	65.148	1.00 74.23	AAAA C
ATOH	1741 C	THR	178		-9.539	67.213	1.00 60.25	
								AAAA C
HOTA	1742 0	THR	178	31.204 -	10.202	68.135	1.00 66.05	AAAA O
ATOH	1743 11	ASN	179		-9.130	67.253	1.00 57.56	
								AAAA II
ATOH	1745 CA	ASH	179		-9.392	68.443	1.00 53.39	AAAA C
ATOH:	1746 CB	ASH	179	35.130 -	10.024	68.068	1.00 48.46	
								AAAA C
ATOH	1747 CG	ASN	179	34.897 -		67.126	1.00 56.25	AAAA C
ATOH-	1748 OD1	ASN	179	34.412 -:		67.553	1.00 51.38	
								AAAA O
ATOH		ASII	179	35.229 -	11.063	65.863	1.00 48.10	AAAA 11
ATOH	1752 C	ASH	179			69.285	1.00 50.78	
								AAAA C
ATOH	1753 0	ASII	179	34.556 -	-8.377	70.426	1.00 57.97	AAAA O
								· -

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ATOU	1754 1756		ARG ARG	180 180	33.626 33.808				AAAA 0	
ATOL	1757	C5		180	34.925				AAAA C	
ATOH	1758			180	36.324				AAAA C	
ATOH HOTA	1759 1760		ARG ARG	180 180	37.288 38.569				AAAA C AAAA N	
ATOH	1762	32	ARG	180	39.298				AAAA C	
ATOH	1763		1 ARG	180	38.877			1.00 80.82	AAAA N	
ATOH	1766 1769		2 ARG ARG	180 180	40.474 32.530				AAAA N AAAA C	
ATOH ATOH	1770		ARG	180	31.862				AAAA O	
ATOH	1771	[1]	CYS	181	32.230	-4.728	71.063	1.00 44.80	H AAAA H	
HOTA HOTA	1773 1774	CA C	CYS	181 181	31.199 31.646			_	AAAA C	•
ATOH	1775	ō	CYS	181	32.835				AAAA O	
ATOH	1776	CB	CYS	181	30.940	-4.282	73.110	1.00 43.88	AAAA C	
ATOH	1777	SG	CYS	181	30.363				AAAA S	
HOTA HOTA	1778 1780	DA CA	GLII	182 182	30.659 30.948				AAAA C	
ATOI1	1781	CB	GLII	182	29.749				AAAA C	
HOTA	1782	CG	GLII	182	29.809				AAAA C	
ATOH ATOH	1783 1784	CD OE1	GLN GLN	182 182	28.757 27.898				AAAA C AAAA O	
ATOH	1785		GLI	182	28.857	4.164			II AAAA	
ATOH	1788	Ç	GLII	182	31.218			1.00 46.07	AAAA C	
ato::	1789 1790	0	GLN LYS	182 183	30.458 32.213	-0.327 0.866		1.00 47.01	AAAA O	
HOTA	1792	CA	LTS	183	32.479			1.00 45.26	AAAA 11 AAAA C	
ATO!!	1793	CB	LYS	183	33.966	1.275	75.185	1.00 48.68	AAAA C	
ATOH	1794	CG	LYS	183	34.865	0.267		1.00 47.95	AAAA C	
IOTA IOTA	1795 1796	CD	LYS LYS	183 183	36.337 37.178	0.734 -0.208	74.523 73.684	1.00 48.06 1.00 46.78	AAAA C AAAA C	
ATOI1	1797	112	LYS	183	38.499	-0.654	74.158	1.00 44.00	AAAA II	
ATOH	1901	3	LYS	193	31.659	2.205	75.477	1.00 48.13	AAAA C	
ATOH ATOH	1802 1803	0	LYS	183 184	31.679 31.165	3.305 2.014	74.946 76.699	1.00 48.84	O AAAA 11 AAAA	
ATON	1805	TA	HET	184	30.388	3.041	77.413	1.00 53.22	AAAA O	
ATOH	1806	2.5	HET	194	29.927	2.613	77.537	1.00 54.27	AAAA C	
ATOH: ATOH:	1907	03 SD	HET	184 184	27.855 26.911	2.955 1.601	76.536 75.912	1.00 56.16	AAAA C AAAA S	
ATOH	1909	CE	HET	184	26.738	1.855	74.171	1.00 46.57	AAAA C	
ATOH	1910	2	HET	184	31.051	3.200	78.770	1.00 50.55	AAAA C	
ATC:1	1911	ଦ ::	CYS	194 185	31.770	2.292	79.115	1.00 48.82	AAAA O	
ATON HOTA	1812 1814	TA.	CYS	185	30.796 31.342	4.195 4.365	79.565 80.892	1.00 53.97 1.00 58.63	AAAA :: AAAA C	
ATCH	1815	:	CYS	185	30.297	4.320	91.989	1.00 65.16	AAAA C	
ATON	1916	<u> </u>	CYS	185	29.133	4.549	81.761	1.00 65.87	AAAA O	
ATON ATON	1817 1818	03 3:3	CYS	195 185	31.965 33.623	5.772 5.771	81.000 80.312	1.00 60.37 1.00 60.09	AAAA C AAAA S	
ATON	1919	::	PRO	185	30.688	3.979	83.206	1.00 69.41	AAAA !!	
ATOH	1820	== ==	PRO	196	32.066	3.777	83.702	1.00 71.11	AAAA S	
ATOH ATOH	1821 1822	CA CB	PRO PRO	186 196	29.717 30.523	3.933 3.487	84.304 85.503	1.00 69.11 1.00 68.03	AAAA C AAAA C	
HOTA	1823	Ċ3	PRO	186	31.910	3.920	85.198	1.00 71.02	AAAA C	
ATOH	1924	č	PRO	196	29.120	5.320	84.431	1.00 69.47	AAAA C	
ATOH ATOH	1825 1826	11	PRO SER	186 187	29.820 27.801	6.345 5.367	84.507 84.546	1.00 65.93 1.00 68.78	aaaa o aaaa ii	
ATOH	1828	CA	SER	187	27.050	6.592	84.750	1.00 69.29	AAAA C	
ATOH	1829	CB	SER	187	25.594	6.287	85.129	1.00 78.29	AAAA C	
ATOH ATOH	1830 1932	OG C	SER SER	187 187	25.474 27.630	4.935	85.566 85.836	1.00 91.78 1.00 67.19	AAAA C AAAA C	
HOTA	1833	Ö	SER	187	27.606	8.708	85.803	1.00 63.98	AAAA O	
ATO!!	1834	11	THR	198	28.108	6.853	86.908	1.00 68.20	M AAAA N	
ATOH ATOH	1836 1837	CA CB	THR THR	188 188	28.870 29.805	7.507 6.459	87.963 88.618	1.00 68.39	D AAAA D AAAA	
ATOH	1838		THR	198	28.943	5.365	89.016	1.00 89.33	AAAA O	
HOTA	1840	CG2	THR	188	30.605	7.048	89.759	1.00 73.71	AAAA C	
ATOH	1841 1842	0	THR THR	198 188	29.802	8.583	87.429	1.00 67.52	AAAA C	
ATOH	1843	N	CYS	189	29.843 30.643	9.739 8.247	87.834 86.446	1.00 68.30 1.00 63.89	О <i>Е</i> БББ И ББББ	
ATOH	1845	CA	CYS	199	31.583	9.116	85.817	1.00 57.29	AAAA C	
ATOH	1846	C	CYS	189	30.951	10.331	85.195	1.00 57.70	AAAA C	
ATOH ATOH	1047 1848	C5 C	CYS	189 189	31.648 32.416	11.327 8.372	85.017 84.769	1.00 57.56 1.00 58.67	AAAA C	
HOTA	1846	S·3	CYS	189	33.347	7.001	85.535	1.00 53.46	AAAA S	
ATOH	1850	14	GLY	190	29.689	10.322	84.806	1.00 56.91	AAAA N	
ATOH ATOH	1852 1853	CA C	GLY GLY	190 190	29.038 29.444	11.521 11.834	84.323 82.886	1.00 57.28 1.00 59.62	AAAA C AAAA C	
ATOH	1854	Ö	GLY	190	29.609	10.932	82.082	1.00 57.91	AAAA O	
ATOH	1855	H	LYS	191	29.842	13.052	82.624	1.00 62.78	II AAAA II	
ATOH ATOH	1857 1858	CA CB	LYS LYS	191 191	30.359 30.058	13.520 15.035	81.364 81.214	1.00 67.72	AAAA C AAAA C	
ATOH	1859	ÇĞ	LYS	191	28.568	15.035	81.214	1.00 /2./6	AAAA C	
ATOH	1860	CD	LYS	191	28.207	16.733	80.723	1.00 90.15	AAAA C	
HOTA	1861	CE	LYS	191	26.713	16.806	80.471	1.00 91.83	AAAA C	

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ATCH	1960 NO LYG	1.21	26.368	16.183	79.152	1.00 97.62	11 AAAA 11
ATOR	1866 T LYS	191	31.868				AAAA C
ATOH	1967 O LYS			_			AAAA O
			32.486				
ATOH	1968 II ARG		32.488				II AAAA II
ATOH	1870 CA ARG		33.885	12.171			AAAA C
ATOH	1871 CB ARG	192	34.505	12.070	83.432	1.00 66.58	AAAA C
ATOH	1870 CG ARG	192	34.670	13.400	84.131	1.00 71.59	AAAA C
ATOH	1973 CD ARG		34.386				AAAA C
ATOL	1874 HE ARG						
			35.622				II AAAA
ATOH	1876 CZ ARG		35.968				AAAA C
ATOH	1877 IIH1 ARG	192	35.026	11.486	87.600	1.00 88.49	II AAAA II
HOTA	1880 HH2 ARG	192	37.162	12.463	87.950	1.00 72.95	II AAAA II
ATOH	1983 C ARG	192	34.321	10.851	81.337	1.00 58.83	AAAA C
ATOH	1884 O ARG	192	33.336				AAAA O
		193					
HOTA	_		35.521				II AAAA
ATOH	1887 CA ALA	193	35.962				AAAA C
HOTA	1889 CB ALA	193	37.167	9.921	79.541	1.00 45.15	AAAA C
ATOH	1989 C ALA	193	36.221	8.525	81.451	1.00 48.97	AAAA C
ATOH	1890 O ALA	193	36.220	8.908	82.616		AAAA O
ATOH	1891 # CYS	194	36.544	7.304			
							II AAAA II
ATOH	1893 CA CYS	194	36.836	6.302			AAAA C
ATOH	1894 C C/S	194	37.834	5.304	81.448	1.00 61.25	AAAA C
ATOH:	1895 O CYS	194	37.952	5.291	80.216	1.00 61.52	AAAA O
ATOH	1896 CB CYS	194	35.510	5.741	82.504	1.00 57.96	AAAA C
ATO(1	1897 SG CYS	194	34.785	4.524	81.402	1.00 54.49	AAAA S
ATOH	1899 II THR	195			82.311		
			38.422	4.499		1.00 58.51	H AAAA H
ATOH	1900 CA THR	195	39.462	3.584	81.913	1.00 57.42	AAAA C
HOTA	1901 CB THR	195	40.237	3.142	83.188	1.00 65.73	AAAA C
ATOH	1902 OG1 THR	195	40.288	4.248	84.091	1.00 70.15	AAAA O
ATOH	1904 CG2 THR	195	41.684	2.864	82.745	1.00 77.91	AAAA C
ATOH	1905 C THR	195	38.857	2.404	81.226	1.00 54.59	
							AAAA C
ATOH	1906 O THR	195	37.633	2.315	81.318	1.00 58.75	AAAA O
HOTA	1907 N GLU	196	39.610	1.408	80.882	1.00 55.95	II AAAA II
ATOI1	1909 CA GLU	196	39.139	0.145	80.364	1.00 60.07	AAAA C
HOTA	1910 CB GLU	196	40.395	-0.612	79.914	1.00 68.06	AAAA C
HOTA	1911 09 310	196	40.479	-1.146	79.526	1.00 73.96	AAAA C
ATOH	1911 72 610	196	39.235	-0.983	77.67	1.00 83.08	
							AAAA C
ATON		196	38.356	-1.884	77.697	1.00 81.19	O EEAA
ATON	1914 OEC GLU	196	39.060	0.041	76.939	1.00 82.13	AAAA O
ATOH	1915 T GLV	196	38.382	-0.579	81.467	1.00 63.91	AAAA C
ATOI :	1916 0 910	196	37.690	-1.537	91.159	1.00 63.51	AAAA O
ATC!!	1917 N ASN	197	39.566	-0.312	82.739	1.00 67.40	H AAAA
ATOH	1919 CA ASH	197	38.025	-0.947	83.886	1.00 69.21	AAAA C
		197					
ATOH	1920 CB ASH		39.021	-1.394	84.966	1.00 68.49	AAAA C
ATOH	1921 CG ASN	197	39.722	-2.692	84.672	0.01 69.09	AAAA C
ATON	1922 CD1 ASN	197	40.364	-3.273	85.551	0.01 69.04	AAAA C
ROTE	1923 ND2 ASH	197	39.522	-3.193	93.443	0.01 68.97	aaaa x
ATOLI	1926 C ASH	197	37.033	0.043	84.495	1.00 69.01	AAAA I
ATOH	1917 O ASN	197			85.664		
			36.945	0.281		1.00 68.24	AAAA O
ATCH	1929 H ASH	198	36.384	0.795	83.607	1.00 69.91	AAAA II
ATOH	1930 CA ASH	198	35.356	1.734	64.048	1.00 68.49	AAAA C
ATOH	1931 TB ASN	198	34.120	0.830	94.373	1.00 60.12	AAAA C
ATOH	1932 CG ASH	198	33.806	0.095	83.103	1.00 69.29	AAAA C
ATOH	1933 OD1 ASN	198	33.475	0.654	82.054	1.00 73.20	AAAA C
ATOH	1934 HD2 ASH	198	33.980	-1.206	83.268	1.00 65.34	AAAA N
ATOH	1937 C ASH	198	35.784	2.563	85.228	1.00 64.01	AAAA C
ATOH		198	34.992	2.827	86.117	1.00 64.20	AAAA O
ATOH	1939 N GLU	199	36.955	3.164	85.157	1.00 64.75	aaaa n
HOTA	1941 CA GLU	199	37.342	4.054	86.255	1.00 64.64	AAAA C
АТОН	1942 CB GLU	199	38.702	3.624	86.744	1.00 66.11	AAAA C
ATOH	1943 CG GLU	199	38.846	3.717	08.233	1.00 77.15	AAAA C
HOTA	1944 CD GLU	199	39.579	2.532	88.832	1.00 89.24	AAAA C
. ATOH	1945 OE1 GLU	199	39.385			1.00 81.65	
				2.406	90.066		AAAA O
ATO!!	1946 CEC GLU	199	40.282	1.821	88.079	1.00 77.94	AAAA O
IOTA	1947 C GLU	199	37.314	5.463	85.690	1.00 62.92	AAAA C
ATOH	1948 O GLU	199	37.922	5.676	84.632	1.00 63.62	O AAAA
ATOH	1949 N CYS	200	36.605	6.393	86.313	1.00 56.16	AAAA 11
ATOH	1951 CA CYS	200	36.600	7.721	85.740	1.00 55.11	AAAA C
ATOH	1952 C CYS	200	37.978	8.315	85.521	1.00 57.77	AAAA C
					-		
ATOH		200	38.884	8.058	86.300	1.00 63.79	AAAA O
ATOH	1954 TB CYS	200	35.824	8.664	86.548	1.00 62.70	AAAA C
ATOH	1955 SG CYS	200	34.196	9.100	87.098	1.00 55.85	AAAA S
MOTA	1956 H CYS	201	38.124	9.192	84.540	1.00 54.50	BAAA N
ATOH	1958 CA CYS	201	39.338	9.389	84.202	1.00 48.19	AAAA C
ATOH	1959 C CYS	201	39.236	11.287	84.786	1.00 42.34	AAAA C
ATOH	1960 O CYS	201					
			38.165	11.704	85.166	1.00 54.32	AAAA O
ATOH	1961 CB CYS	201	39.590	10.070	82.695	1.00 40.90	AAAA C
ATOH	1962 SG CYS	201	39.644	8.597	81.747	1.00 51.42	AAAA S
ATOH	1963 N HIS	202	40.254	12.075	84.675	1.00 39.12	AAAA 11
ATOH	1965 CA HIS	202	40.290	13.461	85.128	1.00 41.55	AAAA C
ATOH	1966 C HIS	202	39.284	14.184	84.289	1.00 46.59	AAAA C
ATOH		202					
			39.176	13.851	83.103	1.00 51.64	AAAA C
ATOH	1968 CB HIS	202	41.712	13.952	84.810	1.00 45.20	AAAA C
ATOH	1969 CG HIS	202 -	41.996	15.330	85.267	1.00 38.71	AAAA C
ATOI1	1970 HD1 HIS	202	41.501	16.404	84.550	1.00 51.32	AAAA II
					-	•	

ATCH 2011 T SLY 207 38.466 9.061 76.058 1.00 47.15 ATCH 2010 O SLY 207 37.668 9.102 76.057 1.00 45.04 ATCH 2013 H SER 208 39.622 9.019 76.760 1.00 50.36 ATCH 2015 CA SER 208 39.832 7.898 77.660 1.00 48.27 ATCH 2016 CB SER 208 40.600 5.597 77.461 1.00 61.34 ATCH 2017 OG SER 208 41.144 8.668 78.377 1.00 49.17 ATCH 2010 O SER 208 41.144 8.668 78.377 1.00 49.17 ATCH 2010 O SER 208 41.144 8.68 78.377 1.00 49.17 ATCH 2020 O SER 208 41.599 7.123 79.199 1.00 52.04 ATCH 2021 H CYS 209 41.599 7.123 79.199 1.00 52.04 ATCH 2023 CA CYS 209 42.924 7.307 79.964 1.00 55.98 ATCH 2024 C CYS 209 43.453 6.035 80.484 1.00 57.41 ATCH 2025 O CYS 209 42.924 7.307 79.964 1.00 55.51 ATCH 2026 CB CYS 209 42.862 4.963 90.423 1.00 58.33 ATCH 2026 CB CYS 209 42.862 8.258 81.146 1.00 52.51 ATCH 2026 CB CYS 209 42.862 8.258 81.146 1.00 52.51 ATCH 2026 CB CYS 209 42.862 8.258 81.146 1.00 52.51 ATCH 2030 CA SER 210 44.734 6.145 90.893 1.00 58.22 ATCH 2031 CB SER 210 47.022 5.083 91.105 1.00 59.10 ATCH 2031 CB SER 210 47.546 6.204 81.813 1.00 64.49 ATCH 2034 C SER 210 45.529 3.614 83.326 1.00 56.34 ATCH 2035 O SER 210 45.529 3.614 83.326 1.00 56.34 ATCH 2035 O SER 210 45.529 3.614 83.326 1.00 54.42 ATCH 2035 O SER 210 45.529 3.614 83.326 1.00 54.42	AAAA C AAAA C AAAA C AAAA O AAAA H AAAA C
ATCH 2038 CA ALA 211 44.980 5.684 85.004 1.00 56.60 ATCH 2039 CB ALA 211 46.333 5.926 85.649 1.00 63.41 ATCH 2040 C ALA 211 43.962 6.747 85.395 1.00 56.58 ATCH 2041 O ALA 211 43.967 7.792 84.711 1.00 50.78 ATCH 2042 H PRO 212 43.117 6.416 86.359 1.00 55.93 ATCH 2043 CD PRO 212 43.042 5.166 87.115 1.00 55.86 ATCH 2044 CA PRO 212 41.951 7.257 86.575 1.00 55.50 ATCH 2044 CG PRO 212 41.104 6.470 87.556 1.00 55.50 ATCH 2046 CG PRO 212 42.021 5.483 88.175 1.00 59.65 ATCH 2046 CG PRO 212 42.409 8.535 87.177 1.00 53.64 ATCH 2048 O PRO 212 42.409 8.535 87.177 1.00 53.64 ATCH 2048 O PRO 212 43.611 8.725 87.393 1.00 57.48 ATCH 2049 H ALA 213 41.537 9.492 87.347 1.00 53.87 ATCH 2051 CA ALA 213 41.537 9.492 87.347 1.00 53.87 ATCH 2051 CA ALA 213 41.783 10.255 89.541 1.00 66.40	AAAA C
ATOH 2053 C ALA 213 43.289 11.300 87.907 1.00 61.40 ATOH 2054 C ALA 213 43.728 12.202 88.652 1.00 60.03 ATOH 2055 H ASH 214 44.068 10.999 86.899 1.00 64.80 ATOH 2057 CA ASH 214 45.366 11.551 86.596 1.00 63.36 ATOH 2063 C ASH 214 45.366 11.551 86.596 1.00 63.36 ATOH 2064 C ASH 214 45.366 11.551 86.596 1.00 63.36 ATOH 2058 CB ASH 214 45.300 12.294 85.251 1.00 61.56 ATOH 2058 CB ASH 214 45.390 12.794 84.117 1.00 58.38 ATOH 2059 CG ASH 214 46.336 10.379 86.608 1.00 67.32 ATOH 2059 CG ASH 214 47.697 10.896 86.362 1.00 75.48 ATOH 2060 ODI ASH 214 48.254 11.105 85.302 1.00 83.64 ATOH 2061 HD2 ASH 214 48.513 11.170 87.427 1.00 90.05 ATOH 2065 H ASP 215 45.666 13.565 85.305 1.00 59.78 ATOH 2066 CB ASP 215 45.618 14.432 84.143 1.00 56.47 ATOH 2068 CB ASP 215 45.618 14.432 84.143 1.00 56.47 ATOH 2069 CG ASP 215 46.671 16.543 84.986 1.00 56.36 ATOH 2070 ODI ASP 215 46.590 17.699 85.473 1.00 56.17	AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C AAAA O AAAA II AAAA II AAAA C AAAA C AAAA C

Aff I	: 2671 902 ASI	n 215	47.76	5 15. 9 2	é 81.51	1 1.00 60.51	
5.701			46.81				AAAA O AAAA C
ATO			46.99		8 82.30	2 1.00 53.58	AAAA O
ATG ATG			47.719 48.883				II AAAA
ATO			50.20			_	AAAA C AAAA C
ICTA.			50.403	3 11.97	_		AAAA O
ATOL			50.436				AAAA C
IOTA IOTA			48.681 49.590				AAAA C
ATO			47.559				AAAA O AAAA N
ATOL			47.259	9.760	81.84	5 1.00 51.83	AAAA C
ATO:			46.908				AAAA C
ATOH			46.207 45.775				AAAA C AAAA O
ATON	•		45.744				II AAAA
ATOR			44.802				AAAA C
ATOH ATOH			45.166 46.300				AAAA C
ATOH			44.536				AAAA O AAAA C
ATOH			44.256	13.494	80.303		AAAA S
ATOH ATOH			44.226				aaaa ii
ATOH			44.575 43.693				AAAA C AAAA C
ATOH			43.952				AAAA C
ATOL			43.811		76.071	1.00 45.51	AAAA C
ATON ATON			44.453 45.303		-		AAAA C
ATOH			43.728				0 AAAA 11 AAAA
ATO:	3106 CA ALA	220	43.630				AAAA C
HOTA			42.536			1.00 28.42	AAAA C
ATON:	2108 T ALA 2109 O ALA	220 220	43.292 42.846	14.071 13.604	75.390 76.455		AAAA C
ATO:	2110 :: CYS	221	43.285	15.334	75.058		O AAAA U AAAA
ATON	2112 CA CYS	221	42.753	16.392	75.875	1.00 35.55	AAAA C
ATON: ATON:	1113 1 TYS	221 221	41.460	17.055	75.452		AAAA C
A7011	note to dve	221	41.265 43.804	17.598 17.479	74.369 76.063		AAAA C AAAA C
ATC:	0116 83 CYS	221	45.494	16.935	76.538		AAAA S
ATG:	2117 Y ARG	222	40.503	17.133	76.396		AAAA N
ATM:	0119 TA ARG	222 222	39.281 38.647	17.906 19.074	76.338 77.712	1.00 51.86	AAAA C
ATO::	IIII IF ARG	222	37.314	19.697	77.854	1.00 54.53 1.00 45.56	AAAA C AAAA C
ATO:	DIDE TO ARG	222	36.538	19.338	79.C87	1.00 54.45	AAAA C
ATON ATON	2123 NE ARG 2125 DE ARG	222 222	36.272	16.947	79.269	1.00 65.53	AAAA II
ATO:	2126 UH1 ARG	222	35.534 34.925	16.080 16.599	78.617 77.533	1.00 67.50 1.00 70.25	AAAA :: AAAA ::
ATOM	2129 DH2 ARG	222	35.342	14.780	79.961	1.00 54.11	AAAA :
ATON	0130 T ARG 0133 D ARG	222	39.562	19.296	75.740	1.00 50.66	AAAA C
ATO:: ATO::	2133 0 ARG 2134 0 HIS	222 223	38.737 40.556	19.845	75.009 76.190	1.00 58.34	AAAA O
A.POI:	2136 TA HIS	223	40.988	21.291	75.821	1.00 45.65 1.00 46.93	II AAAA C AAAA
ATOH	2137 79 HIS	223	41.057	22.251	77.011	1.00 49.51	AAAA C
ATON! ATON	2138 73 HIS 2139 702 HIS	223 223	39.710	22.344	77.647	1.00 58.83	AAAA C
ATOH	2140 HD1 HIS	223	38.820 39.082	23.360 21.388	77.556 78.425	1.00 61.08 1.00 63.28	AAAA C AAAA II
ATOM	2142 CE1 HIS	223	37.881	21.915	78.759	1.00 58.01	AAAA C
ATOH ATOH	2143 NE2 HIS 2145 C HIS	223	37.681	23.010	78.232	1.00 48.56	AAAA N
ATOH!	2145 C HIS 2146 C HIS	223 223	42.363 42.506	21.260 20.753	75.122 74.003	1.00 50.79 1.00 47.43	AAAA C AAAA O
ATOH	2147 H TYR	224	43.359	21.847	75.769	1.00 49.20	AAAA II
IICTA	2149 CA TYR	224	44.712	21.992	75.259	1.00 48.17	AAAA C
HOTA	1150 CB TYR 2151 TG TYR	224 224	45.144 44.318	23.430 24.234	75.426 74.417	1.90 44.07 1.90 51.77	AAAA C
ATOH	2152 CD1 TYR	224	43.193	24.869	74.904	1.00 48.94	AAAA C AAAA C
ATOH	2153 CE1 TYR	224	42.401	25.633	74.089	1.00 48.41	AAAA C
HOTA HOTA	2154 CD2 TYR 2155 CE2 TYR	224	44.623	24.358	73.065	1.00 54.82	AAAA C
ATOH	2156 CD TYR	224 224	43.847 42.739	25.131 25.745	72.233 72.766	1.00 56.09 1.00 54.23	AAAA C AAAA C
ATOH	2157 CH TYR	224	41.915	26.522	72.017	1.00 61.70	AAAA O
ATOH	2159 C TYR	224	45.725	21.095	75.892	1.00 48.19	AAAA C
HOTA HOTA	2160 0 TYR 2161 !! TYR	224 225	45.776 46.584	20.913 20.514	77.111 75.077	1.00 55.75	AAAA O
HOTA	2163 TA TYR	225	47.655	19.653	75.555	1.00 48.79 1.00 43.02	AAAA N AAAA C
HOTA	2164 CB TYR	225	48.020	18.639	74.548	1.00 42.30	AAAA C
ATOH ATOH	2165 CG TYR 2166 CDI TYR	225 225	49.286	17.926	74.954	1.00 46.95	AAAA C
ATON	2167 CEL TYR	225	49.299 50.450	16.858 16.221	75.817 76.173	1.00 43.57 1.00 47.26	AAAA C AAAA C
ATOH1	2168 CD2 TYR	225	50.487	18.407	74.421	1.00 52.82	AAAA C
HOTA	2169 CE2 TYR	225	51.656	17.791	74.781	1.00 53.94	AAAA C
ATOH ATOH	2170 CS TYR 2171 OH TYR	225 225	51.639 52.886	16.707 16.186	75.644 75.905	1.00 52.31 1.00 50.71	AAAA C
ATOH	2173 C TYR	225	48.872	20.507	75.793	1.00 50.71	AAAA O AAAA C
ATOH	2174 © TYR	225	49.080	21.514	75.150	1.00 53.97	AAAA C
HOTA	2175 H TYR	226	49.634	20.253	76.821	1.00 56.8;	AAAA 11

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	ATHE	2177	ťΑ	TYR	226	50.814	21.001	77.172		56.83	AAAA c		
	ATOL	2179	TB CG	TYR	226	50.455 51.741	22.343	77.785 77.941		59.51 65.45	AAAA C AAAA C		
	ATOL:	2179	05 001	TYR	226 226	52.121	23.126 23.557	79.197		69.12	AAAA C		
	ATOLL	2181		TYR	226	53.289	24.275	79.400		70.77	AAAA C		
	ATOH	2192	CDC		226	52.580	23.409	76.864		69.38	AAAA C		
	ATOU ATOU	2183 2184		TYR TYR	226 226	53.758 54.099	24.118	77.020 78.301		70.94 72.96	AAAA C AAAA C		•
	ATOH	2185		TYR	226	55.267	25.254	78.435		70.84	AAAA O		
į	ATO:	2187	Ç	TYR	226	51.784	20.356	78.165		57.55	AAAA C		
	ATOH	2188 2189		TYR ALA	226 227	51.492 52.978	20.133	79.350 77.642		56.90 53.82	AAAA O AAAA N		
	HOTA HOTA	2191		ALA	227	54.061	19.557	78.440		51.82	AAAA C		
	HOTA	2192		ALA	227	54.528	20.629	79.428		55.81	AAAA C		
	ATOH	2193		ALA	227	53.600	18.309	79.170		53.56	AAAA C		
	ATOH ATOH	2194 2195		ALA GLY	227 228	53.663 53.076	18.218 17.360	80.413 78.393		49.63 50.68	AAAA O AAAA N		
	ATOH	2197		GLY	228	52.585	16.135	79.028		49.02	AAAA C		
1	ATOH	2198		GLY	228	51.312	16.330	79.861		51.61	AAAA C		
	ATOH	2199		GLY VAL	228 229	51.028 50.643	15.538 17.495	80.776 79.791		51.10 47.09	O AAAA N AAAA		
	ATOH ATOH	2200		VAL	229	49.489	17.671	80.635		51.11	AAAA C		
	ATOH	2203		VAL	229	49.908	18.610	81.774		56.52	AAAA C		
	INTA	2204		VAL	229	48.627	18.896	82.566		38.39	AAAA C		
	ATOH ATCH	2205	CG2 C	VAL VAL	229 229	51.002 48.255	18.035 18.173	82.682 79.873		50.16 51.37	AAAA C AAAA C		
	ATOH	2207		VAL	229	48.344	19.279	79.309		53.71	AAAA O		
	HOTA	2208	11	CYS	230	47.100	17.518	80.036	1.00	42.21	II AAAA II		
	HOTA	2210		CYS	230	45.881	18.117	79.471 80.228		40.32	AAAA C		
	ATOH ATOH	2211		CYS CYS	230 230	45.456 44.964	19.350 19.248	81.321		38.42 41.62	AAAA C AAAA O		
	HOTA	2213		CYS	230	44.746	17.132	79.370		31.54	AAAA C		
	ATON	2214		CYS	230	45.149	15.753	78.266		43.61	AAAA S		
	HOTA	2215		VAL VAL	231 231	45.637 45.445	20.534	79.731 80.462		39.83 46.57	II AAAA C AAAA		
	ATON	2217 2219		VAL	231	46.619	22.736	80.089		50.99	AAAA C		
	ATOU	2213	731	WAL.	231	46.798	23.878	81.053		50.41	AAAA C		
Ą	ATON:	2222	232	WAL	231	47.838	21.913	80.506	1.00		AAAA C		
	ATOLL ATOLL	====		VAL VAL	231 231	44.111 43.599	22.321	80.057 78.936		52.59 55.30	C AAAA O AAAA		
	ATOH!	2223		PRO	232	43.492	23.105	80.913		54.29	AAAA H		
	ATO!!	2224		FRO	232	43.830	23.395	82.320		54.25	, AAAA C		
	ATOH ATOH	2225 2226		FRO FRO	232 232	42.153 41.537	23.625 23.877	80.575 91.928		54.39 53.73	'AAAA C AAAA C	•	
	ATOL	2227		FRO	232	42.683	24.287	82.765		55.00	AAAA C		
F	ATON:	2229	C	PRO	232	42.361	24.913	79.795		56.37	AAAA C		
	ATOH!	2229		FRO	232	41.498	25.492	79.137 79.901		55.79 54.76	AAAA O AAAA U		
	ATON ATON	0239 2032		ALA ALA	233 233	43.615 43.998	25.400 26.569	79.124		49.93	AAAA C		
	-TOI:	2233		ALA	233	43.440	27.907	79.746		35.43	AAAA C		
	ATOH	1234		ALA	233	45.502	26.662	79.974		49.79	AAAA C		•
	ATOH ATOH	2235 2236		ALA CYS	233 234	46.195 45.984	25.879 27.508	79.516 78.072	1.00	51.41 45.07	O AAAA H AAAA		
	ATOH	2238		CYS	234	47.430			1.00		AAAA C		
<i>د</i> ,	HOTA	2239	C '	CYS	234	48.001	28.340	79.076			AAAA C		
	HOTA	2249		CYS	234	47.650	29.513 28.034	79.250 76.511	1.00	47.57	AAAA C		
	HOTA HOTA	2241		CYS CYS	234 234	47.816 47.608	26.789	75.226		43.04	AAAA S		
	INT	2243		PRO	235	49.127	27.853	79.599	1.00	49.55	II AAAA II		
	HOTA	2244		PRO	235	49.692	26.557	79.207		48.75	AAAA C AAAA C		
	HOTA	2245		PRO PRO	235 235	49.911 50.984	28.569 27.581	80.599 80.975	1.00	51.69 50.80	AAAA C		
	TOIL	2247		PRO	235	50.912	26.417		1.00		AAAA C		
	HOTA	2249		PRO	235	50.487	29.852	80.050	1.00		AAAA C		
	IOTA NOTA	2249		PRO PRO	235 236	50.848 50.676	29.957 30.875	78.870 80.887	1.00		0 AAAA 11 AAAA		
	TOI	2251		PRO	236	50.405	30.822		1.00		AAAA C		
A	1 ICT	2252	CA !	PRO	236	51.323	32.143	80.493			AAAA C		
	TOH	2253		FRO	236 236	51.695 50.652	32.814 32.277		1.00		AAAA C AAAA C		
	IOT/	2254 2255		PRO PRO	236	52.545	31.886	79.671	1.00		AAAA C		
	HOTA	2256		PRO	236	53.218	30.892	79.928	1.00	43.40	AAAA O		
	TOH	2257			237	52.837	32.757		1.00		AAAA II	*	
	TOH TOH	2259 2260		asii Asii	237 237	53.895 55.258	32.623 32.653	77.716 78.456	1.00		AAAA C AAAA C		
	TOH	2261		4511 4511	237	55.357	33.855	79.371	1.00		AAAA C		
A	HOT	2262	001 8	\SN	237	56.044	33.783	80.379	1.00	72.25	AAAA O		
	TOH	2263	HD2 A		237	54.631	34.910	79.051	1.00		AAAA N		
	HOTA	2266 2267		NSN VSII	237 237	53.897 54.962	31.425 30.935	76.788 76.326	1.00		AAAA C AAAA O		
	TOIL	2268		THR	238	52.817	30.657		1.00		AAAA II		
A'	TOH	2270	CA 1	THR	238	52.617	29.567	75.780	1.00		AAAA C		
		2271		HR	238 238	52.461 51.227	28.248	76.466 77.237	1.00		AAAA C AAAA O		
	TOH TOH	2272	OG1 T		238	53.552	28.343		1.00		AAAA C		
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1E, TA	2275	C THE	238	51.279	29.875	75.078	1.90 42.59	2222 6
						-		AAAA C
ATM	2276	O THE	238	50.669			1.00 42.51	AAAA O
ATTH	2277	JJ TYR	239	51.051	29.488	73.832	1.00 42.62	II AAAA II
							_	
ATQU	2279	CA TYR	239	49.949	29.959	73.024	1.00 41.87	AAAA C
ATON	3360	CB TYR	239	50.457	30.907	71.931	1.00 44.86	AAAA C
ATOH	2281	OG TYR	239	51.099			1.00 42.05	AAAA C
ATCN	2292	CD1 TYR	239	52.467	32.086	72.815	1.00 39.41	AAAA C
		CE1 TYR	239					
ATOH	2293			53.092			1.00 43.27	AAAA C
ATO!	2284	CD2 TYR	239	50.376	33.230	72.923	1.00 44.15	AAAA C
	2285	CEC TYR	239	50.972				
ATOH					34.310		1.00 46.22	AAAA C
IOTA	2286	CD TYR	239	52.339	34.243	73.779	1.00 50.49	AAAA C
INTA	2287	OH TYR	239	53.013				AAAA O
							1.00 55.47	
ATOH	2289	C TYR	239	49.232	20.013	72.315	1.00 45.54	AAAA C
HOTA	2290	O TYR	239	49.922	27.810	72.021	1.00 46.66	AAAA O
ATOH	2291	II ARG	240	47.895	28.990	72.126	1.00 40.62	AAAA N
HOTA	2293	CA ARG	240	47.177	27.892	71.426	1.00 38.78	AAAA C
IOTA	2294	CB ARG	240	45.675	28.127	71.452	1.00 39.77	AAAA C
HOTA	2295	CG ARG	240	45.116	28.944	72.588	1.00 43.37	AAAA C
ATOH	2296	CD ARG	240	43.573	28.957	72.683	1.00 38.60	AAAA C
HOTA	2297	HE ARG	240	43.114	29.683	71.455	1.00 53.98	II AAAA
ATOH	2299	CE ARG	240	43.123	31.015	71.530	1.00 48.07	AAAA C
ATOH	2300	HH1 ARG	240	43.513	31.562	72.668	1.00 47.65	II AAAA
ATOH	2303	HH2 ARG	240	42.788	31.778	70.533	1.00 51.03	II AAAA II
ATOH	2306	C ARG	240	47.627	27.737	69.979	1.00 31.72	AAAA C
	2307				-			
ATOII		O ARG	240	47.937	28.730	69.302	1.00 32.37	AAAA O
ATO!!	2308	II PHE	241	47.779	26.542	69.549	1.00 27.95	и баба
HOTA	2310	CA PHE	241	48.182	26.269		1.00 30.41	AAAA C
ATCH	2311	CB PHE	241	49.678	25.940	68.151	1.00 34.83	AAAA C
ATOH	2312	CG PHE	241	50.235	25.653	66.773	1.00 26.84	AAAA C
ATOH	2313	CD1 PHE	241	50.165	26.567	65.753	1.00 25.31	AAAA C
HOTA	2314	CD2 PHE	241	50.785	24.417	66.573	1.00 27.38	AAAA C
ATO:	2315	CE1 PHE	241	50.676	26.232	64.509	1.00 37.24	аааа с
HOTA	2316	CE2 PHE	241	51.294	24.101	65.320	1.00 38.45	AAAA C
ATOH	2317	CS PHE	241	51.281	25.010	64.281	1.00 21.17	AAAA C
ATOH	2318	C PHE	241	47.382	25.089	67.621	1.00 35.77	AAAA C
ATO!!	2319	O PHE	241	47.543	24.013	68.186	1.00 36.77	алал о
ATOH	2320	!: GLU	242	46.739	25.301	66.468	1.00 32.30	H AAAA H
ATOI:	2322	CA GLU	242	45.964				
					24.269	65.805	1.00 35.43	AAAA C
ATCH	2323	ce and	242	46.953	23.144	65.472	1.00 37.98	AAAA C
ATOH	2324	C3 'SLU	242	47.867	23.415	64.314	1.00 39.63	AAAA C
ATO!!	2325	CD GLU	242	47.207	23.965	63.075	1.00 39.27	AAAA C
ATCH	2326	OSI GLU	242	46.380	23.205	62.517	1.00 42.79	AAAA O
ATOH	2327	DEC GLU	242	47.354	25.109	62.626	1.00 36.36	AAAA O
ATQ!!	2329	C GLU	242	44.752	23.771	66.600	1.00 34.36	AAAA C
ATOH	2329	o GLU	242	44.390	22.611	66.511	1.00 28.53	AAAA O
ATO!!	2330	H GLY	243	44.135	24.589	67.449	1.00 36.94	AAAA H
	2332	CA GUY						
ATOH			243	43.043	24.154	60.303	1.00 34.57	аааа с
HOTA.	2333	C GLY	243	43.429	23.107	69.319	1.00 37.76	AAAA C
ATCH	2334	O GLY	243	42.474	22.473	69.745	1.00 43.00	
								AAAA C
ATON:	2335	H TRP	244	44.637	22.536	69.611	1.00 39.53	HAAA H
ATOH	2337	CA TRP	244	44.797	21.536	70.566	1.00 40.85	AAAA C
ATOH	2339	CB TRP	244	44.774	20.271	69.764	1.00 26.76	AAAA C
ATOH	2339	CG TRP	244	46.012	19.885	69.028	1.00 43.19	AAAA C
HOTA	2340	CD2 TRP	244	47.019	18.983	69.498	1.00 39.55	AAAA C
ATOH	2341	CE2 TRP	244	47.998	18.906	68.489	1.00 36.50	AAAA C
ATOH	2342	CE3 TRP	244				1.00 32.19	
				47.186	18.254	70.692		AAAA C
HOTA	2343	CD1 TRP	244	46.424	20.308	67.779	1.00 43.37	AAAA C
ATOH		NE1 TRP	244	47.595	19.727	67.469	1.00 38.89	
								AAAA II
ATOH	2346	CS2 TRP	244	49.150	18.128	68.620	1.00 39.01	AAAA C
HOTA	2347	CE3 TRP	244	48.336	17.478	70.815	1.00 43.98	AAAA C
ATOH		CH2 TRP	244	49.322	17.425	69.784	1.00 42.50	AAAA C
HOTA	2349	C TRP	244	45.998	21.517	71.509	1.00 42.98	AAAA C
- ATOH	2350	O TRP	244	46.253	20.501	72.146	1.00 42.70	AAAA O
I/OTA	2351	N ARG	245	46.888	22.485	71.435	1.00 44.16	II AAAA II
ATOH		CA ARG	245	48.168	22.472	72.095	1.00 46.47	AAAA C
HOTA	2354	CB ARG	245	49.203	21.602	71.367	1.00 47.30	AAAA C
ATOH	2355	CG ARG	245	49.885	22.309	70.203	1.00 48.97	AAAA C
1 KOTA		CD ARG	245	51.129	21.552	69.819	1.00 39.28	AAAA C
HOTA	2357	HE ARG	245	51.586	21.665	68.444	1.00 50.86	AAAA II
HOTA		CZ ARG	245	52.629	21.044	67.895	1.00 46.73	AAAA C
ATOH	2360	NH1 ARG	245	53.344	20.236	68.653	1.00 50.15	AAAA N
ATOH		NH2 ARG	245	53.072	21.126	66.638	1.00 41.69	AAAA II
HOTA	2366	C ARG	245	48.771	23.963	72.271	1.00 46.01	AAAA C
			215					
HOTA		O ARG		48.394	24.793	71.541	1.00 47.44	AAAA O
ATOH	2368	N CYS	246	49.625	23.881	73.317	1.00 42.08	AAAA II
ATOH		CA CYS	246	50.246		73.628		
					25.199		1.00 43.48	AAAA C
ATOH	2371	C CYS	246	51.695	25.217	73.183	1.00 43.38	AAAA C
ATOM		O CYS	246	52.476		73.320		
					24.239		1.00 42.51	AAAA O
ATOH	2373	CB CYS	246	50.102	25.392	75.138	1.00 48.91	AAAA C
ATOH		SG CYS	246	48.386		75.797		
					25.049		1.00 43.68	aaaa s
ATOH	2375 1	I VAL	247	52.121	26.288	72.564	1.00 41.21 .	AAAA N
HOTA		CA VAL	247					
				53.417	26.468	71.982	1.00 36.51	AAÁA C
ATOI1	2378 (CB VAL	247	53.568	26.357	70.444	1.00 36.87	AAAA C
ATOH			247					
		CG1 VAL		53.089	24.988	70.024	1.00 32.71	AAAA C
ATOH	2380 (GG2 VAL	247	53.129	27.602	69.729	1.00 28.20	AAAA C

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AT:30	2391 " VAL	247	53.969	27.812	72.373	1.00 39.37	AAAA C
						1.00 38.80	
ATOH		247	53.230	29.770	72.540		AAAA O
ATUU	2383 II ASE	248	55.291	27.820	72.711	1.00 45.21	AAAA N
ATOU	2385 CA AGE	248	55.895	29.115	73.098	1.00 40.19	aaaa c
HOTA	2386 CB ASP	546	57.091	28.946	73.953	1.00 42.63	AAAA C
ATOH	2387 CG ASP	248	58.126	27.997	73.394	1.00 58.81	AAAA C
ATOM	2388 OD1 ASE	248	59.067	27.795	74.187	1.00 53.06	AAAA O
ATOH	2389 OD2 ASE	248	58.167	27.395	72.313	1.00 69.51	AAAA O
ATOH	2390 C ASP	248	56.315	29.883	71.839	1.00 36.99	AAAA C
	2391 O ASF	248	56.292	29.288	70.772	1.00 39.70	AAAA O
ATCH		249			71.918	1.00 30.72	N AAAA
HOTA	2390 II ARG		56.545	31.163			
HOTA	2394 CA ARG	249	56.950	32.057	70.906	1.00 36.17	AAAA C
INTA	2395 CB ARG	249	57.223	33.485	71.491	1.00 21.29	AAAA C
HOTA	2396 CG ARG	249	57.594	34.424	70.326	1.00 24.96	AAAA C
ATOH	2397 CD ARG	249	57.814	35.811	70.843	1.00 21.23	AAAA C
ATOH	2398 HE ARG	249	56.658	36.150	71.689	1.00 39.75	AAAA N
ATOH.	2400 CC ARG	249	55.632	36.823	71.101	1.00 39.35	AAAA C
ATOH	2401 HH1 ARG	249	55.642	37.118	69.801	1.00 25.41	AAAA 11
ATOH	2404 11H2 ARG	249	54.641	37.118	71.946	1.00 44.04	AAAA N
HOTA	2407 C ARG	249	58.134	31.685	70.010	1.00 40.63	AAAA C
	2408 O ARG	249	58.086	31.923	68.797	1.00 44.79	AAAA O
ATOH	_					1.00 41.87	AAAA II
ATOII	2409 II ASP	250	59.149	30.974	70.468		
ATON	2411 CA ASP	250	60.287	30.739	69.606	1.00 46.90	AAAA C
HOTA	2412 CB ASP	250	61.740	30.726	70.154	1.00 53.11	AAAA C
ATOL	2413 CG ASP	250	62.421	32.122	70.081	1.00 71.49	аааа с
HOTA	2414 OD1 ASP	250	63.124	32.682	69.176	1.00 58.53	AAAA O
ATOI1	2415 OD2 ASP	250	62.272	32.928	71.071	1.00 70.30	aaaa o
HOTA	2416 C ASP	250	59.881	29.536	68.771	1.00 41.22	AAAA C
ATOH	2417 O ASP	250	60.291	29.443	67.616	1.00 39.06	AAAA O
ATOI1	2418 N PHE	251	59.116	28.609	69.299	1.00 36.13	AAAA N
ATOH	2420 CA PHE	251	58.457	27.601	68.489	1.00 34.88	AAAA C
ATOH	2421 CB PHE	251	57.468	26.746	69.256	1.00 29.82	AAAA C
ATO!!	2422 CG PHE	251	56.701	25.801	68.385	1.00 41.50	AAAA C
					68.263	1.00 30.66	AAAA C
ATOH	2423 CD1 PHE	251	57.101	24.479			
ATOH	2424 GD2 PHE	251	55.559	26.213	67.686	1.00 37.78	AAAA C
ATOH	2425 CEL PHE	251	56.414	23.597	67.424	1.00 29.30	AAAA C
ATOH	2426 CEC PHE	251	54.847	25.372	66.856	1.00 36.09	AAAA C
ATOU	0407 00 PHE	251	55.294	24.070	66.715	1.00 36.21	AAAA C
ATC! i	2429 C PHE	251	57.624	28.090	67.338	1.00 39.28	AAAA C
ATO!!	2429 O PHE	251	57.911	28.010	55.144	1.00 30.27	AAAA O
ATOH	2430 H CYS	252	56.734	29.225	67.713	1.00 35.13	BAAA N
ATOH	2432 CA CYS	252	55.895	29.870	66.728	1.00 38.90	AAAA C
ATOH	2433 C CYS	252	56.827	30.599	65.747	1.00 44.73	AAAA C
ATOLL	2434 O CYS	252	56.552	30.534	64.536	1.00 43.20	AAAA O
	2435 CB CYS	252	54.903	30.778	67.379	1.00 35.65	AAAA C
ATON						1.00 39.03	AAAA S
ATOH	2436 SG CYS	252	53.562	31.544	66.459		AAAA N
INTA	2437 N ALA	253	57.872	31.256	66.285	1.00 41.53	
ATOH	2439 CA ALA	253	58.667	32.071	65.415	1.00 40.39	AAAA C
ATQ! I	2440 CB ALA	253	59.529	33.098	55.172	1.00 36.07	AAAA C
ATOH	2441 C ALA	253	59.551	31.167	64.539	1.00 42.89	AAAA C
ATOH	2442 O ALA	253	60.147	31.735	63.640	1.00 47.42	AAAA O
ATCH	2443 H ASH	254	59.657	29.859	64.700	1.00 38.75	II AAAA
ATCH	2445 CA ASH	254	60.546	29.073	63.928	1.00 42.94	AAAA C
ATOH	2446 CB ASH	254	61.667	28.497	64.847	1.00 48.09	AAAA C
INTA	2447 CG ASN	254	62.696	29.635	65.031	1.00 49.54	AAAA C
HOTA	2449 OD1 ASH	254	63.468	29.940		1.00 61.38	AAAA O
ATOH	2449 HD2 ASH	254	62.607	30.321	66.144	1.00 48.38	aaaa n
ATOH	2452 C ASN	254	59.907	27.959	63.135	1.00 53.72	AAAA C
ATO!1	2453 O ASN	254	60.552	26.965	62.804	1.00 51.19	AAAA O
ATOH	2454 N ILE	255	58.612	28.136	62.766	1.00 57.77	AAAA N
ATOH	2456 CA ILE	255	57.828	27.107	62.134	1.00 53.29	AAAA C
		255	56.329		62.304	1.00 50.41	AAAA C
ATOH	2457 CB ILE			27.322		1.00 50.41	AAAA C
ATOH	2458 CG2 ILE	255	55.477	26.595	61.246		
ATOH	2459 CG1 ILE	255	55.778	26.675	63.553	1.00 40.59	AAAA C
ATOH	2460 CD1 ILE	255	54.479	27.317	64.006	1.00 38.97	AAAA C
INTA	2461 C ILE	255	58.127	26.886	60.651	1.00 52.62	AAAA C
HOTA	2462 O ILE	255	58.196	25.709	60.252	1.00 53.96	aaaa o
ATOH	2463 II LEU	256	58.290	27.960	59.918	1.00 49.96	AAAA N
HOTA	2465 CA LEU	256	58.680	27.764	58.516	1.00 63.69	AAAA C
ATOI1	2466 CB LEU	256	58.175	29.012	57.799	1.00 56.80	AAAA C
ATOH	2467 CG LEU	256	56.671	29.196	57.864	1.00 59.11	AAAA C
ATOH	2468 CD1 LEU	256	56.310	30.654	57.645	1.00 43.31	AAAA C
HOTA	2469 CD2 LEU	256	55.965	28.222	56.928	1.00 55.88	AAAA C
ATOH	2470 C LEU	256	60.193	27.622	58.355	1.00 66.23	AAAA C
ATOH	2471 O LEU	256	60.691	27.511	57.245	1.00 70.29	AAAA O
ATON	2472 N SER	257	60.942	27.559	59.430	1.00 64.61	AAAA N
		257	62.352	27.529	59.534	1.00 69.23	AAAA C
ATOH							AAAA C
ATOH	2475 CB SER	257	62.924	27.318	60.955	1.00 62.45	
ATOH	2476 OG SER	257	63.381	25.980	61.074	1.00 56.18	AAAA O
ATOH	2478 C SER	257	62.973	26.497	58.610	1.00 70.77	AAAA C
ATOH	2479 O SER	257	64.127	26.731	58.246	1.00 72.50	AAAA O
HOTA	2480 N ALA	258	62.322	25.389	58.320	1.00 74.61	AAAA N
ATOH	2482 CA ALA	258	62.933	24.498	57.343	1.00 76.34	AAAA C
ATOI1	2483 CB ALA	258	62.570	23.039	57.584	1.00 80.82	AAAA C
ATOH	2484 C ALA	258	62.663	24.964	55.921	1.00 78.21	AAAA C

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ATMI	2495		ALA		62.880				aaaa o
ATOH	2466		SLU		62.069				aaaa ii
ATO!!	2499	ÇA			61.742	26.621			AAAA C
ATOH	5160				60.226				AAAA C
ICTA	2490				59.687	25.049			AAAA C
ATOH	2491	CD	GLU 1 GLU		58.364	25.032			AAAA C
ATOL	2490			259	58.000	24.088		· ·	AAAA O
ATOH	2493	30	GLU GLU	25 <u>9</u>	57.598	26.002			AAAA O
ATOH	2494	c	GLU	259	62.117	28.078			AAAA C
ATOH	2495	0		259	62.059	29.009			AAAA O
ATOL	5466	CA 11	SER SER	260	62.298	28.338			H AAAA
ATOH	2499 2499	CB CA		260 260	62.725	29.625		1.00 84.03	AAAA C
	2500	03		260	63.753 63.306	29.269		- · · · · · · - ·	AAAA C
ATO!!	2500	C.	SER	260		29.419 30.466		1.00 93.65	AAAA O
ATOH	2503	õ	SER	260	61.558			1.00 80.84	AAAA C
I TOTA	2504	11	SER	261	61.496 60.617	30.889		1.00 81.31	AAAA O
ATOH	2506	CA	SER	261	59.423	30.785 31.540		1.00 78.56	AAAA II
ATOI	2507	CB	SER	261	58.179	31.297	52.308 53.170	1.00 72.13	AAAA C
ATOH	2508	OG	SER	261	57.436	30.334	52.451	1.00 74.74	AAAA C
ATOH	2510	ç	SER	261	59.683	33.032	52.318	1.00 66.90	AAAA C
ATOLI	2511	ō	SER	261	60.049	33.588	53.334	1.00 63.24	AAAA O
ATOH	2512	ŭ	ASF	262	59.364	33.659	51.204	1.00 65.30	II AAAA
ATOH	2514	ÇA	ASP	262	59.358	35.071	50.915	1.00 58.55	AAAA C
ATOH	2515	CB	ASP	262	59.268	35.285	49.400	1.00 64.85	AAAA C
ATOH	2516	CG	ASP	262	59.389	36.713	48.931	1.00 76.42	AAAA C
ATO:	2517		LASP	252	59.473	37.708	49.701	1.00 79.81	AAAA O
ATOH	2518		2 ASP	262	59.404	36.873	47.671	1.00 80.46	AAAA O
HOTA	2519	C	ASP	262	58.121	35.706	51.529	1.00 56.88	AAAA C
HOTA	2520	0	ASP	262	57.851	36.918	51.510	1.00 52.48	AAAA O
ATCH	2521	11	SER	263	57.259	34.849	52.118	1.00 53.43	AAAA N
HOTA	2523	C.A.	SER	263	56.047	35.352	52.734	1.00 52.84	AAAA C
112TA	2524	CB	SER	263	55.020	34.245	52.885	1.00 46.60	AAAA C
ATOH	2525	03	SER	263	55.149	33.348	51.791	1.00 66.80	AAAA O
ATCH	2527	Э·	SER	263	56.310	35.965	54.117	1.00 49.52	AAAA C
ATCH	2529	0	SER	263	57.396	35.737	54.709	1.00 42.33	AAAA O
ATON	2529	::	GLU	264	55.320	36.783	54.540	1.00 38.93	AAAA H
ATSI:	2831	CA	GLU	264	55.362	37.002	55.921	1.00 36.70	AAAA C
AT SE	2532	23	GLU	264	54.359	39.337	56.208	1.00 43.71	AAAA C
ATO:	3533	03	GEU	264	54.575	39.482	55.219	1.90 37.74	AAAA C
ATC:	2534	92	GLU	254	55.374	40.632	55.793	1.00 34.36	AAAA C
ATCH:	2535		GLU	364	55.493	40.600	57.034	1.00 41.55	AAAA C
ATCH	2536	೦೭೨		364	55.832	41.576	55.146	1.00 39.60	O EAAA
ATO:	3537	3	GLU	264	55.099	36.056	56.827	1.00 35.84	AAAA C
ATCH!	2539	<u>.</u>	GLU	254	54.369	35.151	56.355	1.00 39.60	AAAA O
ATC::	2539	::	GLY	265	55.801	35.938	57.962	1.00 35.64	AAAA H
ATOH:	2541	ÇĀ	GLY	265	55.671	34.690	59.727	1.00 40.30	AAAA C
ATO:	2542	:	GLY	265	54.622	34.716	59.829	1.00 39.51	AAAA C
ATOL: ATOL:	2843 2844	;: ::	GLY PHE	265 266	53.951	35.699	60.135	1.00 37.20	AAAA C
ATOH:	2546	CA	PHE	266	54.537 53.637	33.569	60.516	1.00 35.75	AAAA ::
ATON	25:7		PHE	266	53.924	33.434 32.155	61.625	1.00 33.70	AAAA C
ATOH	2548	-3	FHE	266	53.356	30.958	62.386 61.671	1.00 28.20 1.00 37.07	AAAA C
ATOH!	2549	CD1		266	53.760	30.518		1.00 37.07	AAAA C AAAA C
ATOH	2550		PHE	266	52.383	30.185	62.313	1.00 25.65	AAAA C
ATCI:	2551		PHE	266	53.225	29.506	59.760	1.00 23.03	AAAA C
HOTA	2552		PHE	266	51.879	29.094	61.672	1.00 24.63	AAAA C
HOTA	2553	CZ	PHE	266	52.260	29.708	60.402	1.00 23.58	AAAA C
HOTA	2554	C	PHE	266	53.571	34.570	62.608	1.00 35.82	AAAA C
ATON	2555	0	PHE	266	54.446	35.372	62.879	1.00 39.23	AAAA O
HOTA	255€	11	VAL	267	52.360	34.763	63.161	1.00 37.10	II FAAA
ATOH	2558	CA	VAL	267	52.118	35.812	64.113	1.00 36.09	AAAA C
HOTA	2559	CB	VAL	267	51.315	36.974	63.567	1.00 39.01	AAAA C
ATOH	2560		VYL	267	51.626	37.601	62.230	1.00 31.10	AAAA C
ATOH	2561		VAL	267	49.890	36.400	63.570	1.00 36.88	AAAA C
ATOH	2562	C	VAL	267	51.506	35.260	65.400	1.00 33.55	AAAA C
ATOH	2563	0	VAL	267	51.202	34.098	65.515	1.00 32.41	AAAA O
ATOH	2564	11	ILE	268	51.539	36.988	66.477	1.00 35.88	N FARA
ATOH	2566	CA	ILE	268	50.867	35.573	67.691	1.00 39.79	AAAA C
ATOH	2567	CB	ILE	268	51.791	35.232	68.849	1.00 31.17	aaaa c
ATOI1	2568		ILE	268	50.922	35.253	70.150	1.00 -32.66	AAAA C
HOTA	2569		ILE	268	52.403	33.966	68.724	1.00 23.56	AAAA C
ATOH	2570		ILE	268	53.421	33.546	69.806	1.00 25.93	AAAA C
ATOH	2571 2572	C	ILE	268	49.806	36.608	69.060	1.00 42.44	AAAA C
ATCH ATCH	2573	0	ILE HIS	268	50.116	37.767	68.327	1.00 39.99	AAAA O
ATOH	2575	II CA	HIS	269 269	48.528	36.292	67.864	1.00 44.26	AAAA N
ATON	2576	CB	HIS	269	47.491 46.885	37.320	68.173	1.00 44.29	AAAA C
ATOH	2577	CG	HIS	269		37.876	66.901	1.00 45.48	AAAA C
ATOH	2578	CD2		269	45.915 44.551	39.986 39.014	67.079	1.00 54.33	AAAA C
ATOH	2579	NDI		269	46.356	40.280	67.096 67.307	1.00 46.61 1.00 51.86	AAAA C
HOTA	2581	CEI		269	45.282	41.057	67.437	1.00 55.17	АААА Н АААА С
ATOH	2582	HE2		269	44.175	40.324	67.309	1.00 46.97	K AAAA :
ATOH	2584	C	HIS	269		36.740	69.074	1.00 45.54	AAAA C
ATOH	2585	ō	HIS	269		35.552	69.027	1.00 42.94	AAAA O
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ATOT	2580		AGE	275	45.95	37.504	5 70.05%	9 1.00 40.80	AAAA II
ATOL	2585	CA	AGE	270	44.946	37.025	31.000	1.00 48.03	AAAA C
HOTA	2589	CB	ASP	270	43.57	37.01	70.336	3 1.00 63.63	AAAA C
ATOH	2590	03	ASP	270	42.919	38.39	70.294	1.00 80.82	AAAA C
LICTA	2591	OD	1 ASF	270	41.737				AAAA O
ATOH	2592	: OD	2 ASP	270	43.407				AAAA O
ATOH	2593		ASP		45.226				AAAA C
ATOH	2594		ASF		44.357				AAAA O
ATOH	2595		GLY		46.477				AAAA N
ATOL	2507				46.839				
			GLY						AAAA C
ATOH	2598			271	46.818				AAAA C
ATO!!	2599		GLi	271	46.775				AAAA O
INTA	2600		GLU	272	47.015				AAAA 11
ATOH	2602			272	47.108		69.371		AAAA C
ATOH	2603		GLU	272	45.752	31.737	68.876	1.00 37.58	аааа с
ATOH	2694			272	45.778	30.600	67.839	1.00 45.30	AAAA C
ATOH	2605	CD	GLU	272	44.413	30.528	67.149	1.00 36.92	AAAA C
ATOH	2606	OE.	1 GLU	272	43.545	31.345	67.533	1.00 48.41	AAAA O
INTA	2607	OE.	2 GLU	272	44.223	29.696	66.286	1.00 44.10	AAAA O
HOTA	2608	C	GLU	272	48.211	32.324	68.335	1.00 40.32	AAAA C
ATOH:	2609	C	GLU	272	48.445	33.447			AAAA O
HOTA	2610	11	CYS	273	48.942				AAAA 11
ATOH	2612	CA	CYS	273	50.046				AAAA C
ATOH	2613	C	CYS	273	49.321				AAAA C
ATO!!	2514	ō	CYS	273	48.713				AAAA O
ATOH	2615	Œ8	CYS	273	51.098				AAAA C
HOTA	2616	3:3	CYS	273					
	2617			274	52.337				AAAA S
ATOH		11	TEI		49.373				AAAA N
HOTA	2619	CA	HET	274	48.586		63.720	1.00 36.68	AAAA C
ATOH	2620	CB	HET	274	47.136		63.847	1.00 29.11	AAAA C
ATOIL	2621	CG	! IET	274	46.923		63.691	1.00 36.51	AAAA C
ATO!!	2532	SD	HET	274	45.477	33.921	64.677	1.00 40.00	AAAA S
ATOI!	2623	Œ	HET	274	45.659	35.658	64.754	1.00 22.47	AAAA C
ATO!!	2624	c	!:ET	274	49.426	31.900	62.608	1.00 39.35	AAAA C
ATC!:	2628	ラ	HET	274	50.167	32.880	62.673	1.00 41.00	O AAAA
ATC!!	2626	::	GLH	275	49.378	31.353	61.428	1.00 42.55	AAAA II
ATCH	262	ca.	31:1	275	50.041	31.934	60.232	1.00 37.69	AAAA C
ATCH	2609	73	311	275	49.519	30.765	59.242	1.00 34.01	AAAA C
ATO::	2637	73	31::	275	49.329	31.274	57.864	1.00 56.40	AAAA C
ATOM:	2831	35	31!	275	49.275	30.190	56.812	1.00 65.46	AAAA C
ATCH:	2632	321	32:1	275	49.941	29.151	56.910	1.00 67.24	AAAA O
ATO:	2433	::53	311	275	48.451	30.436	55.799	1.00 78.29	AAAA II
ATOI:	2636	-	35:1	275	49.721				
ATC!:	263	-	31.1	275		33.195	59.720	1.00 35.41	AAAA C
				276	50.526	33.831	59.064	1.00 35.95	O AAAA
ATO:	2638	::	GLU		49.566	33.754	60.056	1.00 41.70	AAAA H
ATO:	2640	TA.	317	276	48.222	35.080	59.571	1.00 43.96	AAAA C
ATO!	2641	23	GLV	276	47.387	34.884	58.245	1.00 42.40	AAAA C
ATO::	2642	73	320	276	47.154	36.269	57.650	1.00 53.94	C AAAA
ATON:	2643	??	GLU	276	48.359	37.198	57.460	1.00 61.37	AAAA C
ATON	2544	OE1	3LU	275	49.356	36.595	56.943	1.00 67.32	AAAA O
ATOH	264€	CE2		276	48.242	39.411	57.811	1.00 45.10	AAAA O
ATO(:	2646	=	311	276	47.444	35.935	60.540	1.00 39.74	AAAA C
ATON	2647	Ç	3 LU	276	46.760	35.449	61.444	1.00 45.96	AAAA O
ATOH	3946	::	TYS	277	47.495	37.235	60.500		II AAAA
ATON	2650	CA	C: S	277	46.718	39.089	61.332	1.00 46.11	aaaa c
ATOH	2651	C	TTS	277	45.205	37.938	60.994	1.00 52.70	AAAA C
HOTA	2652	C	CYS	277	44.760	37.511	59.936	1.00 49.43	AAAA O
ATOH	2653	CB	CYS	277	47.039	39.537	61.111	1.00 45.56	AAAA C
ATOH	2654	S:3	CYS	277	48.629	40.083	61.645	1.00 52.86	AAAA S
ATOH	2655	1:	PRO	278	44.380	38.261	61.993	1.00 54.63	AAAA 11
HOTA	2656	CD	PRO	278	44.824	38.778	63.311	1.00 57.20	AAAA C
ATC:1	2657	CA	280	278	42.946	38.185	61.899	1.00 55.82	AAAA C
HOTA	2658	CB	PRO	278	42.445	38.635	63.267	1.00 55.61	AAAA C
ATOH	2659	CG	PRO	278	43.605	38.670	64.153	1.00 55.58	AAAA C
ATOH	2660	C	FRO	278	42.487	39.116	60.781	1.00 52.55	AAAA C
HOTA	2661	e e	FRO	278	43.083	49.195	60.631	1.00 48.76	AAAA O
ATOH	2662	11	SER	279	41.370	38.845	60.143	1.00 49.35	AAAA N
ATOH	2664	CA	SER	279	40.815	39.720	59.140		AAAA C
ATOI	2665	CB	SER	279	39.280	39.572	58.975	1.00 52.03 1.00 47.62	AAAA C
ATOH	2666	C/3	SER	279	39.320	39.778		1.00 47.62	AAAA O
ATOH	2669	03	SER	279			57.785		
ATOH	2669		SER	279	41.003	41.209	59.173	1.00 55.40	AAAA C
ATOH	2670	0	GLY	290	41.225	41.740	58.059	1.00 55.40	AAAA O
ATOH	2672	ti CA			40.775	41.962	60.247	1.00 55.32	AAAA N
			GLY	290	10.968	43.406	59.868	1.00 48.58	AAAA C
ATON	2673	Ç	GLT	290	42.248	43.990	60.479	1.00 55.98	AAAA C
ATOH	2674	0	GLY	280	42.249	45.097	60.772	1.00 56.00	AAAA O
ATOH	2675	11	PHE	281	43.213	42.983	60.742	1.00 55.42	AAAA N
ATOH	2677	CA	345	291	44.506	43.411	61.262	1.00 52.94	AAAA C
ATO:	2678	CB	PHE	281	44.938	42.644	62.523	1.00 61.20	AAAA C
ATOH	2679	CG	PHE	281	43.958	42.792	63.637	1.00 53.66	AAAA C
ATOH	2680	CDI		291	44.142	43.702	64.630	1.00 60.47	AAAA C
ATOH	2681	CD2		281	42.839	41.992	63.712	1.00 60.98	AAAA C
HOTA	2692	CEI		291	43.272	43.901	65.678	1.00 64.71	AAAA C
ATOH:	2683	CEC		281	41.931	42.162	64.756	1.00 63.18	AAAA C
ATOH	1681	93	PHE	281	42.141	43.115	65.744	1.00 58.88	AAAA C

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ATM	2685	G BHE	291	45.530	43.217	60.240	1.00 48.00	AAAA C
ATOH		O PHE	281	45.738	42.395			AAAA O
ATCH		n ife	282	46.570	43.990		1.00 49.55	II AAAA II
ATOH	2689	CA ILE	282	47.907	43.984	59.748	1.00 45.00	AAAA C
ATOH	_	CB ILE	282	47.945	45.198	58.799	1.00 30.25	AAAA C
ATOH	_	CG2 ILE	282	48.041	16.494	59.507	1.00 24.60	AAAA C
ATOH	2692	CG1 ILE	282	49.092	45.022	57.795	1.00 38.71	AAAA C
ATOH	2693	CD1 ILE	282	49.194	46.043	56.669	1.00 33.38	AAAA C
ATOH	5654	C ILE	282	49.081		- 60.673	1.00 44.30	AAAA C
ATOH	2695	O ILE	282	49.078	44.447	61.759	1.00 48.49	AAAA O
ATOH	2696	II ARG	283	50.126	43.153	60.298	1.00 48.68	H AAAA H
			283	51.396		61.048		
ATOH	_				43.094		1.00 39.30	AAAA C
IIOTA	2699	CP ARG	283	52.300	42.000	60.286	1.00 41.10	AAAA C
ATOH	2700	CG ARG	283	52.295	40.696	60.515	1.00 29.19	AAAA C
	_	CD ARG	283	53.078	39.996	59.451	1.00 29.85	AAAA C
INTA								
ATOH	2702	HE ARG	283	52.823	38.545	59.404	1.00 29.39	aaaa n
INTA	2704	CE ARG	283	51.862	38.024	50.646	1.00 37.61	AAAA C
HOTA		HH1 ARG	283	51.065	38.846	57.944	1.00 31.41	AAAA N
ATOH	-	NH2 ARG	283	51.651	36.722	58.596	1.00 31.97	n aaaa
HOTA	2711	Ç ARG	283	51.945	44.498	61.190	1.00 42.27	AAAA C
HOTA	2712	O ARG	283	51.931	45.228	60.173	1.00 43.42	AAAA O
ATOH			284	52.362	44.686	62.422	1.00 39.49	AAAA 11
ATOH	2715	ca asii	284	52.733	46.311	62.574	1.00 42.07	AAAA C
ATOH	2721	C ASII	284	54.078	46.656	61.929	1.00 41.64	AAAA C
ATCH		O ASII	284	54.431	47.798	61.742	1.00 39.01	AAAA O
ATOH		CB ASII	284	52.734	46.760	64.032	1.00 37.33	AAAA C
ATOH	2717 (TS ASH	284	53.917	46.028	64.611	1.00 50.21	AAAA C
ATCH	2719	MEA IGC	284	54.609	45.104	64.192	1.00 44.30	AAAA O
ATOH		ID2 ASH	284	54.323	46.432	65.842	1.00 42.46	аааа н
HOTA	2723	I GLY	285	54.931	45.699	61.562	1.00 40.10	N AAAA
HOTA	2725	CA GLY	285	55.971	45.815	60.593	1.00 26.91	AAAA C
			285					
ATOH				56.091	44.468	59.848	1.00 33.12	AAAA C
HOTA	2727 (O GLY	285	55.584	43.331	60.187	1.00 29.51	AAAA O
ATOH	2728 1	J SER	286	56.915	44.619	59.766	1.90 26.53	H AAAA
ATOH		CA SER	286	57.109	43.395	57.975	1.00 32.67	AAAA C
ATOH		CO SER	296	57.944	43.681	56.757	1.00 33.19	AAAA C
ATC!!	2732 (DG SËR	296	58.283	42.490	5€.014	1.00 31.95	O AAAA
ATOH	2734 0	SER S	286	\$7.750	42.310	58.836.	1.00 34.57	AAAA C
			286	58.700		59.607	1.00 44.29	
ATO:	- 35				42.495			O AAAA
ATO:		: 3Li;	297	57.227	41.149	58.940	1.00 34.45	n aaaa
ATO!!	2739 3	IA GLN	297	57.738	40.005	59.634	1.00 35.25	AAAA C
ATO:		:2 31H	297	59.139	39.610	59.083	1.00 27.97	AAAA C
ATOH		og GLN	287	59.037	39.234	57.664	1.00 26.61	AAAA C
ATOH	2749 0 2741 0	io gun	287	58.539	37.963	57.130	1.00 21.25	AAAA C
: ICTA		NEI GLN	297	58.192	37.023	57.845	1.00 28.18	AAAA O
		IEC GLII	287		37.838	55.782	1.00 27.55	
ATO:				58.492				II AAAA II
ATO!!	2746 0	31.1	297	57.773	40.298	51.111	1.00 30.25	AAAA C
ATOH	2747 () GLN	297	58.163	39.415	€1.908	1.00 32.78	aaaa o
ICTA	2748 (298	57.021	41.217	61.624	1.00 32.49	AAAA H
	2.43							
ATQ!:		TA JER	288	<u>.</u> 56.696	41.322	63.043	1.00 28.98	AAAA C
ATO!!	2751 0	e ser	288	56.024	42.675	63.313	1.00 35.79	AAAA C
ATON	2782 0	G SER	288	55.639	42.512	64.701	1.00 36.61	AAAA O
	2754 0		298		40.285		1.00 29.96	AAAA C
ATOI:				55.665		63.442		
ATOH	2755 0) SER	288	54.993	39.776	62.553	1.00 31.16	AAAA O
ATOH	2756 1	I HET	289	55.774	39.720	64.621	1.00 32.51	II AAAA II
ATOH	2759 C	A MET	289	54.875	38.697	65.105	1.00 34.53	AAAA C
				57.073				
HOTA		B HET	289	55.507	37.823	66.153	1.00 30.31	AAAA C
ATOH	2760 C	G MET	289	56.571	36.872	65.680	1.00 40.50	AAAA C
ATOH	2761 S	D HET	289	56.977	35.623	66.881	1.00 31.65	AAAA S
HOTA		E MET	289	55.745	34.315	66.508	1.00 30.47	AAAA C
			289				-	
HOTA	2763 C			53.557	39.286	65.703	1.00 35.55	AAAA C
ATOH	2764 C		289	52.630	38.512	66.014	1.00 38.37	AAAA O
HCTA	2765 I	TYR	290	53.380	40.565	65.742	1.00 29.54	II AAAA II
ATOH		A TYR	290	52.363	41.358	66.297	1.00 38.81	AAAA C
ATOH			290		42.589		1.00 36.72	
				52.947		67.042		AAAA C
ATOH		G TYR	290	53.570	42.184	68.351	1.00 41.94	AAAA C
HOTA	2770 C	D1 TYR	290	54.932	41.780	68.350	1.00 37.79	AAAA C
ATOH		E1 TYR	290	55.548	41.369	69.503	1.00 32.60	AAAA C
ATOH		D2 TYR	290	52.887	42.157	69.570	1.00 39.93	AAAA C
ATOH:	2773 C	E2 TYR	290	53.501	41.750	70.748	1.00 36.16	AAAA C
ATOH	2774 C		290	54.822	41.355	70.693	1.00 38.85	AAAA C
	2775 0		290	55.581				AAAA O
ATOH					40.923	71.751	1.00 43.41	
ATOH	2777 @		290	51.361	41.955	65.270	1.00 45.54	AAAA C
HOTA	2778 0	TYR	290	51.733	42.520	64.227	1.00 47.10	AAAA O
ATOH	2779 !!		291	50.971	41.699	65.537	1.00 44.68	II AAAA
ATOH	2781 @		291	49.017	42.205	64.695	1.00 47.20	AAAA C
HOTA	2782 C	CYS	291	48.295	43.434	65.194	1.00 46.06	AAAA C
ATOH	2783 0		291	47.892	43.550	66.343	1.00 49.45	AAAA O
ATOH	2784 C		291	47.973	41.103	64.483	1.00 43.44	AAAA C
ATOH:	2785 S	G CYS	291	48.766	39.715	63.683	1.00 45.49	AAAA S
ATOH	2786 11		292	48.136	44.453	64.365	1.00 46.82	AAAA N
			292					
ATOH	2788 C			47.399	45.651	64.755	1.00 50.64	AAAA C
TOTA	2789 C		292	48.267	46.932	64.779	1.00 39.19	AAAA C
ATOH	2790 0	G2 ILE	292	49.291	46.885	65.861	1.00 44.39	AAAA C
ATOH		G1 ILE	292	48.920	47.095	63.402	1.00 44.25	AAAA C
ALC:	7.81 O			40.529	41.055	03.402	1.00 44.23	7000A C

ATOM	3.11 107 C975	292	49.234 49.56	8 63.108	1.00 32.80	AAAA C	
ATUL		292	46.240 46.00		1.00 50.01	AAAA C	
ATOH		292	46.165 45.52		1.00 46.64	AAAA O	
ATOH		293	45.150 46.50		1.00 51.86	и аааа	•
ATOH	2796 CD PRO	293	45.009 46.80	4 65.839	1.00 51.05	AAAA C	
ATOH	2797 CA PRO	293	43.958 46.93	0 63.675	1.00 51.40	AAAA C	
ATOH		293	43.170 47.78	4 64.681	1.00 49.00	AAAA C	
ATOH		293	43.533 47.11		1.00 53.73	AAAA C	
ATOH		293	44.253 47.87		1.00 51.68	AAAA C	
ATOH		293	45.953 48.78		1.00 51.92	AAAA O	
IOTA .	2802 H CYS	294	43.607 47.62	1 61.408	1.00 50.66	и аааа	
HOTA	2804 CA CYS	294	43.811 48.46	4 60.254	1.00 57.90	AAAA C	
ATOIL		294	43.219 49.84		1.00 59.59	AAAA C	
		294	43.744 50.81			AAAA O	
ATOH					1.00 60.87		
ATOH		294	43.229 47.68		1.00 57.59	AAAA C	
ATOH	2808 SG CYS	294	44.408 46.46	0 58.563	1.00 51.12	AAAA S	
ATOH	2809 II ALA	295	42.009 50.03	1 60.854	1.00 65.87	H AAAA	
ATOH		295	41.391 51.38		1.00 71.19	AAAA C	
ATOH		295	42.311 52.45		1.00 63.82	AAAA C	
HOTA		295	40.971 51.770		1.00 69.17	AAAA C	
ATOH		295	41.421 52.71		1.00 64.70	aaaa o	
ATOH	2815 N GLY	296	40.153 50.926	58.775	1.00 71.30	aaaa n	
HOTA	2817 CA GLY	296	39.640 51.049	9 57.416	1.00 72.66	AAAA C	
ATOH	2818 C GLY	296	39.895 49.686		1.00 74.20	AAAA C	
ATOH!	2819 O GLY	296	40.408 48.819		1.00 75.04	AAAA O	
ATOH	2820 II FRO	297	39.561 49.540		1.00 71.88	AAAA N	
ATOH	2821 CD PRO	297	38.928 50.561	54.637	1.00 72.15	AAAA C	
HOTA	2822 CA PRO	297	39.958 48.344	54.777	1.00 68.23	AAAA C	
ATOI-I	2823 CB PRO	2 9 7	39.488 48.603	53.369	1.00 72.57	AAAA C	
ATOH	2824 CG PRO	297	38.470 49.687		1.00 74.04	AAAA C	
ATO!	2825 C PRO	297	41.480 48.306		1.00 65.78	AAAA C	
ATOH	2826 O PRO	297	42.147 49.323		1.00 62.72	AAAA O	
HOTA	2827 H CYS	298	42.039 47.135	55.073	1.00 63.85	AAAA N	
ATOH	2829 CA CYS	298	43.464 46.953	55.248	1.00 54.47	AAAA C	
ATOI!	2830 C CYS	298	44.109 47.303		1.90 54.56	AAAA C	
	_	298					
ATCH			43.621 47.030		1.00 54.83	AAAA O	
ATOU	1630 OB CAR	298	43.665 45.544		1.00 47.65	AAAA C	
ATOH	2933 SG CYS	299	43.501 45.115		1.00 46.12	aaaa s	
ATON	2934 N FRO	299	45.310 47.976	53.967	1.00 49.83	AAAA N	
ATC!:	1835 TD FRO	299	46.087 48.168		1.00 48.14	AAAA C	
ATOH:	2836 CA FRO	299	46.055 48.212		1.00 43.67	AAAA C	
ATOH	2837 CB FRO	299	47.267 49.965		1.00 44.08	AAAA C	
ATOH	2838 GG FRO	299	47.454 49.361		1.00 51.38	AAAA C	
HOTA	2939 C PRO	299	46.341 46.969	52.010	1.00 38.96	AAAA C	
ATON	1940 O PRO	299	46.372 48.874	52.546	1.00 42.85	AAAA O	
HOTA	2841 N LYS	300	46.310 47.073		1.00 38.30	AAAA II	
ATOH	2843 TA LYS	300	45.484 45.953		1.00 42.62	AAAA C	
ATOLL	0944 GB LYS	300	45.176 45.226		1.00 34.28	AAAA C	
ATOH	2845 OG LYS	300	45.346 43.901	49.920	1.00 41.45	AAAA C	
ATOH	2846 DD LYS	300	44.013 43.413	48.378	1.00 49.31	AAAA C	
ATOH	2847 CE LYS	300	44.388 42.027	47.787	1.00 48.57	AAAA C	
ATOH	2848 NG LYS	300	43.662 42.031	46.478	1.00 63.70	AAAA II	
ATOH	2852 C LYS	300	46.964 46.479		1.00 48.72	AAAA C	
ATOH	2853 O LYS	300	46.413 47.393		1.00 46.09	AAAA O	
ATOI I	2854 H VAL	301	48.150 45.984	48.054	1.00 48.15	AAAA II	
ATOH:	2856 CA VAL	301	48.802 46.462	46.871	1.00 44.52	AAAA C	
I-fota	2857 CB VAL	301	50.292 46.729	47.074	1.00 51.52	AAAA C	
ATOH	2858 CG1 VAL	301	51.008 47.200		1.00 43.07	AAAA C	
IOTA	2859 CG2 VAL	301	50.495 47.794	48.141	1.00 49.50	AAAA C	
ATON:	2860 C VAL	301	48.526 45.410		1.00 44.59	AAAA C	
ATO! I	2861 O VAL	301	48.913 44.291	46.060	1.00 43.70	C FAAA	
ATO!!	2862 H CYS	302	47.910 45.816	44.718	1.00 47.99	II AAAA	
HOTA	2864 CA CYS	302	47.645 44.735	43.739	1.00 55.19	AAAA C	
HOTA	2865 C CYS	302	48.594 44.968	42.583	1.00 57.64	AAAA C	
ATOH	2866 O CYS	302			1.00 60.23		
				42.343		AAAA O	
HOTA	2867 CB CYS	302	46.186 44.630	43.330	1.00 68.30	AAAA C	
ATOH	2868 SG CYS	302	45.070 41.360	44.751	1.00 70.31	AAAA S	
HOTA	2869 II GLU	303	49.183 43.921	12.075	1.00 58.15	II AAAA	
ATOH	2871 CA GLU	303	50.174 43.932		1.00 62.85	AAAA C	
ATOH	2872 CB GLU	303	51.603 44.006	41.595	1.00 67.85	AAAA C	
		303					
ATOH	2873 CG GLU		51.760 43.487	43.014	0.01 67.46	AAAA C	
ATOH	2874 CD GLU	303	51.989 41.992		0.01 67.94	AAAA C	
ATOH	2875 OE1 GLU	303	53.011 41.514	42.561	0.01 67.67	AAAA O	
HOTA	2876 OE2 GLU	303	51.147 41.290	43.697	0.01 67.65	AAAA O	
ATOH	2877 C GLU	303	50.096 42.662		1.00 64.12	AAAA C	•
ATOH	2878 O GLU	303			1.00 65.08	AAAA O	
HOTA	2879 N GLU	304	49.867 42.794		1.00 67.37	AAAA II	
ATON	2881 CA GLU	304	49.672 41.583	38.094	1.00 74.63	AAAA C	
ATOH	2882 CB GLU	304	48.285 41.596	37.458	1.00 71.71	AAAA C	
I-IOTA	2883 CG GLU	304	47.339 42.663		1.00 84.54	AAAA C	
HOTA	2884 CD GLU	304	45.930 42.152		1.00 87.56	AAAA C	
HOTA	2885 OE1 GLU	304	45.438 41.571		1.00 89.13	AAAA O	
IOTA	2886 OE2 GLU	304	45.249 42.269		1.00 93.19	C KAAA	
ATOH	2887 C GLU	304	50.866 41.307	37.190	1.00 76.10	AAAA c	
HOTA	2888 O GLU	304	51.911 41.962		1.00 74.78	AAAA O	

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* ***	2806				50.00				
ATH		!!	SLU		50.89				II AAAA II
ATOH	2891	ÇΛ	らしい		51.93				AAAA C
ATOH	2892	CB	GLU		51.46	7 38.389	34.970	1.00 79.95	AAAA C
ATOH	2893	C:3	っことしり	305	52.30	37.937	33.807	1.00 87.28	AAAA C
ATOH	2894	CD	GLU	305	51.758	36.091			AAAA C
ATOH	2895		GLU	305	50.763				AAAA O
ATOH	2896		GLU	305	52.310				
									AAAA O
ATOH	2897	C	GLU	305	52.276			1.00 75.97	AAAA C
ATOH	2668	0	GLU	305	53.383	41.268	34.613	1.00 76.54	AAAA O
ATOH	2899	11	LTS	306	51.291	41.181	33.888	1.00 78.22	II AAAA II
ATCH	2901	CA	LYS	306	51.479				AAAA C
ATOH	2900	CB	LTS	306	50.467				
			LTS	306					AAAA C
ATOH	5903	C:3			51.208				AAAA C
ATOU	2904	ĊБ	LYS	306	50.313			1.00 92.78	AAAA C
ATCH	2905	CE	LYS	306	50.740	43.227	28.261	1.00 97.10	AAAA C
ATOH	2906	HS	LïS	306	50.938	44.554	28.929	1.00 84.87	H AAAA H
HOTA	2910	Ç	LYS	306	51.381				AAAA C
ATOH	2911	ō	LYS	306	50.703			1.00 76.08	AAAA O
ATOH	2912	ĬĬ.	LYS	307					
					52.000				N AAAA
ATOH	2914	CA	LYS	307	51.934			1.00 69.45	AAAA C
ATOH	2915	CB	LYS	307	53.022	46.903	33.008	1.00 79.64	AAAA C
ATOH:	2916	CG	LYS	307	54.419	46.837	33.564	1.00 78.88	AAAA C
ATOH	2917	CD	LYS	307	55.257	48.084		1.00 85.84	AAAA C
ATOH	2918	CE	LYS	307	55.708			1.00 97.07	AAAA C
HOTA	2919	112	LYS	307					
					54.649			1.00 97.80	N AAAA
ATOU	2923	Ç	LYS	307	50.562			1.00 67.97	AAAA C
ATOH	2924	O	LYS	307	50.010	47.369	34.431	1.00 64.46	AAAA O
IOTA	2925	11	THR	308	49.979	46.661	32.323	1.00 65.84	II AAAA II
ATO!	2927	CA	THR	308	48.709			1.00 64.56	AAAA C
HOTA	2928	CB	THR	308	48.714			1.00 59.91	AAAA C
ATOH:	2929		THR	308					
					49.834	48.843		1.00 61.97	AAAA O
ATOH	2931		THR	308	47.392	48.742		1.00 63.64	AAAA C
ATOR	2932	Ç	THR	308	47.514	45.379	32.234	1.00 61.82	AAAA C
ATOH	2933	C	THR	308	47.412	45.415	31.477	1.00 62.05	AAAA O
ATOH	2934	i i	173	309	46.675	46.719		1.00 55.66	H FAAA
ATO!	2936	CA	7.7.2	309	45.456	45.926		1.00 54.67	AAAA C
ATO:	2937	25	LYS LYS	309					
			LYS		45.043	45.880		1.00 55.82	AAAA C
ATOH	2939	23	_:3	309	43.601	45.541	35.223	1.00 57.50	AAAA C
ATO:	2939	22	LYS	309	43.390	44.039	35.086	1.00 59.50	AAAA C
AT OIL	2940	Œ	1:5	309	42.703	43.449	36.324	1.00 57.31	AAAA C
ATO!:	2941	::5	173	309	42.758	41.954	36.236	1.00 57.22	AAAA II
ATOH:	2945	-	175	309	44.391	46.570	32.549	1.00 51.21	AAAA C
ATOH	2946	5	LYS	309					
		::			44.074	47.763	32.680	1.00 47.23	O AAAA
ATO:	29:7		THR	310	43.895	45.772	31.610	1.00 47.67	II AAAA
ATOH	2949	CA	THR	310	42.862	46.329	30.733	1.00 51.89	AAAA C
ATOH:	2950	73	THR	310	43.161	46.015	29.266	1.00 54.81	AAAA C
ATM:	3951	0.31	THR	310	41.909	45.710	28.635	1.00 66.29	AAAA C
ATC:	2953	232	THR	310	44.032	44.791	29.139	1.00 55.18	AAAA C
ATON	1954	:	THR	310	41.468	45.941	31.117	1.00 51.15	
									AAAA C
ATO!!	2955	2	THR	310	41.162	44.590	30.991	1.00 49.27	AAAA O
	2956	::	ΞLΞ	311	40.684	46.706	31.732	1.00 50.18	AAAA X
	2958	ΞÄ	ILE	311	39.363	46.453	32.276	1.00 48.67	AAAA C
ATOH	2959	23	ILE	311	39.120	47.396	33.462	1.00 49.27	AAAA C
IKCTA	2960	7.52	ILE	311	37.655	47.596		1.00 50.72	AAAA C
	2951	CG1		311	39.896	45.930	34.699	1.00 41.34	AAAA C
	2962	CDI		311	39.847	49.073		1.00 52.22	AAAA C
							35.739		
	2963	Ċ	ILE	311	38.334	46.729	31.186	1.00 45.37	D KAAA
	2964	0	ILE	311	38.132	47.975	30.758	1.00 37.14	aaaa o
	2965	71	ASP	312	37.871	45.578	30.524	1.00 50.10	H AAAA H
ATOH	2967	CA	ASP	312	36.991	45.842	29.377	1.00 56.35	AAAA C
HOTA	2968	CB	ASP	312	37.546	45.152	28.128	1.00 59.45	AAAA C
ATOH .	2969	CG	ASP	312	37.761	43.671	28.382	1.00 65.64	AAAA C
	2970	ODI		312	38.525				
	2971	CD2				43.034	27.636	1.00 72.60	AAAA O
				312	37.154	43.175	29.349	1.00 66.86	C AAAA
	2972		ASP	312	35.589	45.337	29.693	1.00 59.39	AAAA C
	2973	O	ASP	312	34.729	45.007	28.867	1.00 61.00	C AAAA
ATOH :	2974	11	SER	313	35.278	45.290	30.976	1.00 61.17	AAAA ::
ATOH :	2976	CA	SER	313	34.053	44.683	31.459	1.90 55.73	AAAA C
ATOH :	2977		SER	313	34.121	43.201	31.083	1.00 48.22	AAAA C
			SER	313					
			SER		34.373	42.514	32.282	1.00 57.89	O AAAA
				313	33.998	44.918	32.941	1.00 57.87	AAAA C
			SER	313	34.802	45.506	33.537	1.00 66.47	AAAA C
			VAL	314	33.001	44.205	33.545	1.00 64.35	II AAAA II
ATOH 3	2984	CA	VAL	314	32.849	44.305	35.016	1.00 64.39	AAAA C
			VAL	314	31.360	44.340	35.343	1.00 69.57	AAAA C
		CG1		314	31.024	43.693		1.00 65.60	
		CG2					36.681		AAAA C
				314	30.927	45.823	35.319	1.00 65.27	AAAA C
			VAL	314	33.492	43.088	35.638	1.00 62.65	AAAA C
			VAL	314	34.029	43.141	36.704	1.00 63.92	AAAA O
ATOH 2	5990	и .	THR	315	33.468	42.011	34.878	1.90 61.82	AAAA II
			THR	315	34.029	40.752	35.284	1.00 63.44	AAAA C
			THR	315	33.618	39.628	34.314	1.00 65.54	
									AAAA C
		CGI (315	32.403	40.004	33.634	1.00 74.05	AAAA C
		CG2 1		315	33.339	39.366	35.104	1.00 64.86	AAAA C
ATOH 2	997	c :	THR	315	35.541	40.971	35.323	1.90 65.62	AAAA C

Aren	2929 O THE	315	36.217	40.339	36.200	1.00 66.41	AAAA O
ATOU	2999 II SER	316	36.071	41.593	34.333	1.00 63.28	II AAAA
ATOH ATOH			37.500				AAAA C
ATOI			37.785 37.298				AAAA C AAAA O
ATOH			38.977	42.573	35.387	1.00 58.91	AAAA C
ATOH ATOH			39.293 37.310				O AAAA 11 AAAA
ATOH			37.750				AAAA C
ATOH			36.833				AAAA C
ATOI1		317 317	37.689 37.702	43.487	38.538 39.599		AAAA C AAAA O
HOTA		318	37.361	42.205	38.523		II AAAA
HOTA			37.185				AAAA C
HOTA HOTA		318 318	36.857 36.624	39.956 38.947	39.293 40.383		AAAA C AAAA C
ATOH	3018 CD GLN	318	35.265	39.080		1.00 92.69	AAAA C
ATOH	3019 OE1 GLH 3020 HE2 GLH	318 318	34.256	39.907	40.391		AAAA O
IOTA IOTA	3023 C GLH	318	35.356 38.380	39.509 41.413	42.308 40.653		АААА И АААА С
ATOH	3024 O GLH	318	38.294	41.855	41.804	1.00 68.92	AAAA O
1 IOTA	3025 II HET 3027 CA HET	319 319	39.562 40.846	41.062	40.153 40.826		AAAA H
ATOI	3028 CB MET	319	41.950	40.960	39.772	1.00 71.85	AAAA C AAAA C
ATO!	3029 CG HET	319	41.740	39.644	39.050	1.00 91.16	AAAA C
IIOTA IOTA	3030 SD HET 3031 CE HET	319 319	43.123 42.486	38.482 37.105	39.185 38.231	1.00106.72 1.00 97.56	AAAA S AAAA C
ATCH	3032 C HET	319	41.118	42.509	41.471	1.00 67.68	AAAA C
ATOH	3033 O HET	319	41.597	42.541	42.612	1.00 69.73	AAAA O
11OTA 11OTA	3034 H LEU 3036 CA LEU	320 320	40.740 40.907	43.639 44.938	40.887 41.531	1.00 62.95 1.00 62.31	aaaa ii aaaa c
IOTA	3037 CB LEU	320	40.440	46.085	40.623	1.00 54.93	AAAA C
INTA	3038 CG LEU	320	41.091	46.163	39.238	1.00 53.49	AAAA C
HOTA	3039 CD1 LEU 3040 CD2 LEU	320 320	41.005 42.557	47.552 45.709	38.692 39.403	1.00 51.31 1.00 58.43	AAAA C AAAA C
110TA	3041 C LEU	320	40.209	45.008	42.881	1.00 60.30	AAAA C
ATOH ATOH	3040 0 LEV 3043 N 3LN	320 321	40.344 39.267	45.959 44.106	43.661	1.00 58.72 1.00 59.62	AAAA O
ATO!	3048 CA 31N	321	38.482	44.128	43.112	1.00 63.50	aaaa ii aaaa c
ATOH	3046 CB GLN	321	37.373	43.789	44.250	1.00 62.52	AAAA C
ATOH ATOH	3047 OG GLN 3048 OD GLN	321 321	36.611 35.337	42.884 42.864	45.522 45.291	1.90 56.83 1.00 68.77	AAAA C AAAA C
HCTA	3049 OE1 GLN	321	35.362	40.969	44.713	1.00 70.37	AAAA O
HOTA	3650 NEC GLN 3653 C GLN	321 321	34.210 39.367	40.632	45.764	1.00 63.77	AAAA H
ATOH	3054 6 GLN	321	40.262	44.030 43.196	45.594 45.782	1.00 60.97 1.00 57.29	AAAA C AAAA O
ATON	3185 H GLY	302	39.092	44.939	46.546	1.00 57.62	AAAA 3
ATOL: ATOL:	3087 TA GLY 3088 C GLY	322 322	39.855 41.126	44.928 45.773	47.790 47.812	1.00 60.63 1.00 61.79	AAAA C AAAA C
ATOI:	3089 O GLY	322	41.594	46.199	43.999	1.00 60.16	AAAA o
HOTA HOTA	3060 H CYS 3060 CA CYS	323 323	41.719	46.134	46.676	1.00 60.03	AAAA ::
ATOH	3063 C CYS	323	42.938 42.924	46.845 48.307	46.528 46.910	1.00 54.20 1.00 53.43	AAAA C AAAA C
ATOH	3064 O CYS	323	42.105	49.148	46.503	1.00 56.43	AAAA O
ATOH ATOH	3065 CB CYS 3066 SG CYS	323 323	43.458 43.325	46.822 45.222	45.086 44.248	1.00 53.33 1.00 66.22	AAAA C AAAA S
ATO!!	3067 H THR	324	43.994	48.718	47.580	1.00 49.83	AAAA H
ATCH ATOH	3069 CA THR 3070 CB THR	324 324	44.164	50.161 50.324	47.811	1.00 52.29	AAAA C
ATOH	3071 OG1 THR	324	44.623 45.245	49.087	49.264 49.634	1.00 52.84 1.00 59.92	AAAA C AAAA O
ATOH	3073 CG2 THR	324	43.432	50.517	50.193	1.00 60.00	AAAA C
HOTA :	3074 C THR 3075 O THR	324 324	45.154 45.277	50.802 52.016	46.844 46.710	1.00 48.91	C AAAA O AAAA
IOTA	3076 N ILE	325	46.021	49.963	46.251	1.00 46.87	AAAA N
HOTA HOTA	3078 CA ILE 3079 CB ILE	325 325	47.114 48.473	50.511 50.577	45.445	1.00 45.10	AAAA C
ATOM	3080 CG2 ILE	325	49.586	50.905	46.183 45.163	1.00 43.60 1.00 47.47	AAAA C AAAA C
HOTA	3081 CG1 ILE	325	48.394	51.623	47.294	1.00 34.03	AAAA C
HOTA HOTA	3082 CD1 ILE 3083 C ILE	325 325	49.595 47.265	52.010 49.642	48.028 44.229	1.00 41.94 1.00 42.89	AAAA C AAAA C
HOTA	3084 O ILE	325	47.406	48.429	14.469	1.00 42.99	AAAA O
ATOH ATOH	3085 II PHE 3087 CA PHE	326 326	47.170	50.238	43.042	1.00 41.19	II AAAA
ATON	3098 CB PHE	326	47.312 46.166	49.334 49.437	41.880 49.877	1.00 42.89	AAAA C AAAA C
HOTA	3089 GG PHE	326	46.403	49.474	39.738	1.00 38.03	AAAA C
ATOH ATOH	3090 CD1 PHE 3091 CD2 PHE	326 326	46.186 46.917	47.125 48.892	39.951 38.525	1.00 39.68 1.00 37.31	AAAA C AAAA C
ATO:1	3092 CE1 PHE	326	46.447	46.139	39.023	1.00 36.52	AAAA C
ATOI1	3093 CE2 PHE 3094 CC PHE	326	47.136	47.919	37.551	1.00 45.74	AAAA C
ATOH ATOH	3094 CC PHE 3095 C PHE	326 326	46.924 48.682	46.570 49.673	37.787 41.280	1.00 39.92 1.00 48.78	AAAA C AAAA C
ATOH	3096 O PHE	326	49.024	50.826	40.966	1.00 51.39	AAAA O
ATOH ATOH	3097 H LYS 3099 CA LYS	327 327			41.379 40.831	1.00 50.22 1.00 51.49	AAAA N AAAA C
ATOH	3100 CB LYS	327			41.519	1.00 58.64	AAAA C

ATG			53.25			1 1.00 59.15	AAAA C
AT'A			54.52	8 49.25	7 41.61	7 1.00 63.49	AAAA C
ATO	: 3103 CE LYS	327	55.40	0 48.95	1 40.59	2 1.00 68.12	AAAA C
ATO	1 3104 NG LYS	327	56.26	47.989			AAAA 11
ATCI	: 3109 C LYS	327	50.89				AAAA c
ATO			50.90				
							O AAAA
ATON		328	50.76				н аааа
ATON		328	50.647	49.038	37.08	0 1.00 39.44	AAAA C
ATCO	3113 C GLY	328	49.849	50.161	36.42	7 1.00 39.49	AAAA C
ATON	3114 O GLT	328	49.858				AAAA O
ATOH		329	49.286				
							M AAAA N
ATOR		329	49.467				AAAA C
ATOH		329	49.185	50.942	33.21	1.00 42.50	AAAA C
ATOH	i 3119 CG ASH	329	50.624	51.406	33.35	7 1.00 42.26	AAAA C
ATOL	3120 OD1 ASH	329	50.954	52.331	34.156	5 1.00 34.77	AAAA O
HOTA		329	51.425				
ATOH		329	47.038				II AAAA II
							AAAA C
ATOH		329	46.736			9 1.00 50.17	AAAA O
HOTA		330	46.090		34.413	3 1.00 47.13	N AAAA
ATOH	3129 CA LEU	330	44.691	59.860	34.151	1.00 42.53	AAAA C
ATOH	3129 CB LEU	330	43.751				
ATOH		330					AAAA C
			43.768				AAAA C
ATO!!		330	42.864		37.417	1.00 38.12	AAAA C
ATO!!	3130 CD2 LEU	330	43.283	49.565	36.669	1.00 38.74	AAAA C
ATOH	3133 C LEU	330	44.352				AAAA C
ATCI:	3134 O LEU	330	44.509				
ATOH							AAAA O
		331	43.933				AAAA N
INTA	3137 CA LEU	331	43.367	50.869	30.625	1.00 43.10	AAAA C
ATOH	3139 CB LEU	331	43.958	49.894	29.585	1.00 42.29	AAAA C
HOTA	3139 CG LEU	331	43.301	49.960			AAAA C
ATOIT	3140 CD1 LEU	331					
			43.501	51.319			AAAA C
ATOH	3141 CD2 LEU	331	43.844	48.834	27.367	1.00 48:76	AAAA C
ATOH	3142 C LEU	331	41.872	50.568	30.705	1.00 41.12	AAAA C
ATOH	3143 O LEU	331	41.562	49.365	30.779		AAAA O
ATC!	3144 H ILE	332	41.029	51.566			
ATOH	3146 TA ILE	332	39.606				H FAAA
				51.241	31.044		AAAA C
ATO!!	3147 CB ILE	332	3₹.885	52.095	32.076	1.00 34.77	AAAA C
ATC:	3149 TGC ILE	332	37.413	51.613	32.195	1.00 34.66	AAAA C
ATO::	3149 731 212	332	39.550	51.895	33.452		AAAA C
ATON:	3150 CD1 ILE	332	39.479	53.152	34.337	1.00 48.21	AAAA C
ATOH	BISL T TEE	332	38.959				
ATO:				51.367	29.688		AAAA C
		332	39.867	52,499	29.200		AAAA O
ATCI:	3153 N ASN	333	38.569	50.273	29.094	1.00 35.25	aaaa n
ATOH	3188 CA ASH	333	39.014	50.293	27.737	1.00 40.34	AAAA C
ATOH	3156 CB ASH	333	38.960	49.499	26.797	1.00 50.50	AAAA C
ATOH	3157 CG ASN	333					
ATO!!			38.669	49.493	25.310	1.00 59.29	AAAA C
		333	37.845	49.711	24.794	1.00 64.54	AAAA O
ATOH	3159 NOO ASN	333	39.290	50.350	24.457	1.00 45.83	AAAA ::
ATON	3161 T ASK	333	36.666	49.591	27.755	1.00 47.63	AAAA C
ATCH!	3163 C ASN	333	36.462	48.409	27.398	1.00 44.40	AAAA O
ATOM:	3164 H ILE	334	35.544	50.213	28.315		
ATOI!	Blas CA ILE	334				1.00 54.13	AAAA N
			34.332	49.537	28.460	1.00 59.07	AAAA C
ATOH	3167 CB ILE	334	33.798	49.826	29.876	1.00 61.98	AAAA C
PLOTE	3148 CGC ILE	334	32.362	49.355	30.047	1.00 54.04	AAAA C
ATOH	3169 TG1 ILE	334	34.737	49.224	30.915	1.00 60.43	AAAA C
ATO!	3170 CD1 ILE	334	34.346	49.687	32.317	1.00 68.57	AAAA C
HOTA	3171 C ILE	334	33.271				
ATOH				50.032	27.476	1.00 59.45	AAAA C
		334	32.726	51.136	27.635	1.00 56.22	aaaa o
ATOH	3173 N ARG	335	32.919	49.181	26.550	1.00 59.69	AAAA N
HOTA	3175 CA ARG	335	31.910	49.567	25.573	1.00 73.93	AAAA C
ATOH	3176 CB ARG	335	32.262	49.903	24.240	1.00 74.44	AAAA C
ATOH	3177 CG ARG	335	33.729	49.932	23.918	1.00 82.97	
ATOH	3179 CD ARG	335		_			AAAA C
ATOH	_		34.102	49.289	22.500	1.00 86.49	AAAA C
		335	34.361	49.040	21.777	1.00 89.83	aaaa n
HOTA	3181 CD ARG	335	34.011	47.838	20.496	1.00 93.67	AAAA C
ATOH	3192 NHI ARG	335	33.409	48.852	19.843	1.00 87.24	AAAA II
HOTA	3185 HH2 ARG	335	34.256	46.674	19.877	1.00 75.31	AAAA N
ATOH	3189 C ARG	335	30.492	49.233			
ATOH	3189 O ARG	335			26.021	1.00 81.52	AAAA C
			29.664	50.115	26.239	1.00 84.11	AAAA O
ATOH	3190 H ALA	336	30.208	47.953	26.234	1.00 87.51	AAAA N
HOTA	3192 CA ALA	336	28.878	47.484	26.601	1.00 82.40	AAAA C
ATCH!	3193 CB ALA	336	28.835	45.980	26.633	1.00 94.03	AAAA C
HOTA	3194 C ALA	336	28.479	49.058	27.953	1.00 96.61	AAAA C
ATOH:	3195 C ALA	336	29.316				
ATOH				49.019	28.855	1.00 96.96	AAAA O
		337	27.298	48.685	28.039	1.00 99.74	AAAA N
ATOH	3199 CA GLY	337	26.986	49.385	29.272	1.00103.11	AAAA C
ATOH	3199 C GLY	337	25.568	49.303	29.763	1.00105.51	AAAA C
ATOH	3200 O GLY	337	24.801	50.267	29.596	1.00106.64	AAAA O
ATOH	3201 II ASN	338	25.243				
ATOH				48.146	30.346	1.00105.41	AAAA N
		338	23.886	49.017	30.908	1.00106.92	AAAA C
ATOH	3204 CB ASH	338	23.714	46.689	31.624	1.00109.14	AAAA C
HOTA	3205 CG ASN	338	24.403	45.544	30.928	1.00112.30	AAAA C
ATOH	3206 ODE ASN	338	25.598	45.595	30.625	1.00117.94	AAAA O
HOTA	3207 HDC ASH	338	23.604	44.508			
ATON					30.683	1.00113.72	AAAA II
WI CALL	3010 C ASH	338	23.790	49.160	31.931	1.00105.84	AAAA C

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	3211 O ASH	330	~ ~ ~		71 770	1.00103.97	
ATCU		338 339	23.544	50.345			AAAA O
ATOU	3010 II ASII 3014 CA ASII	339	24.290				AAAA H
ATCU		339	24.529	49.740	_		AAAA C
ATOI!	3215 CB ASN		23.252	49.915			AAAA C
ATOU	3216 CG ASN	339	22.777	51.351	35.003		AAAA C
ATOU	3217 OD1 ASH	339	22.715	51.931	36.088		AAAA O
ATOU	3218 HDC ASH	339	22.441	51.932	33.859		II AAAA
ATOH	3221 C ASH	339	25.697	49.237	35.007		AAAA C
PLOTE	3200 O ASH	339	25.520	48.390			AAAA O
HOTA	3223 N ILE	340	26.897	49.527	34.510		N AAAA N
ATOH	3225 CA ILE	340	28.136	49.101	35.138	1.00 97.43	AAAA C
HOTA:	3226 CB ILE	340	29.040	48.354	34.151	1.00 93.63	AAAA C
ATO!	3227 CGC ILE	310	28.194	47.252	33.489	1.00 99.38	AAAA C
ATO!!	3229 OG1 ILE	340	29.726	49.158	33.070	1.00 85.50	AAAA C
I POTA	3229 CD1 ILE	340	28.897	49.634	31.915	1.00 92.53	AAAA C
ATOH	3230 C ILE	340	28.783	50.357	35.706	1.00 95.32	AAAA C
ATOH	3231 O ILE	340	29.472	51.099	34.997	1.00 97.86	AAAA O
ATOH	3232 II ALA	341	28.409	50.739	36.915	1.00 89.89	II AAAA II
ATON	3234 CA ALA	341	28.892	52.008	37.450		AAAA C
ATOH	3235 CB ALA	341	28.068	53.201	37.006		AAAA C
ATO!	3236 C ALA	341	28.786	51.968	38.970		AAAA C
ATOH	3237 O ALA	341	28.910	52.935	39.690		AAAA O
ATOH	3238 II SER	342	28.204	50.877	39.386		AAAA N
ATOL	3240 CA SER	342	27.910	50.601	40.780		AAAA C
ATO!!	3241 CB SER	342	26.426	50.667		1.00 85.51	AAAA C
ATOI	3240 OG SER	342	26.145	51.271	41.112 42.361	1.00 85.31	AAAA O
HOTA	3241 C SER	342	28.487	49.196	40.965	_	AAAA C
ATOH	3245 O SER	342	29.119	48.966	41.964	1.00 70.02	AAAA O
ATOH		343	28.373	48.409	39.905	1.00 76.23	II AAAA
ATOH	3249 CA GLU	343	29.001	47.109	39.820		AAAA C
ATOH	3249 CB GLU	343	28.595	46.300	38.616	1.00 78.62	AAAA C
ATOH	3250 CG GLU	343	27.118	46.105	38.316	1.00 85.33	AAAA C
ATOH	3251 CD GLW	343	26.898	45.121	37.169	1.00 92.76	AAAA C
ATON	3250 OE1 GLV	343	27.209	43.911	37.310	1.00 96.41	O AAAA
ATOLL	3253 <u>0</u> E2 GLV	343	26.423	45.517	36.082	1.00 98.55	O AAAA
ATO:	3254 C 310	343	30.525	47.319	39.804	1.00 77.75	AAAA C
ATOH:	3055 9 910	343	31.273	46.797	40.637	1.00 75.73	AAAA O
ATON	3256 H LEV	344	31.022	49.237	39.966	1.00 75.65	II AAAA
ATON:	BOSS CA LEV	344	32.415	48.596	38.833	1.00 72.36	AAAA C
ATO::	3089 DB LEV	344	32.760	43.697	37.809	1.00 64.33	AAAA C
ATO!!	3261 DB LEV	344	32.687	49.397	36.311	1.00 50.12	AAAA C
ATCI:	3041 CD1 LEV	344	33.224	50.577	35.519	1.00 57.00	AAAA C
ATO!:	3262 CCC LEV	344	33.401	48.127	35.905	1.00 51.62	AAAA C
ATOM:	3263 T LEV	344	32.963	49.130	40.174	1.00 69.74	AAAA C
ATON	3264 C LEU	344	34.079	48.739	40.551	1.00 69.12	aaaa o
ATOH:	3268 W 31V	345	32.166	49.959	40.822	1.00 63.10	H AAAA II
ATO::	306" TA 317	345	32.555	50.891	42.061	1.00 65.42	AAAA C
ATO::	3069 TB GLT	345	31.592	51.714	42.478	1.00 55.59	AAAA C
ATC::	3069 09 300	345	32.267	52.607	13.486	1.00 68.78	AAAA C
ATO::	327: 70 310	345	31.324	53.374	44.376	1.00 81.31	AAAA C
ATOM:	3271 0E1 GLU	345	30.514	54.320	43.976	1.00 85.60	AAAA O
ATO::	3070 CEO GLU	345	31.237	53.078	45.595	1.00 88.79	AAAA O
ATO::	3273 0 614	345	32.706	49.652	43.255	1.00 63.31	AAAA C
ATO!:	3274 O GLU	345	33.501	49.913	44.134	1.00 60.06	AAAA O
ATOM	3275 II ASII	346	32.151	48.462	43.202	1.00 62.25	II AAAA II
ATOH:	3277 CA ASH	346	32.285	47.403	44.173	1.00 63.82	AAAA C
ATO!!	3279 CB ASH	346	31.024	46.498	44.095	1.00 61.66	AAAA C
ATO!!	3279 CG ASN	346	31.110	45.292	45.006	1.00 58.73	AAAA C
ATOH	3290 OD1 ASN	346	31.188	45.352	46.224	1.00 69.11	AAAA O
ATOH	3281 ND2 ASN	346	31.155	44.092	44.444	1.00 51.10	AAAA N
ATOI!	3294 C ASN	346	33.532	46.580	43.870	1.00 63.71	AAAA C
ATC: 1	3295 O ASN	316	33.636	45.336	43.905	1.00 65.65	AAAA O
ATOH	3296 N PHE	347	34.419	47.173	43.066	1.00 63.23	N AAAA
HOTA	3298 CA PHE	347	35.540	46.411	42.506	1.00 61.39	AAAA C
HOTA	3089 CB PHE	347	35.123	45.854	41.170	1.00 61.38	AAAA C
ATOH	3090 CG PHE	347	34.457	44.534	41.142	1.00 65.57	AAAA C
ATO!!	3291 CD1 FHE	347	33.090	44.438	40.982	1.00 75.25	AAAA C
HOTA	3292 CD2 PHE	347	35.148	43.351	41.267	1.00 77.15	AAAA C
ATOH1	3293 CE1 PHE	347	32.425	43.224	40.951	1.00 75.55	AAAA C
HOTA	3294 CE2 PHE	347	34.512	42.130	41.249	1.00 72.86	AAAA C
ATOH	3295 CC PHE	347	33.152	42.051	41.095	1.00 72.74	AAAA C
ATOH	3296 C PHE	347	36.712	47.375	42.440	1.00 57.70	AAAA C
ATOH	3297 O PHE	347	37.770	46.920	42.354	1.00 59.92	AAAA C
HOTA	3299 H HET	348	36.492	18.676		1.00 50.56	AAAA H
ATOH	3300 CA HET	348	37.500	49.630	41.964	1.00 42.86	AAAA C
ATOH	3301 CB HET	348	37.402	50.096		1.00 31.72	AAAA C
ATOH	3302 CG HET	348	37.425	18.933	39.471	1.00 33.42	AAAA C
ATOH	3303 SD MET	348	37.566	49.448	37.732	1.00 44.79	AAAA S
ATOH	3304 CE HET	348	38.408	50.999	37.732	1.00 44.79	AAAA C
ATOH		348	37.368			1.00 45.88	AAAA C
		348		50.831	42.867		
HOTA		349	38.210	51.772	42.901	1.00 43.33	AAAA O
ATOH	3307 H GLY		36.296	50.783	43.683	1.00 45.30	AAAA II
ATOH	3309 CA GLY	349	35.998	51.965	44.504	1.00 49.19	AAAA C
ATOH	3310 C GLY	315	36.980	52.189	45.620	1.00 52.77	AAAA C
ATOH	3311 O GLY	313	37.033	53.299	46.156	1.00 53.43	AAAA O

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ATG	: 3312 # LEU	350	37.79	1 51.15	9 45.92	5 1.00 56.17	II AAAA II
ATO	: 3314 CA LEU	350	38.73	5 51.25			AAAA C
ATOU	: 3315 CB LEU	350	38.87				AAAA C
ATOR			37.87				
ATON							AAAA C
			37.70				AAAA C
ATOR			38.24		6 50.038	8 1.00 56.11	AAAA C
ATON			40.14	4 51.72	7 46.685	5 1.00 61.34	AAAA C
ATOR	3320 O LEU	350	40.93	1 51.962			AAAA O
ATON	3321 H ILE	351	40.446			-	AAAA II
ATOL			41.729				77777 11
							AAAA C
ATOI			41.81				AAAA C
ATOH			43.121	l 52.416	42.757	7 1.00 40.01	AAAA C
ATOH	3326 CG1 ILE	351	41.535	5 50.418	3 43.058	3 1.00 36.87	AAAA C
ATOH	3327 CD1 ILE	351	41.173	50.351	41.581		AAAA C
ATOL	3329 C ILE	351	42.031				
ATOH		351	41.367				AAAA C
							AAAA O
ATOH		352	43.002		46.015	1.00 50.61	ii aaaa
ATOH		352	43.381	. 55.241	46.248	1.00 51.20	аааа с
ATOH	3333 CB GLU	352	43.907	55.353	47.678	1.00 52.12	AAAA C
ATOH	3334 CG GLU	352	42.912				
ATOH		352	43.034				AAAA C
ATOH							AAAA C
		352	43.881				AAAA O
ATOH		352	42.330	53.799	50.009	1.00 76.07	AAAA O
ATOH		352	44.502	55.751	45.314	1.00 47.43	AAAA C
ATO(1	3339 O GLU	352	44.798				AAAA O
ATOH	3340 II VAL	353	45.342				
ATOH	3342 CA VAL	353	46.512				N AAAA
ATOH							AAAA C
		353	47.759			_	AAAA C
ATO(1	3344 CG1 VAL	353	47.766		46.387	1.00 30.84	AAAA C
IICTA	3345 CG2 VAL	353	48.988	54.844	44.310	1.00 42.55	AAAA C
ATOH	3346 C VAL	353	46.828	54.233			AAAA C
HOTA	3347 O VAL	353	46.843			1.00 39.19	AAAA O
ATOH	3348 II VAL	354	47.074				
ATOH	3350 CA VAL	354			_		H AAAA
			47.586		40.651	1.00 43.97	AAAA C
ATOH	3351 CB VAL	354	46.725		39.407	1.00 40.96	AAAA C
ATOH	3352 C31 VAL	321	47.347	53.896	39.123	1.00 36.72	AAAA C
HOTA	3353 032 VAL	354	45.293	53.849	39.678	1.00 35.35	AAAA C
ATOH	3354 C VAL	354	49.043	54.510	40.388	1.00 44.56	AAAA C
ATOH	3355 O VAL	354	49.366	55.718	40.289	1.00 43.32	
ATOR	3356 :: THR	355	49.972				AAAA O
ATOH	3358 CA THR			53.561	40.431	1.00 43.93	AAAA W
		355	51.392	53.914	40.284	1.00 44.85	AAAA C
ATON	3359 CB THR	355	52.374	52.799	40.653	1.00 42.40	AAAA C
ATOH	3360 OG1 THR	355	52.273	51.744	39.695	1.00 45.30	AAAA O
ATOH	3360 CGC THR	355	52.210	52.194	42.039	1.00 38.13	AAAA C
ATQI!	3363 C THR	355	51.746	54.339	38.851	1.00 43.84	AAAA C
HCTA.	3364 C THR	355	52.463	55.334	38.697	1.00 44.26	
ATOH	3365 H GLY	356	51.127				AAAA O
ATOH	3367 CA GLY			53.704	37.870	1.00 41.16	AAAA II
		356	51.358	54.073	36.470	1.00 37.81	AAAA C
ATON	3369 C GLY	356	50.505	55.004	35.955	1.00 38.07	AAAA C
ATO(1	3369 O GLY	356	50.364	56.261	36.615	1.00 34.65	AAAA O
ATOH	3370 H TYR	357	49.910	55.004	34.800	1.00 38.47	AAAA ::
ATOH	3372 CA TYR	357	49.982	55.973	34.205	1.00 38.03	AAAA T
ATOH	3373 CB TYR	357	49.557	56.343	32.805	1.00 31.44	AAAA C
ATOH	3374 CG TYR	357	49.473		31.812		
ATOH	3375 CD1 TYR	357					AAAA C
HOTA	3376 CE1 TYR		48.333	54.842	31.077	1.00 32.86	AAAA C
		357	48.352	53.779	30.175	1.00 32.83	AAAA C
ATOH	3377 CD2 TYR	357	50.639	54.465	31.606	1.00 34.28	AAAA C
ATOH:	3378 CE2 TYR	357	50.706	53.402	30.720	1.00 32.51	AAAA C
HOTA	3379 CZ TYR	357	49.552	53.068	30.007	1.00 37.26	AAAA C
ATOH	3380 OH TYR	357	49.726	51.997	29.166	1.00 35.85	O KAAK
ATOH	3382 C TYR	357	47.582	55.368	34.150	1.00 38.55	AAAA C
HOTA	3383 O TYR	357	47.458	54.127		1.00 36.11	
ATOH	3394 H VAL	358			34.088		O AAAA
ATOH			46.593	56.216	33.814	1.00 40.98	II AAAA II
		358	45.197	55.798	33.639	1.00 38.90	AAAA C
HOTA	3387 CB VAL	358	44.211	56.502	34.610	1.00 49.15	AAAA C
ATOH	3398 CG1 VAL	358	42.815	55.883	34.484	1.00 33.12	AAAA C
HOTA	3389 CG2 VAL	358	44.748	56.437	36.043	1.00 29.20	AAAA C
ATOH	3390 C VAL	358	44.750	56.194	32.234	1.00 35.64	AAAA C
ATOH	3391 O VAL	358	44.792	57.358	31.888	1.00 34.58	
ATOH	3392 N LYS	359					AAAA O
ATOH	3394 CA LYS		44.387	55.188	31.461	1.00 36.00	II AAAA
		359	43.898	55.419	30.117	1.00 41.27	AAAA C
ATOH	3395 CB LYS	359	14.815	54.707	29.174	1.00 37.40	AAAA C
ATOH	3396 CG LYS	359	44.340	54.473	27.770	1.00 45.19	AAAA C
HOTA	3397 CD LYS	359	45.040	55.317	26.750	1.00 43.40	AAAA C
ATOH	3398 CE LYS	359	15.958	54.402	25.986	1.00 43.56	AAAA C
ATOH	3399 NE LYS	359	45.416	53.937			
ATOH	3403 C LYS				24.680	1.00 47.98	AAAA II
		359	42.423	54.979	29.939	1.00 42.14	AAAA C
ATO(1	3404 O LYS	359	42.056	53.791	30.006	1.00 40.40	AAAA O
ATOH:	3405 N ILE	360	41.602	55.974	29.572	1.00 37.16	AAAA II
1 IOTA	3407 CA ILE	360	40.164	55.742	29.334	1.00 40.02	AAAA C
ATC/1	3408 CB ILE	360	39.297	56.804	30.048	1.00 38.10	AAAA C
ATOH	3409 CG2 ILE	360	37.887				
ATOH				56.277	29.932	1.00 39.42	AAAA C
	3410 CG1 ILE	360	39.769	57.111	31.481	1.00 29.54	AAAA C
ATOH	3411 CD1 ILE	360	39.423	56.037	32.491	1.00 33.16	AAAA C
ATOH	3412 C ILE	360	39.888	55.837	27.834	1.00 39.49	AAAA C

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ATOU		360	40.014				AAAA O
ATOR HOTA		361 361	39.567 39.472				II AAAA
ATOIL	and the second s	361	40.783				AAAA C
ATC!!		361	40.805				AAAA C
ATOH		361	41.943				AAAA C
ATOH		361	41.473				II AAAA II
ATOH		361	42.297				AAAA C
HOTA		361 361	43.612				II AAAA
IOTA IOTA	3426 HH2 ARG 3429 C ARG	361 361	41.834 38.382	49.719 53.866			AAAA II AAAA C
ATOH	3430 O ARG	361	38.336				
ATOH	3431 N HIS	362	37.514	54.342			AAAA II
ATOU	3433 CA HIS	362	36.372	53.555			AAAA C
ATOH	3434 CB HIS	362	37.000	52.300			AAAA C
ATOH	3435 CG HIS 3436 CD2 HIS	362	37.849	52.610			AAAA C
HOTA	3436 CD2 HIS	362. 362	38.049 38.628	53.765 51.676			AAAA C
ATON	3439 CE1 HIS	362	39.256	52.247	20.465		AAAA C
ATOH	3440 HE2 HIS	362	38.923	53.515			II AAAA
ATOH	3442 C HIS	362	35.295	53.113	24.913		AAAA C
HOTA	3443 O HIS	362	34.686	52.030	24.795		AAAA O
ATOH	3444 II SER	363	35.222	53.875	26.013		II AAAA
HOTA	3446 CA SER 3447 CB SER	363 363	34.402 35.231	53.456 53.837	27.139 28.400		AAAA C
ATOH	3448 OG SER	363	35.713	52.558	28.816		AAAA C AAAA O
ATON	3450 C SER	363	33.005	54.072	27.046		AAAA C
ATOH	3451 O SER	363	32.653	55.040	27.694	1.00 37.49	AAAA O
ATOH	3452 II HIS	364	32.243	53.577	26.058	1.00 52.25	N AAAA
ATOH ATOH	3454 CA HIS	364	30.954	54.173	25.717	1.00 53.66	AAAA C
ATOH	3455 C HIS 3456 O HIS	364 364	29.879 29.297	53.937 54.899	26.760 27.280	1.00 48.77 1.00 51.44	AAAA C AAAA O
HOTA	3457 CB HIS	364	30.485	53.699	24.349	1.00 49.83	AAAA C
ATOH	3458 CG HIS	364	31.493	54.182	23.330	1.00 51.51	AAAA C
ATOH	3459 HD1 HIS	364	31.970	55.502	23.156	1.00 44.83	AAAA H
ATOH	3460 CE1 HIS	364	32.798	55.533	22.214	1.00 28.57	AAAA C
ATON ATON	3461 CD2 HIS 3463 MED HIS	364 364	32.194 32.992	53.393 54.274	22.472	1.00 38.62	AAAA C AAAA H
ATOH!	3464 H ALA	365	29.949	52.819	27.427	1.00 47.53	AAAA ::
ATOH:	3466 CA ALA	365	29.211	52.488	28.621	1.00 44.41	AAAA C
ATOH	3467 CB ALA	365	29.678	51.133	29.150	1.00 40.28	AAAA C
ATON	3468 T ALA	365	29.318	53.473	29.768	1.00 44.70	AAAA D
ATOH	3469 0 ALA 3470 N LEU	365	28.576	53.206	30.726	1.00 45.23	AAAA O
ATOH ATOH	3470 H LEU 3472 CA LEU	366 366	30.158 30.415	54.517 55.243	29.762 30.969	1.00 40.80	AAAA N AAAA C
ATOH	3473 CB LEU	366	31.985	55.241	31.350	1.00 43.78	AAAA C
ATOM	3474 GB LEU	366	32.740	54.037	31.667	1.00 51.52	AAAA C
ATON	3475 DD1 DEU	366	34.192	54.373	32.043	1.00 51.77	AAAA C
ATOH	3476 002 180	366	32.119	53.305	32.834	1.00 51.17	AAAA C
ATOH ATOH	3477 0 LEV 3478 0 LEV	366 366	29.974 30.305	56.687 57.248	30.896 29.849	1.00 46.36 1.00 48.40	AAAA C
ATOH	3479 H VAL	367	29.521	57.275	32.015	1.00 43.69	AAAA D AAAA H
ATOH	3491 CA VAL	367	29.072	58.575	31.940	1.00 44.19	AAAA C
MOTA	3492 CB VAL	367	27.557	50.727		1.00 48.80	AAAA C
HOTA	3483 CG1 VAL	367	26.923	60.073	32.571	1.00 41.69	AAAA C
ATOH ATOH	3484 CG2 VAL 3485 C VAL	367 367	26.697 29.923	57.949 59.518		1.00 34.00 1.00 44.90	AAAA C AAAA C
ATOH	3485 O VAL	367	29.965	60.751		1.00 44.75	AAAA O
ATOH	3497 !: SER	368	30.591	59.818	33.757	1.00 48.72	AAAA N
ATOH	3499 CA SER	368	31.487	59.465	34.742	1.00 52.70	AAAA C
ATOH	3490 CB SER	368	30.658	59.706		1.00 55.32	AAAA C
ATOH ATOH	3491 OG SER 3493 C SER	368 368	31.300 32.590	60.298 58.497	37.091 35.179	1.00 64.86 1.00 52.76	AAAA C AAAA C
ATOH	3494 O SER	368	32.352	57.299		1.00 32.76	AAAA O
ATOI1	3495 II LEU	369	33.631	59.012	35.831	1.00 53.86	AAAA II
ATOH	3497 CA LEU	369	34.716	58.129	36.274	1.00 60.15	AAAA C
ATOH	3499 CB LEU 3499 CG LEU	369	36.073	58.630	35.784	1.00 55.91	AAAA C
ATOH ATOH	3499 CG LEU 3500 CD1 LEU	369 369	36.325 37.669	58.736 59.428	34.271 34.154	1.00 45.96 1.00 53.97	AAAA C AAAA C
ATOH	3501 CD2 LEU	369	36.207	57.384	33.619	1.00 38.77	AAAA C
ATOH	3502 C LEU	369	34.645	58.036	37.811	1.00 62.52	AAAA C
ATOH	3503 O LEU	369	35.569	57.700	38.595	1.00 59.33	AAAA C
HOTA	3504 N SER	370	33.437	58.401	38.285	1.00 56.26	AAAA II
MOTA HOTA	3506 CA SER 3507 CB SER	370 370	33.089 31.673	58.431 59.052	39.690 39.816	1.00 53.89 1.00 57.50	AAAA C AAAA C
ATON	3508 CG SER	370		58.061	39.261	1.00 57.50	AAAA O
ATOH	3510 C SER	370	33.060	57.085	40.412	1.00 47.97	AAAA C
ATOH	3511 O SER	370			41.596	1.00 41.93	AAAA C
HOTA	3512 N FHE	371			39.792	1.00 45.49	AAAA II
ATOH ATOH	3514 CA PHE 3515 CB PHE	371 371			40.356 39.287	1.00 46.29 1.00 43.53	AAAA C AAAA C
ATOH	3516 CG PHE	371			39.287	1.00 43.53	AAAA C
ATOH	3517 CD1 PHE	371	34.805		37.764	1.00 58.95	AAAA C
11OTA	3518 CD2 PHE	371			37.004	1.00 53.92	AAAA C
INTA	3519 CE1 PHE	371	35.498	52.842	36.570	1.00 59.50	AAAA C

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ATM 3605 GLU 380 54,980 55.449 35.157 1.00 53.56 AAAA N 3607 CA GLU 1.00 48.15 ATOL 382 55.091 33.766 55.018 AAAA C 3628 CB GLU 33.532 1.00 35.27 ATOL 382 55.051 53.550 AAAA C 3629 1.00 49.69 ATOH 00 GLU 382 54.739 53.225 32.051 AAAA C ATOH 3630 CD GLU 382 54.676 51.719 31.807 1.00 56.45 AAAA C 3631 OE1 GLU 382 32.705 1.00 61.66 ATOH 55.062 50.924 AAAA O 3632 OE2 GLU 382 30.745 1.00 57.69 54.264 51.201 AAAA O 3633 382 ATOH C GLU 54.006 55.732 32.973 1.00 50.84 AAAA C 3634 GLU 382 53.097 56.282 33.598 1.00 49.44 AAAA O ATO: 3635 п GLII 383 54.347 31.780 1.00 52.25 AAAA II **ATOH** 56.256 3637 CA GLN 383 53.498 57,153 31,016 1.00 40.15 AAAA C ATO!! 58.609 1.00 28.50 AAAA C CB GLII 383 HOTA 3638 53.914 31.155 HOTA 3639 CG GLN 383 54.489 58.909 32.542 1.00 31.10 AAAA C 3640 CD GLII 383 54.950 60.301 32.752 1.00 33.19 AAAA C ATOH 3641 OE 1 GLII 383 55.186 60.840 1.00 40.34 ATCH 31.683 AAAA O 3642 HE2 **GLII** 383 55.043 60.943 33.934 1.00 36.30 AAAA H ATOH 3645 c GLII 383 53.426 1.00 40.45 56.744 29,563 AAAA C HOTA GLII 383 3646 0 55.858 **HOTA** 54.131 29.139 1.00 43.45 AAAA O 384 3647 ы LEU 1.00 42.54 ATOH 52.375 57.195 28.860 AAAA N ATOH 3649 CA LEU 384 52.257 56.889 27.443 1.00 43.24 AAAA ¢ ATOH 3650 CB LEU 384 50.814 57.011 26.949 1.00 43.79 AAAA ATOH 3651 CG LEU 381 49.818 56.235 27.861 1.00 41.21 AAAA C 3652 CDI LEU 384 ATOH 48.611 57.095 28.221 1.00 33.99 AAAA C CD2 LEU 384 ATOI: 3653 49.405 54.968 27.149 1.00 33.20 AAAA C 3654 LEU 384 53.204 26.672 1.09 40.51 ATOH 57.809 AAAA C ATOH 3655 LEU 384 53.582 27.177 1.00 29.66 AAAA O 58.872 3656 н GLU 385 53.659 ATO!! 57.319 25.531 1.00 45.22 AAAA N 3658 CA GLU 385 1.00 49.98 **ATOH** 54.410 58.116 24.570 AAAA C 3659 CB GLU 385 54.424 HOTA 57.475 23.174 1.00 60.50 AAAA С 3660 GLU 385 AAAA C HOTA CG 55.045 56.095 23.106 1.00 68.76 **ATOH** 3551 CD GLU 385 54.195 54.951 23.592 1.00 72.07 AAAA ATOH 3662 OE1 GLU 385 53.150 1.00 81.88 AAAA O 55.213 24.244 ATOU 3663 OE2 GLU 385 54.565 53.786 23.301 1.00 73.13 AAAA O ATON 3654 C GLU 385 53.828 59.515 24.450 1.00 47.41 AAAA C ATOU 3665 C GLU 395 52,635 59,706 1.00 54.43 AAAA O 24,184 3555 :: 317 386 60.470 ATO!! 54.614 24,902 1.00 43.69 H KAAA II 3LT 61.870 62.449 ATOH 3659 CA 336 24.897 1.00 40.34 AAAA 54.191 ATO: 3559 396 317 54.286 26.309 1.00 40.65 AAAA: O ATOH 3670 2 GLY 396 53.930 63.615 26.491 1.00 39.75 AAAA O 3671 ATC:: 3311 337 54.441 61.837 27.272 1.00 40.75 AAAA 3673 54.479 61.912 ATO: CA ASH 397 28.675 1.00 49.18 عممم 3674 3675 ATOH 25 ASH. 397 55.500 63.094 28.874 1.00 44.41 AAAA. ATOH! 7:3 ASH 397 56.925 62.541 28.722 1.00 61.51 AAAA. 3676 3677 001 387 ATOM ASH 57.199 61.313 28.677 1.90 57.85 AAAA O 397 58.063 ATOH 1102 A.511 63.251 28.592 1.00 61.96 AAAA N 327 ATO! 3590 ASH 53.095 62,100 1.00 48.46 29.299 AAAA C HOTA: 397 3681 ASH 52.536 62.891 30.218 1.00 48.99 O AAAA ATON TYR 398 3600 :: 61.116 52.214 29.058 1.00 46.29 AAAA M TIR 389 ATOM: 3684 50.846 61.199 29.540 1.00 45.09 AAAA 3595 333 ATQU: €₽ TYR 49.823 60.957 28.399 1.00 40.70 AAA ATQU: 3596 23 TYR 339 49.925 62.056 27.373 1.00 42.24 AAAA C 3687 CD1 TYR 388 50.343 ATOH 61.854 26.064 1.00 44.38 AAAA ATOH: 3689 CEL TYR 388 50.401 62.895 25.157 1.00 35.51 AAAA C ATOH 3689 CD2 TYR 398 49.625 63.356 27.709 1.00 44.67 AAAA ATOH 3690 CE2 TYR 388 49.699 1.00 38.14 26.830 AAAA C 64.428 CE 388 ATOH 3591 50.087 TYR 25.555 1.00 41.27 AAAA C 64.148 OH 388 AAAA O ATOH 3692 TYR 50.151 65.181 24.604 1.00 50.18 ATOH 3694 \subset TYR 388 50.563 60.288 30.714 1.00 41.88 AAAA C ATOH 3695 0 TYR 388 50.727 59.092 30.511 1.00 32.99 AAAA O ATOH: 3696 :1 SER 389 50,020 60.917 31.763 1.00 45.42 AAAA 11 32.931 LICTA 3698 ÇA SER 389 49.591 60.131 1.00 50.13 AAAA ATOH 3600 CB SER 389 49.798 1.00 45.57 AAAA C 60.894 34.261 1.00 51.11 HOTA 3700 CG SER 389 51.185 60.899 34.504 AAAA O ATOH 3702 c SER 389 48.097 59.813 32.804 1.00 48.11 AAAA C HOTA 3703 SER 389 47.686 1.00 49.25 AAAA O 58.792 33.336 ATOH 3704 11 PHE 390 47.321 1.00 42.56 AAAA N 60.685 32.196 3706 CA PHE 390 ATO(1 45.867 1.00 40.76 AAAA C 60.595 32.146 3707 ATOM CB PHE 390 AAAA C 45.241 61.581 33.139 1.00 44.80 3708 ATOH CG PHE 390 43.764 61.358 33.328 1.00 40.53 AAAA C ATOH 3709 CD1 PHE 390 43.406 60.273 34.089 1.00 40.80 AAAA C HOTA 3710 CD2 PHE 390 42.768 62.157 32.748 1.00 35.59 AAAA C ATOH 3711 CEL PHE 390 42.050 59.985 34.312 1.00 47.09 AAAA C 3712 PHE 390 ATO!! CEC 41.454 61.824 32.965 1.00 44.50 AAAA C PHE ATOH 3713 CZ 390 41.063 60.745 33.739 1.00 34.54 AAAA C HOTA 3714 PHE 390 45.372 60.929 30.720 1.00 38.54 AAAA C 3715 390 ATOM PHE 45.542 30.126 1.00 40.29 61.918 AAAA O TYR 391 ATOH 3716 11 AAAA N 14.819 59.818 30.096 1.00 33.48 1.00 38.58 ATOU 3719 CA TYR 391 44.596 59.782 28.663 AAAA C ATOH 3719 CB TYR 391 45.579 58.871 27.972 1.00 38.95 AAAA C ATOL 3720 CG TYR 391 45.760 59.006 26.503 1.00 44.54 AAAA C ATOH 3721 CD1 TYR 391 46.822 59.815 AAAA C 26.052 1.00 47.14 HOTA 3722 CEL TYR 391 47.057 59.993 1.00 46.03 AAAA C 24.722 3723 CD2 TYR 391 ATOH 44.927 AAAA C 58.390 25.584 1.00 46.94 391 1.00 47.45 ATON 1724 CEC TTR 45.157 58.560 24.242 AAAA C CC TYR 391 ATOM 37.25 46.207 59.350 23.830 1.00 45.84 AAAA

ATO			46.37				
ATO			43.19		2 28.34	9 1.00 39.74	AAAA C
ATO			42.843	1 50.10	3 28.73	1.00 38.49	AAAA O
ATO			42.417			9 1.90 37.07	
ATO			40.958		4 27.603	3 1.00 39.50	AAAA C
ATO			40.079			1.00 41.12	AAAA C
ATC			38.613		4 28.47	1.00 37.96	AAAA C
ATO			40.666		1 29.841	1.00 33.19	
ATO			40.531	60.09	25.182		
ATO			40.508	61.27	7 25.804		AAAA O
ATO			40.299	59.11			
OTA	1 3740 CA LEU	393	39.948	59.259			AAAA C
ATO	1 3741 CB LEU	393	41.200				
ATO	1 3742 OG LEU	393	41.023				AAAA C
ATO	1 3743 CD1 LEU	393	41.129				AAAA C
ATO	1 3744 CD2 LEU	393	42.078				
ATO		393	38.821				AAAA C
ATO		393	38.760				AAAA C
ATO		394	38.015				AAAA O
ATO		394	36.888				AAAA N
ATO		394	37.445				AAAA C
ATOI-		394	36.466				AAAA C
ATON		394	36.750				AAAA C
ATOI		394	35.311				AAAA O
ATOH		394		56.948			AAAA O
ATOL		394	35.936	57.619		1.00 43.17	AAAA C
ATOU			35.831	56.385		1.00 43.51	AAAA O
ATON		395	35.299				II AAAA II
ATOH		395	34.305	58.158		1.00 46.32	AAAA C
ATON		395	34.804	58.512		1.00 42.96	AAAA C
		395	35.992	57.619		1.00 36.92	AAAA C
HOTA		395	36.013	56.394		1.00 21.65	AAAA O
ATOH		395	37.075	58.409		1.00 27.87	AAAA II
ATOH		395	32.932	58.816	24.541	1.00 40.44	AAAA C
ATON		395	32.749	59.982	24.882	1.00 37.06	AAAA O
ATOH		396	32.073	58.055	23.877	1.00 46.74	AAAA H
ATON		396	30.771	50.582	23.421	1.00 52.93	AAAA C
ATOH:	3779 08 920	396	29.848	57.567	22.744	1.00 52.29	AAAA C
ATO:	3771 03 918	396	30.173	57.405	21.257	1.00 46.42	AAAA C
ATOH	3770 CD GUH	396	29.817	55.991	20.840	1.00 55.21	AAAA C
ATOM	3773 021 311	396	28.935	55.421	21.312	1.00 61.17	AAAA O
ATO!!	3774 (882 35)	396	30.528	55.411	19.971	1.00 55.79	II AAAA
ATOL	3777 0 320	396	29.974	59.224	24.458	1.00 49.64	AAAA C
ATOM	ayya o am	396	29.407	60.287	24.113	1.00 51.63	AAAA O
HOTA	3779 N ASN	397	29.717	58.681	25.633	1.00 48.95	AAAA II
ATOH	3791 TA ASH	397	28.783	59.196	26.632	1.00 51.72	AAAA C
ATOH	3792 TB ASH	397	27.969	57.959	27.093	1.00 35.94	AAAA C
ATO:	3793 TG ASN	397	27.231	57.439	25.860	1.00 49.09	AAAA C
ATON	3794 CD1 ASH	397	26.591	58.304	25.229	1.00 49.32	AAAA O
ATOH:	3788 ::D2 A3H	397	27.258	56.175	25.431	1.00 43.31	AAAA 11
ATO:	3799 C Asii	397	29.367	59.945	27.800	1.00 52.98	AAAA C
ATON	3789 O ASH	397	28.586	60.344	28.627	1.00 53.33	AAAA O
ATOU	3790 H LEV	358	30.682	59.990	29.001	1.00 55.73	AAAA II
ATOH	3790 CA LEU	398	31.312	60.550	29.179	1.00 52.12	AAAA C
ATOH	3793 CB LEU	338	32.827	60.388		1.00 48.47	AAAA C
ATOH	3794 CG LEU	398	33.606	60.283	30.460	1.00 41.81	AAAA C
ATOH	3795 CD1 LEU	398	33.417	58.939	31.136	1.00 40.35	AAAA C
HOTA	3796 CD2 LEU	398	35.070	60.608	30.082	1.00 39.03	AAAA C
HOTA	3797 C LEU	398	30.923	61.995	29.353	1.00 52.35	AAAA C
ATOH	3798 O LEU	398	31.422	62.909	28.681	1.00 49.91	AAAA O
ATOH	3799 N GLN	399	30.241	62.225	30.469	1.00 58.76	AAAA N
HOTA	3801 CA GLN	399	29.688	63.558	30.796	1.00 60.03	AAAA C
ATOH	3802 CB GLN	399	28.236	63.331	31.262	1.00 59.55	AAAA C
ATOH	3803 CG GLH	399	27.235	63.962	30.316	1.00 73.07	AAAA C
ATOH	3804 CD GLii	399	25.944	63.146	30.340	1.00 78.39	AAAA C
HOTA	3805 OE1 GLH	300	25.097	63.455	31.194	1.00 71.79	AAAA O
ATOH	3806 NE2 GLN	399	25.856	62.158	29.440	1.00 69.88	AAAA II
ATOH	3809 C GLN	399	30.490	64.252	31.888	1.00 54.49	AAAA C
ATOH	3910 O GLN	399	30.528	65.477	32.068	1.00 51.96	AAAA O
ATOH	3811 N GLN	490	31.058	63.389	32.734	1.00 50.44	AAAA N
ATOH	3813 CA GLN	400	31.938	63.948	33.756	1.00 53.83	AAAA C
ATO(1	3814 CB GLN	400	31.215	64.314	35.049	1.00 54.97	AAAA C
ATOH:	3815 CG GLN	400		63.150	35.887	1.00 58.99	AAAA C
ATOH	3816 CD GLH	100		63.430	37.389	1.00 65.82	AAAA C
HOTA	3817 OE1 GLN	400		64.502	37.962	1.00 68.10	AAAA O
ATOH	3819 NEC GLN	100		62.444	38.222	1.00 55.35	AAAA II
ATON	3821 C GLN	400		63.008		1.00 52.08	AAAA C
HOTA	3822 O GLN	100				1.00 51.90	AAAA O
HOTA	3823 II LEU	401	_			1.00 49.58	AAAA N
ATOH	3825 CA LEU	401				1.00 49.57	AAAA C
ATOH	3806 CB LEU	401				1.00 47.94	AAAA C
HOTA	3827 CG LEU	401				1.00 46.61	AAAA C
ATOH	3828 CD1 LEU	401				1.00 39.09	AAAA C
ATOH	3829 CDC LEU	401	36.919			1.00 40.72	AAAA C
ATOH:	3830 C LEU	401				1.00 51.23	AAAA C
HOTA		401				1.00 49.06	AAAA O
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ATCH! 3830 11 TRE 492 35.297 63.140 37.699 1.00 54.58 AAAA II 3634 ATOH CA TRP 402 34.975 63.090 39.097 1.00 59.76 AAAA C ATCH 3835 CB TRP 402 39.933 36.279 62.953 1.00 59.56 AAAA C **ATOH** 3836 C/3 TRP 402 36.971 39.737 1.00 58.17 61.624 AAAA C ATOH 3837 CD2 TRP 402 37.981 38.784 61.243 1.00 53.18 AAAA C 39.002 HOTA 3838 CE2 TRP 402 38.286 59.897 1.00 56.61 AAAA ATOH 3839 CE3 TRP 402 37.764 38.643 61.917 1.00 43.25 AAAA 3840 **ATOH** CD1 TRP 402 36.719 60.517 40.459 1.00 53.50 AAAA C 3841 HEL TRP 1.00 57.66 ATOH: 402 37.488 59.467 40.032 II AAAA 3843 ATO!! CZZ TRP 402 39.212 59.160 38.249 1.00 51.44 AAAA C ATO! 3844 CZ3 TRP 402 39.546 61.199 37.026 1.00 53.69 AAAA C 3845 CH2 TRP 402 HOTA 39.820 59.857 37.263 1.00 50.75 AAAA C 3846 TRP 402 ATO!1 34.223 64.389 39.429 1.00 64.09 AAAA C HOTA 3847 TRP 402 34.408 65.449 38.808 1.00 61.98 AAAA O 3848 11 ASP 403 33.503 HOTA 64.418 40.551 1.00 68.85 AAAA N 3850 CA ASP ATO!! 403 32.947 65.668 41.068 1.00 67.83 AAAA C 3851 ASP 403 ATO! CB 31.918 65.343 42.151 1.00 72.19 AAAA 3852 ASP 403 CG HOTA 30.853 66.417 42.306 1.00 73.08 AAAA C 3853 ODI ASP 103 ATOU 31.177 67.625 42.297 1.00 71.67 AAAA O **ATOI**1 3854 OD2 ASP 403 29.693 65.979 42.454 1.00 75.08 AAAA O ATON 3855 ASP 403 34.005 66.607 41.607 1.00 66.63 AAAA C **ATOH** 3856 О ASP 403 34.245 66.672 42.811 1.00 67.18 AAAA O HOTA 3857 11 TRP 404 34.449 67.588 40.846 1.00 69.29 AAAA H ATOH: 3859 CA TRP 404 35.412 68.588 41.291 1.00 77.11 AAAA ¢ 3860 ATOH CB TRP 404 35.859 69.409 40.063 1.00 79.10 AAAA C HOTA 3861 CG TRE 494 36.504 68.509 39.047 1.00 82.59 AAAA C ATOH: 3862 CD2 TRP 404 37.294 67.346 39.322 1.00 84.82 AAAA C HOTA 3863 CE2 TRP 404 37.586 66.813 38.081 1.00 84.56 AAAA C ATO!! 3864 CE3 TRP 404 37.703 66.710 40.506 1.00 80.95 AAAA С **ATOH** 3865 CD1 TRP 404 36.460 68.622 37.694 1.00 83.37 AAAA C **ATOI1** 3866 NE1 TRP 404 37.165 67.617 37.111 1.00 80.33 AAAA N NOTA 3868 CS2 TRP 404 38.477 37.982 65.562 1.00 85.91 AAAA ATO: 1 3869 003 TRP 404 38,471 65.573 40.392 1.00 86.36 AAAA ATOM 3870 CH2 TRP 404 38.860 65.051 39.133 1.00 85.05 AAAA ATO: 3671 TRP 404 35.034 69.517 42.420 1.00 81.60 AAAA ATOH 3872 TRP 404 70.709 35.387 42.504 1.00 84.57 AAAA O ATOH 3873 11 23P 105 34.281 69.063 43.393 1.00 84.45 AAAA !! 3875 ATON CA AS? 405 33.771 69.861 44.495 1.00 87.48 AAAA C ATOI: 3875 CB ASP 105 32.352 70.365 44.262 1.00 88.04 AAAA C 3877 ATON ŢĞ 405 ASP 32.274 71.612 43.409 1.00 92.54 AAAA C ATOL 3878 ASP 405 33.306 72.285 43.207 1.00 94.82 AAAA O 3979 ATO!! 002 ASP 405 31.130 71.954 42.955 1.00 95.26 AAAA C 3980 ATO!! ASP 405 33.730 68,906 45.693 1.00 87.90 AAAA ROH 3881 ASP 405 69.224 34.245 46.743 1.00 92.19 AAAA O :: ATOH: 3882 ALA 106 33.239 45.460 1.00 84.45 AAAA II CA CB ATOH 3884 ALA :06 33.176 66.671 46.451 1.00 82.57 AAAA C ALA ALA ATOH 3895 106 31.943 68.905 AAAA C 46.133 1.00 76.32 ATOH 3886 406 34.445 68.840 1.00 85.77 45.459 AAAA ATOH 3997 0 ALA 405 34.470 64.923 66.073 47.185 45.577 1.00 89.39 1.00 83.74 AAAA O ATOH 3929 :: ARG 407 35.433 AAAA :: ATOH 3890 ARG 107 65.151 CA. 36.541 45.400 1.00 79.60 AAAA C 407 **ATOH** 3891 C3 AR/3 64.140 36.165 1.00 77.94 44.297 AAAA C **HOTA** 3892 ARG 407 C:3 35.457 62,950 44.921 1.00 81.91 AAAA C ATOH 407 3893 CD ARG 35.362 61.688 44.113 1.00 86.97 AAAA C ATOH 3894 ARG 407 HE 36.281 60.660 44.607 1.00 86.94 AAAA N HOTA 3896 C 407 ARG 37.564 60.583 44.279 1.00 92.14 AAAA C NHI ARG HOTA 3897 407 38.169 61.441 43.469 1.00 97.06 AAAA N ATOH 3900 DH2 ARG 407 38.309 59.616 44.770 1.00 96.33 AAAA H HOTA 3903 С ARG 407 37.880 65.749 45.048 1.00 76.72 AAAA C ATO: 3904 0 ARG 407 37.989 66.774 44.410 1.00 77.47 AAAA O ATOL 3905 ASN 408 38.958 65.081 45.453 1.00 75.75 AAAA N 3907 ATOH CA ASN 408 40.311 65.556 45.173 1..00 73.79 AAAA C HOTA 3908 CB ASN 498 40.938 66.240 46.388 1.00 74.45 AAAA C HOTA 3909 408 CG **ASN** 41.986 67.242 45.947 1.00 82.51 AAAA C 3910 NOTA OD1 ASN 408 41.813 68.429 46.240 1.00 90.33 AAAA O ATO11 3911 ND2 ASM 108 43.028 66.821 45.253 1.00 84.46 M AAAA N ATOM 3914 \mathbf{c} ASH 408 41.257 64.468 44.654 1.00 65.97 AAAA C ATOH 3915 0 ASN 408 41.251 63.374 45.151 1.00 63.82 AAAA O ATOH 3916 М LEU 409 42.041 64.793 43.650 1.00 61.41 AAAA N 3918 ATON CA LEU 409 42.896 63.872 42.947 1.00 60.90 AAAA C NOTA 3919 CB LEU 409 42.153 63.250 41.768 1.00 62.98 AAAA C **ATOH** 3920 CG LEU 409 42.992 62.553 40.704 1.00 59.77 AAAA C ATO/1 3921 CDI LEU 409 43.488 61.205 41.197 1.00 54.06 AAAA C HOTA 3922 CD2 LEU 409 42.094 62.445 39.486 1.00 55.74 AAAA C **ATON** 3923 C LEU 109 44.151 64.599 42.485 1.00 61.19 AAAA C ATOH 3924 O LEU 109 44.141 42.370 65.809 1.00 60.64 AAAA O **ATOM** 3925 H THR 410 45.281 63.903 42.424 1.00 63.74 AAAA N ATO! 3927 CA THR 410 46.588 64.462 42.131 AAAA C 1.00 60.44 ATOH 3928 CB THR 410 47.454 64.676 43.385 1.00 67.08 AAAA C ATOH 3929 OG1 THR 410 46.870 65.746 44.157 1.00 74.29 AAAA O **ATOH** 3931 CG2 THR 410 48.909 65.103 43.162 1.00 48.56 AAAA C ATOH 3932 THR 410 C 47.426 63.565 41.218 1.00 56.62 AAAA 410 ATOH 3933 0 THR 47.382 41.317 62.354 1.00 54.99 AAAA O ATO: 3934 11 ILE 411 48.977 64.245 40.288 1.00 53.97 II AAAA 3936 HOTA CA ILE 411 48.897 63.562 AAAA C 39, 291 1.00 53.29

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ATMI ATMI ATMI ATMI ATMI ATMI ATMI ATMI	3945 3943 3944 3944 3939 3939 3939			411 411 411 411 411 411 412 412	49.409 49.216 46.911 46.322 50.319 50.656 51.073 52.434 53.071	63.854 63.128 63.489 63.547 64.018 65.179 63.182 63.502	36.338 39.568 39.291 40.270 40.689	1.00 30.86 1.00 40.83 1.00 38.51 1.00 55.38 1.00 57.59 1.00 54.26 1.00 54.46	\$ AAAA C AAAA C AAAA C AAAA C AAAA O AAAA II AAAA C
ATOII ATOII ATOII ATOII ATOII ATOII	3947 3949 3950 3951 3953 3954	05 0 0 11 CA 03 0	SER SER SER ALA ALA ALA	412 412 412 413 413 413	53.756 53.326 54.081 53.254 54.064 55.334 53.301	62.536 63.910 64.876 63.124 63.402 62.520 63.078	42.434 39.523 39.527 38.438 37.281 37.365	1.00 67.12 1.00 55.52 1.00 55.04 1.00 50.12 1.00 50.01	AAAA C AAAA II AAAA C AAAA II AAAA C AAAA C
ATOII ATOII ATOII ATOII ATOII ATOII	3956 3957 3959 3960 3961 3961	O II GA C O II GA	ALA GLY GLY GLY GLY LYS LYS	413 414 414 414 414 415 415	52.495 53.675 53.057 52.017 51.684 51.385 50.289	62.168 63.690 63.454 64.524 65.370 64.406 65.317	35.998 34.895 33.607 33.294 34.114 32.138 31.759	1.00 48.81 1.00 47.92 1.00 51.75 1.00 52.77 1.00 53.23 1.00 56.31 1.00 52.49	AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C
HOTA HOTA HOTA HOTA HOTA HOTA	3965 3966 3967 3968 3969 3973 3974	0 0 0 0 0 0 0 0 0	LYS LYS LYS LYS LYS LYS LYS	415 415 415 415 415 415	50.884 51.198 52.288 52.785 52.426 49.110	66.358 65.855 66.691 66.151 67.032 64.576 63.337	30.833 29.429 28.765 27.441 26.284 31.155 31.036	1.00 50.94 1.00 54.39 1.00 53.96 1.00 56.01 1.00 66.36 1.00 50.04 1.00 49.77	AAAA C AAAA C AAAA C AAAA II AAAA II AAAA C
HOTA HOTA HOTA HOTA HOTA HOTA HOTA	3975 3977 8 3977 8 3998 3998 3998 3998	II CA CB CG	HET HET HET HET HET HET HET HET	416 416 416 416 416 416 416 416	48.091 46.890 45.629 45.836 44.501 44.002 46.623 46.963	65.353 64.734 65.186 65.880 65.636 67.366 65.064 66.137	30.771 30.186 30.949 32.273 33.517 33.690 28.723 28.247	1.00 48.34 1.00 46.77 1.00 42.79 1.00 40.91 1.00 56.20 1.00 35.94 1.00 40.40 1.00 34.94	AAAA N AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C
ATOH ATOH ATOH ATOH ATOH ATOH ATOH	3999	11 CA CB CCI CCI CCI CD2	TYR TYR TYR TYR TYR TYR TYR	417 417 417 417 417 417 417	45.893 45.355 46.156 45.583 45.730 45.196 44.894	64.169 64.387 63.471 63.430 64.501 64.429 62.321	28.104 26.765 25.831 24.428 23.511 22.253 24.005	1.00 38.49 1.00 39.50 1.00 39.48 1.00 39.29 1.00 34.56 1.00 36.91	AAAA O AAAA H AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C
ATOH ATOH ATOH ATOH ATOH ATOH ATOH ATOH	3993 3994 3994 3996 3996 4000 4001	082 00 00 00 00 00 00 00 00 00 00 00 00 00	TYR TYR TYR TYR TYR PHE PHE	417 417 417 417 417 418 418	44.379 44.535 44.053 43.853 43.376 43.968 41.644 40.772	62.241 63.292 63.361 64.065 62.974 64.971 64.701 65.657	22.722 21.872 20.552 26.699 27.135 26.100 25.910 26.730	1.00 38.80 1.00 44.20 1.00 58.10 1.00 44.18 1.00 42.19 1.00 45.84 1.00 45.87	AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C
ATOH ATOH ATOH ATOH ATOH ATOH ATOH	4003 4004 4005 4006 4007 4008	CG CD1 CD2 CE1 CE2 CG	PHE PHE PHE	418 418 418 418 418 418 418	40.675 41.552 39.638 41.402 39.486 40.358 41.251	65.264 65.685 64.417 65.291 64.023 64.454 64.730	28.177 29.132 28.544 30.440 29.845 30.801 24.440	1.00 43.44 1.00 38.43 1.00 51.21 1.00 46.44 1.00 46.63 1.00 44.68	AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C
HOTA HOTA HOTA HOTA HOTA HOTA HOTA	4009 4010 4012 4013 4014 4015 4016 4019		PHE ALA ALA ALA ALA PHE PHE	418 419 419 419 419 419 420 420	41.375 40.554 40.015 41.090 38.837 38.871 37.829	65.762 63.713 63.793 63.562 62.846 61.629 63.398	23.812 23.936 22.607 21.555 22.366 22.557 21.618	1.00 47.60 1.00 43.06 1.00 39.21 1.00 30.88 1.00 41.77 1.00 36.08 1.00 40.41	AAAA O AAAA H AAAA C AAAA C AAAA C AAAA O AAAA O
ATOH ATOH ATOH ATOH ATOH ATOH ATOH	4019 4020 4021 4022 4023 4024 4025	CB CG CD1 CD2 CE1 CE2	PHE PHE PHE PHE PHE	420 420 420 420 420 420 420 420	36.742 37.157 37.832 39.221 37.006 39.783 37.572 38.964	62.621 61.430 61.909 61.987 62.345 62.496 62.833 62.928	21.070 20.180 18.912 18.751 17.871 17.567 16.725 16.549	1.00 40.03 1.00 45.54 1.00 54.18 1.00 49.23 1.00 47.65 1.00 46.00 1.00 51.10	AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C
ATOH ATOH ATOH ATOH ATOH ATOH ATOH	4026 4027 4028 4030 4031 4032 4033	COCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO	PHE PHE ASN ASN ASN ASN	420 420 421 421 421 421 421	35.762 35.352 35.459 34.477 35.183 36.407 36.426	62.146 60.991 63.024 62.960 63.276 62.401 61.147	22.126 22.215 23.049 24.112 25.449 25.654 25.714	1.00 41.65 1.00 38.35 1.00 45.35 1.00 46.86 1.00 43.60 1.00 47.90	AAAA C AAAA N AAAA C AAAA C AAAA C AAAA C
ATOH ATOH ATOH	4037		ASH ASH ASN	421 421 421	37.541 33.432 33.617	63.101 64.069 65.233	25.732 23.835 24.237	1.00 37.46 1.00 47.83 1.00 38.85	AAAA N AAAA C AAAA O

ATMI INTA INTA INOTA INOTA	4//39 H PRO 4//40 CD PRO 4//41 CA PRO 4//42 CB PRO 4//43 CG PRO 4//44 C PRO	422 422 422 422 422 422	32.213 31.463 30.731 30.947	52.423	2.372 1 2.605 1 1.446 1 1.606 1	1.00 47.86 1.00 44.11 1.00 47.85 1.00 44.86 1.00 43.01 1.00 51.16	AAAA II AAAA C AAAA C AAAA C AAAA C	
ATOH ATOH ATOH ATOH ATOH	4045 O PRO 4046 II LYS 4048 CA LYS 4049 CB LYS 4050 CG LYS	422 423 423 423 423	30.223 (30.320 (29.431 (28.556 (56.486 2. 54.487 2. 54.908. 2. 53.721 2.	3.744 1 4.774 1 5.865 1 6.360 1	1.00 48.54 1.00 52.90 1.00 58.82 1.00 52.93	AAAA C AAAA C AAAA C AAAA C	
HOTA HOTA HOTA HOTA	4051 CD LYS 4052 CE LYS 4053 NC LYS 4057 C LYS 4058 O LYS	423 423 423 423 423	26.743 (26.030 (25.949 (30.158 (52.448 24 53.374 24 54.748 24 55.482 21	4.996 1 4.021 I 4.614 1 7.071 1	.00 73.79 .00 77.06 .00 64.99 .00 57.43	AAAA C AAAA C AAAA N AAAA C AAAA O	
HOTA HOTA HOTA HOTA HOTA	4059 N LEU 4061 CA LEU 4062 CB LEU 4063 CG LEU 4064 CD1 LEU	424 424 424 424 424	31.425 6 32.261 6 33.463 6 34.390 6	55.859 26 66.162 26 55.250 28 55.748 29	6.862 1 8.017 1 8.237 1 9.370 1	.00 55.95 .00 57.07 .00 49.16 .00 68.27 .00 60.66	AAAA N AAAA C AAAA C AAAA C AAAA C	
HOTA HOTA HOTA HOTA HOTA	4065 CD2 LEU 4066 C LEU 4067 O LEU 4068 H CYS 4070 CA CYS	424 424 424 425 425	32.709 6 33.696 6 31.995 6 32.342 6	7.585 27 7.861 27 8.488 28	7.878 1 7.201 1 8.492 1 8.406 1	.00 60.35 .00 56.29 .00 59.98 .00 58.76 .00 60.39	AAAA C AAAA C AAAA O AAAA II AAAA C	
HOTA HOTA HOTA HOTA HOTA HOTA	4071 C CYS 4072 O CYS 4073 CB CYS 4074 SG CYS 4075 II VAL 4077 CA VAL	425 425 425 425 426 426	34.288 6 31.249 7 29.916 7 34.529 7	9.665 29 0.644 29 1.303 28 0.953 28	9.831 1 9.214 1 9.086 1 9.102 1	.00 62.59 .00 64.45 .00 68.23 .00 81.03 .00 65.31	AAAA C AAAA O AAAA C AAAA S AAAA N AAAA C	
HOTA HOTA HOTA HOTA HOTA	4078 CB VAL 4079 CG1 VAL 4080 CG2 VAL 4081 C VAL 4082 O VAL	426 426 426 426 426	36.644 7 36.715 7 35.962 7 36.105 7	2.022 27 1.413 25 3.365 27 1.711 29	.310 1 .925 1 .239 1 .757 1	.00 66.66 .00 62.49 .00 60.92 .00 65.99	AAAA C AAAA C AAAA C AAAA C AAAA C	
ATOH ATOH ATOH ATOH ATOH	4093 H SER 4095 CA SER 4096 CB SER 4097 OG SER 4099 C SER	427 427 427 427 427	35.090 7 35.091 7 33.685 7 34.088 7 35.515 7	2.361 30 2.927 31 3.499 31 4.660 32 1.972 32	.267 1 .599 1 .864 1 .098 1 .701 1	.00 67.67 .00 66.85 .00 61.16 .00 67.05 .00 64.24	AAAA N AAAA C AAAA C AAAA O AAAA C	
ATOL: ATOL: ATOL: ATOL: ATOL: ATOL:	4090 O SER 4091 H GLU 4093 CA GLU 4094 CB GLU 4095 CB GLU 4096 CD GLU	427 428 428 428 428 428	34.965 7 35.384 6 34.594 6 33.115 6	0.771 32 9.753 33 9.495 33 8.560 33	.618 1 .585 1 .240 1 .537 1	.00 63.66 .00 58.75 .00 63.39 .00 68.67 .00 66.59	AAAA O AAAA N AAAA C AAAA C AAAA C AAAA C	
ATOLL ATOLL ATOLL ATOLL ATOLL	4097 0E1 GLU 4099 0E2 GLU 4099 0 GLU 4100 0 GLU 4101 N ILE	428 428 428 428 428	32.729 6 32.581 6 36.870 6 37.671 6 37.265 6	7.522 35 9.638 35 9.485 33 9.696 34 9.262 32	.722 1. .517 1. .429 1. .307 1.	.00 81.62 .00 70.97 .00 61.63 .00 62.03	AAAA C AAAA O AAAA C AAAA O AAAA N	
HOTA HOTA HOTA HOTA HOTA	4103 CA ILE 4104 CB ILE 4105 CG2 ILE 4106 CG1 ILE 4107 CD1 ILE 4108 C ILE	429 429 429 429 429 429	38.759 68 40.257 68 37.968 67 38.038 67	3.933 30 3.915 29 7.719 29 7.555 28	.263 1. .895 1. .794 1. .285 1.	.00 61.09 .00 59.32 .00 45.93 .00 57.66 .00 53.49	AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C	
HOTA HOTA HOTA HOTA HOTA	4109 O ILE 4110 H TYR 4112 CA TYR 4113 CB TYR 4114 CG TYR		40.592 70 38.987 71 39.729 72 39.180 73	0.017 32 384 32 2.543 32 3.822 32	.867 1. .200 1. .719 1.	00 61.99 00 61.28 00 65.34 00 68.10 00 71.02 00 75.98	AAAA C AAAA H AAAA C AAAA C AAAA C	
ATOH ATOH ATOH ATOH HOTA	4115 CD1 TYR 4116 CE1 TYR 4117 CD2 TYR 4118 CE2 TYR 4119 CE TYR 4120 OH TYR	430 430 430 430 430 430	38.953 73 40.810 74 41.155 74 40.221 74	.977 28. .401 30. .575 28. .359 27.	.270 1. .260 1. .937 1.	00 77.60 00 75.72 00 75.95 00 74.81 00 78.51 00 85.40	AAAA C AAAA C AAAA C AAAA C AAAA C AAAA C	
ATOH ATOH ATOH ATOH ATOH	4122 C TYR 4123 O TYR 4124 N ARG 4126 CA ARG 4127 CB ARG	430 430 431 431 431	39.779 72 40.654 73 38.819 72 38.747 72 37.348 71	.634 34. .321 34. .017 34. .043 36.	241 1. 758 1. 907 1. 356 1.	00 63.72 00 58.26 00 65.53 00 68.15 00 73.32	AAAA C AAAA O AAAA II AAAA C AAAA C	
ATOH ATOH ATOH ATOH ATOH ATOH	4129 CG ARG 4129 CD ARG 4130 NE ARG 4132 CZ ARG 4133 NH1 ARG 4136 NH2 ARG	431 431 431 431 431 431	37.270 73 37.698 73 36.835 73 35.610 72	.279 38. .472 40. .258 41. .872 40.	860 1. 258 1. 259 1. 872 1.	00 82.99 00 88.39 00 92.48 00 94.93 00 87.40	AAAA C AAAA C AAAA C AAAA C AAAA N	
HOTA HOTA HOTA HOTA	4139 C ARG 4140 O ARG 4141 H MET 4143 CA HET	431 431 432 432	39.718 70 40.637 71 39.541 69	.986 36. .292 37. .791 36.	877 1. 629 1. 305 1.	00 95.17 00 67.75 00 66.74 00 63.87 00 64.40	AAAA C AAAA C AAAA II AAAA C	

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ATM:	4144 UB HET	432	40.23	7 67.523	35.71	9 1.90 54.25	
AT/30	4145 CG HET	432	41.25	66.426			AAAA C AAAA C
ATON ATON			40.829				AAAA S
ATOH			41.583 41.891				AAAA C AAAA C
HCTA			42.530	68.992	37.65	3 1.00 65.88	AAAA O
ATOU			42.331 43.623				AAAA N AAAA C
ATOH	4153 CB GLU	433	43.704	71.506			AAAA C
ATOH ATOH			44.121 44.623				AAAA C
ATOH			44.718				AAAA C AAAA O
ATON			44.905	72.050	31.043	1.00 88.26	AAAA O
ATOH ATOH	4158 C GLU 4159 O GLU		44.016 45.133				AAAA C AAAA O
ATOH	4160 II GLU	434	43.178	72.120	37.280	1.00 72.93	II AAAA
HOTA HOTA	4162 CA GLU 4163 CB GLU		43.505 42.458				AAAA C
ATOM	4164 CG GLU		41.191				AAAA C AAAA C
HOTA	4165 CD GLU 4166 OE1 GLU		40.181				AAAA C
ATON	4167 OE2 GLU		39.521 40.080				AAAA O AAAA O
ATOH	4168 C GLU		43.675	71.886	39.632	1.00 71.46	AAAA C
ATOH ATOH	4169 O GLU 4170 H VAL	434 435	44.728 42.670				AAAA O
ATOH	4172 CA VAL	435	42.711				AAAA C
ATOH ATOH	4173 CB VAL 4174 CG1 VAL	435 435	41.451				АААА С
ATOI	4175 CG2 VAL	435	41.547 40.203				AAAA C AAAA C
ATON	4176 C VAL	435	43.939	69.253	41.018	1.00 60.74	AAAA C
HOTA	4177 O VAL 4178 H THR	435 436	44.607 44.282	69.165 68.506			О АААА И АААА
ATOR	4180 CA THR	436	45.335	67.516	39.936	1.00 56.36	AAAA C
ATON ATON	4181 CB THR 4182 OG1 THR	436 436	45.199 44.913				AAAA C
ATOM:	4184 CG2 THR	436	44.108	67.283 65.526	37.503 38.901		AAAA C AAAA C
ATOM	4195 C THR	436 136	46.701	68.184	39.930	1.00 60.55	AAAA C
ATOM: ATOM	4196 O THR 4197 N BLY	436 437	47.714 46.835	67.490 69.496	40.024 39.835	1.00 60.61 1.00 60.65	0 AAAA 11 AAAA
ATC!:	4189 CA 3LY	437	48.100	79.164	39.749		AAAA C
ATOH: ATOH:	4193 C 3LY	437 437	48.800 49.983	69.964 79.254	38.424 38.245	1.90 64.78 1.90 62.79	AAAA C
ATG:	4192 N THR	438	48.112	69.387	37.390		O AAAA !! AAAA
ATO:: ATO::	4194 CA THR 4195 CB THR	138 138	48.731	69.169	36.076		AAAA C
ATOH	4196 OG1 THR	138	47.967 46.600	68.027 68.385	35.411 35.731	1.90 66.87 1.90 62.22	AAAA C AAAA O
ATO:	4199 TG1 THR	438	48.209	66.659	36.019	1.00 68.74	AAAA C
AT M: AT M:	4199 C THR 4200 O THR	438 438	48.590 49.003	70.415 70.543	35.220 34.070	1.00 66.14 1.00 69.05	D AAAA O AAAA
ATON	4201 H LYS	139	48.089	71.491	35.822	1.00 67.37	H AAAA H
ATOH ATOH	4203 CA LYS 4204 CB LYS	439 439	47.927 47.114	72.757 73.708	35.154	1.00 71.08 1.00 69.23	AAAA C AAAA C
ATON	4205 CG LYS	139	46.677	74.938	35.265	1.00 77.25	AAAA C
HOTA	4206 OD LYS 4207 OE LYS	439 439	45.832 44.385	75.942 75.475	36.014 36.192		AAAA C
ATOH:	4208 NZ LYS	139	43.667	76.431	37.100	1.00 87.39 1.00 93.85	AAAA C AAAA N
ATOH ATOH	4212 C LYS 4213 O LYS	439	49.249	73.396	34.752	1.00 73.01	AAAA C
ATON	4213 O LYS 4214 N GLY	439 440	49.996 49.517	73.986 73.453	35.541 33.441	1.00 74.60 1.00 73.33	О АААА И АААА
IICTA	4216 CA GLY	440	50.733	74.167	33.014	1.00 71.39	AAAA C
HOTA HOTA	4217 C GLY 4218 O GLY	440 440	51.716 52.684	73.204 73.650	32.389 31.822	1.00 71.20 1.00 72.70	AAAA C AAAA O
HCTA .	4219 N ARG	441	51.445	71.908	32.436	1.00 72.99	M AAAA
HOTA	4221 CA ARG 4222 CB ARG	441 441	52.343 52.617	70.945 69.740	31.831	1.00 74.12	AAAA C
HOTA	4223 CG ARG	441	51.847	69.695	32.716 34.003	1.00 69.44 1.00 63.34	AAAA C AAAA C
HOTA	4224 CD ARG 4225 NE ARG	441	52.060	68.314	34.595	1.00 67.64	AAAA C
ATOH	4227 CS ARG	441 441	52.244 52.326	68.395 67.357	36.030 36.831	1.00 61.00 1.00 59.21	AAAA N AAAA C
HOTA	4228 NH1 ARG	441	52.258	66.117	36.395	1.00 60.57	AAAA N
ATOH ATOH	4231 HH2 ARG 4234 C ARG	441 441	52.468 51.760	67.596 70.446	38.128 30.511	1.00 72.94 1.00 73.50	AAAA N AAAA C
ATOH	4235 O ARG	441	52.195	69.424	30.012	1.00 74.73	AAAA O
ATOH ATOH	4236 H GEH 4239 CA GEH	442 442	50.732 49.959	71.114	30.043	1.00 74.69	II AAAA
ATOH	4239 CB GLII	112	49.959	70.646 70.875	28.914 29.126	1.00 75.13 1.00 68.73	AAAA C AAAA C
ATOH	4240 CG GUI	442	47.669	69.576	29.195	1.00 71.20	AAAA C
ATOH HOTA	4241 CD GLN 4242 OE1 GLN	442 442	47.623 47.714	69.028 67.822	30.607 30.868	1.00 70.98 1.00 78.66	AAAA C AAAA O
ATOH	4243 NE2 GLN	442	47.477	69.907	31.584	1.00 66.86	K AAAA
ATOH ATOH	4246 C GLII 4247 O GLN	442 442	50.326 50.227	71.359 72.569	27.627 27.530	1.00 77.69 1.00 75.57	AAAA C
HOTA	4248 H ALA	113	50.474	70.554	26.575	1.00 /5.5/	AAAA O AAAA N
HOTA	4250 CA ALA	443	50.643	71.148	25.236	1.00 82.95	AAAA C
UT:YI	4251 CB ALA	113	51.104	70.118	24.220	1.00 81.69	AAAA C

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ATOM:	4052 C ALA	443	49.259	71.706	04.950	1.00 83.73	AAAA C
HOTA	4053 O ALA	143	48.398				AAAA O
ATOH	4254 II LYS	444	48.914				II AAAA II
ATOIT	4256 CA LYS	444	47.559				AAAA C
ATOH	4257 CB LYS	444	47.426				AAAA C
	4258 CG LYS	444					
ATOH			46.673				AAAA C
ATOH	4259 CD LYS	444	45.883				AAAA C
ATOH	4260 CE LYS	444	46.390				AAAA C
ATOU	4261 HZ LYS	444	45.368	73.090	27.473	1.00 97.22	H AAAA H
ATOH	4265 C LYS	444	46.659	71.779	22.508	1.00 84.20	AAAA C
ATOH	4266 O LYS	444	45.428	71.901	22.635	1.00 85.63	AAAA O
ATOH	4267 H GLY	445	47.214				AAAA H
	4269 CA GLY	445	46.368				AAAA C
ATOH	4270 C GLY	445	45.903				AAAA C
ATO!							
ATOH	4271 O GLY	445	44.963				AAAA O
ATOH	4272 II ASP	446	46.300				M AAAA N
HOTA	4274 CA ASP	446	45.914			1.00 62.81	AAAA C
ATO:1	4275 CB ASP	446	46.754	68.552	25.873	1.00 55.24	AAAA C
ATOH	4276 CG ASP	446	48.213	68.169	25.801	1.00 54.07	AAAA C
ATOH	4277 OD1 ASF	446	48.693				AAAA O
ATOH	4278 OD2 ASP	446	49.091	68.595			AAAA O
	4279 C ASP	446	44.438	68.274	25.016	1.00 58.07	AAAA C
ATOH							
ATOH	4280 O ASP	446	43.610			1.00 55.59	AAAA O
ATOU	4291 N ILE	447	44.043	69.527	25.226	1.00 54.13	II AAAA N
ATO!!	4283 CA ILE	447	42.652	69.822	25.510	1.00 54.09	AAAA C
HOTA	4284 CB ILE	447	42.505	70.502	26.877	1.00 48.92	аааа с
ATOH	4285 CG2 ILE	447	41.030	70.663	27.182	1.00 41.02	AAAA C
ATOH	4286 CG1 ILE	447	43.211	69.621	27.932	1.00 52.36	AAAA C
HOTA	4287 CD1 ILE	447	43.468	70.329	29.237	1.00 48.47	AAAA C
HOTA	4288 C ILE	447	42.027	70.591	24.364	1.00 53.06	AAAA C
HOTA		447	41.718	71.772	24.423	1.00 56.08	AAAA O
ATOH	4290 II ASN	448	41.625	69.915	23.307	1.00 53.17	N AAAA
ATOH	4292 CA ASH	448	41.013	70.642	22.202	1.00 54.61	AAAA C
HOTA	4293 CB ASN	418	41.283	69.982	20.863	1.00 49.17	AAAA C
ATOH	4294 CG ASN	448	40.415	68.786	20.577	1.00 49.40	AAAA C
ATOH:	4295 OD1 ASH	448	39.287	68.977	20.113	1.00 52.34	AAAA O
ATON:	4296 HD3 ASH	449	40.990	67.622	20.871	1.00 52.49	AAAA II
ATOH	4299 C ASH	448	39.518	70.824	22.402	1.00 56.44	AAAA C
ATO:	4300 0 A311	118	38.916	69.974	22.939	1.00 55.83	AAAA O
		149					II AAAA
ATOI!			39.071	71.917	21.764	1.00 58.52	
ATOH	4303 CA THR	449	37.692	72.351	21.901	1.00 58.62	AAAA C
ATOH	4304 TB THR	449	37.497	73.945	22.169	1.00 55.90	AAAA C
ATO!!	4305 OG1 THR	449	37.913	74.495	20.943	1.00 68.89	O AAAA
ATOH:	4307 030 THR	449	38.354	74.352	23.310	1.00 59.06	AAAA C
ATOI!	4309 C THR	115	36.920	72.053	20.628	1.00 56.82	AAAA C
ATOH	4369 O THR	449	35.750	72.381	20.473	1.00 60.87	O AAAA O
ATOH	4310 H ARG	450	37.539	71.304	19.757	1.00 55.76	AAAA !!
ATOH	4312 CA ARG	450	36.827	70.935	18.507	1.00 54.66	AAAA C
ATOH	4313 CB ARG	450	37.945	71.179	17.377	1.00 48.33	AAAA C
ATO!!	4314 CG ARG	450	38.395	69.975	16.645	1.00 54.81	AAAA C
						1.00 44.92	
ATOLL		450	39.497	70.561	15.696		AAAA C
ATOH	4316 NE ARG	450	40.706	70.719	16.488	1.00 52.49	AAAA II
ATOH	4318 CD ARG	450	41.544	69.757	16.892	1.00 39.09	AAAA C
HOTA	4319 NH1 ARG	450	41.176	68.572	16.466		H AAAA
HOTA	4322 HH2 ARG	450	42.601	70.001	17.610	1.00 45.18	n aaaa
HOTA	4325 C ARG	450	36.267	69.553	18.557	1.00 56.82	AAAA C
ATO!1	4326 O ARG	450	35.186	69.303	17.992	1.00 58.15	AAAA O
ATO!!	4327 II ASII	451	36.800	68.583	19.324	1.00 56.66	AAAA H
HOTA	4329 CA ASH	451	36.107	67.311	19.434	1.00 50.27	AAAA C
ATOH	4330 CB ASH	451	36.725	66.127	18.760	1.00 48.54	AAAA C
ATOH	4331 CG ASH	451	38.243	66.143	18.764	1.00 60.51	AAAA C
ATOH	4332 OD1 ASH	451	38.779	66.279	19.855	1.00 53.45	AAAA O
		451				_	AAAA N
ATOH			38.707	65.976	17.506	1.00 54.88	
ATOH	1336 C ASII	451	35.849	66.854	20.869	1.00 52.97	AAAA C
ATOI:1	4337 O ASN	451	35.330	65.750	21.096	1.00 49.71	AAAA O
HOTA	4338 II ASII	452	36.126	67.668	21.851	1.00 51.98	II AAAA II
ATOM	4340 CA ASN	452	35.769	67.485	23.229	1.00 55.88	аааа с
ATOH:	4341 CB ASN	452	36.947	67.873	24.136	1.00 54.62	AAAA C
ATOH	4342 CG ASH	452	37.936	66.736	24.285	1.00 60.96	AAAA C
ATO!1	4343 OD1 ASN	452	37.646	65.633	24.735		AAAA O
ATOM	4344 HD2 ASH	452	39.153	67.098	23.855	1.00 56.75	AAAA N
ATOH	4347 C ASN	452	34.603	68.385	23.688		AAAA C
ATOM	4349 O ASH	452	34.785	69.629	23.657		AAAA O
HOTA		153				1.00 55.08	AAAA II
			33.444	67.813	23.985		
ATOM	4351 CA GLY	453	32.313	68.658	24.296	1.00 59.47	AAAA C
ATOH	4352 C GLY	453	31.500	69.269	23.174	1.00 64.95	AAAA C
ATON	4353 O GLY	153	30.302	69.603	23.276	1.00 65.71	AAAA O
ATOM:	4354 N GLU	454	31.910	69.109	21.910	1.00 67.44	AAAA N
ATOH	4356 CA GLU	154	31.266	69.543	20.690	1.00 63.63	AAAA C
ATOH	4357 CB GLU	454	31.739	68.818	19.401	1.00 53.71	AAAA C
ATOH	4358 CG GLU	454	32.348	67.430	19.738	1.00 49.50	AAAA C
ATOH	4359 CD GLU	454	32.368	66.620	18.454	1.00 54.61	AAAA C
ATOH	4360 OE1 GLU	154	31.368	66.637	17.702	0.01 54.10	AAAA O
HOTA	4361 OE2 GLU	454	33.417	66.003		0.01 54.10	AAAA O
					18.160		AAAA C
ATOH	4362 C GLU	151	29.762	69.301	20.767	1.00 65.41	AAAA C

		(
ATM1 4363 0 GEC 454 ATM1 4364 II ARG 455	29.022 70.089 20.169 1.00 67.86	, AAAA O
ATCH 4366 CA ARG 455	29.298 68.187 21.333 1.00 66.45 27.943 67.997 21.371 1.00 69.33	AAAA II
ATOH 4368 CG ARG 455	27.448 66.733 20.652 1.00 73.38 28.467 65.912 19.924 1.00 74.27	AAAA C AAAA C
ATOH 4370 HE ARG 455	27.775 64.740 19.240 1.00 79.54 27.301 63.638 20.052 1.00 86.31	AAAA C AAAA N
ATOH 4372 CE ARG 455 ATOH 4373 HH1 ARG 455	27.802 62.412 20.189 1.00 88.60 28.890 61.997 19.538 1.00 84.51	AAAA C AAAA N
ATOH 4376 HH2 ARG 455 ATOH 4379 C ARG 455	27.225 61.523 21.003 1.00 87.36 27.213 67.934 22.756 1.00 67.35	AAAA N AAAA C
ATOH 4380 O ARG 455 ATOH 4381 H ALA 456	26.423 67.025 22.961 1.00 66.26 27.499 68.879 23.623 1.00 66.52	AAAA O AAAA N
ATOH 4383 CA ALA 456 ATOH 4384 CB ALA 456	26.947 68.906 24.964 1.00 72.01 27.832 68.147 25.939 1.00 61.84	AAAA C
ATOI 4385 C ALA 456 ATOI 4386 O ALA 456	26.802 70.379 25.371 1.00 75.25 27.706 71.219 25.202 1.00 81.30	AAAA C
ATOH 4387 H SER 457 ATOH 4389 CA SER 457	25.653 70.720 25.939 0.50 71.91 25.431 72.095 26.358 0.50 69.64	O AAAA II AAAA
ATOH 4390 CB SER 457 ATOH 4391 OG SER 457	23.991 72.247 26.836 0.50 73.30	AAAA C AAAA C
ATOH 4393 C SER 457 ATOH 4394 O SER 457	26.418 72.510 27.437 0.50 69.27	AAAA C
ATOH 4395 II CTS 458	27.197 73.531 27.117 0.50 70.44	AAAA O AAAA N
ATOH 4398 C CTS 458	28.287 73.960 27.972 0.50 72.57 27.949 75.205 28.757 0.50 72.54	AAAA C AAAA C
ATOH 4400 CB CYS 458	27.965 75.128 29.606 0.50 76.63 29.527 74.171 27.089 0.50 75.38	AAAA O AAAA C
ATOH 4401 SG CYS 458 ATOH 4402 H ALA 459	30.844 73.032 27.490 0.50 72.18 28.607 76.306 28.441 0.50 70.13	AAAA S AAAA N
ATOH 4404 CA ALA 459 ATOH 4405 CB ALA 459	28.445 77.572 29.116 0.50 70.05 27.046 78.149 28.996 0.50 70.57	AAAA C AAAA C
ATOH 4406 C ALA 459 ATOH 4407 O ALA 459	28.826 77.461 30.601 0.50 70.13 29.080 78.556 31.154 0.50 69.96	AAAA C AAAA O
ATCH 4497 OT ALA 459 ATCH 4522 CI HAG 461	28.855 76.301 31.054 0.50 68.22 59.581 7.102 61.119 1.00 88.13	AAAA C
ATON 4524 02 NAG 461 ATON 4526 NO NAG 461	59.964 7.338 59.697 1.00 91.94 58.739 7.699 58.920 1.00 92.72	AAAA C II AAAA
ATOH 4529 07 HAG 461 ATOH 4529 07 HAG 461	58.400 9.020 58.999 1.00 96.97 58.879 9.774 59.726 1.00 98.62	AAAA C AAAA C
ATOH 4539 C3 HAG 461 ATOH 4534 C3 HAG 461	57.303 9.390 58.043 1.00100.60 60.725 6.225 59.085 1.00 94.77	AAAA C AAAA C
ATGH 4536 03 HAG 461 ATGH 4539 04 HAG 461	61.417 6.725 57.930 1.00 98.51 61.673 5.869 60.064 1.00 96.01	AAAA C AAAA C
ATOH 4540 04 MAG 461 ATOH 4542 05 MAG 461	62.661 4.821 59.484 1.00 99.20 61.359 5.529 61.474 1.00 95.13	AAAA O AAAA C
ATON 4545 OF NAG 461 ATON 4548 OF NAG 461	62.465	AAAA C
ATON 4544 05 NAG 461 ATON 4550 TI NAG 463	60.625 6.648 61.949 1.00 91.92 33.954 15.249 72.938 1.00 43.58	O AAAA O AAAA
ATON 4552 CC NAG 463 ATON 4554 NC NAG 463	31.644 15.292 73.412 1.00 43.62	AAAA C AAAA C
ATOH 4556 07 HAG 463 ATOH 4557 07 HAG 463	29.912 13.584 73.099 1.00 40.84	AAAA N
ATOH 4558 CB HAG 463 ATOH 4562 C3 HAG 463	28.975 12.694 72.394 1.00 35.47	AAAA C
ATOM 4564 03 MAG 463 ATOM 4566 C4 MAG 463	29.979 16.555 74.196 1.00 45.99	AAAA C AAAA O
ATOH 4568 04 HAG 463	32.117 17.617 74.171 1.00 50.36 31.596 18.919 73.891 1.00 53.97	AAAA C AAAA O
ATOH 4572 C6 HAG 463	33.589 17.477 73.725 1.00 48.50 34.490 17.996 74.742 1.00 49.34	AAAA C AAAA C
ATOH 4571 05 NAG 463	34.906 18.739 75.671 1.00 57.11 33.942 16.120 73.583 1.00 48.58	AAAA O AAAA O
ATOH 4576 C1 FUC 464 ATOH 4578 C2 FUC 464	34.544 19.954 76.083 1.00 81.45 35.179 21.173 75.463 1.00 86.35	AAAA C
ATO1 4579 02 FUC 464 ATO1 4582 C3 FUC 464	35.153 21.169 74.021 1.00 92.94 34.252 22.284 75.945 1.00 86.79	AAAA O AAAA C
ATOH 4594 03 FUC 464 ATOH 4596 C4 FUC 464	34.691 23.613 75.596 1.00 87.83 33.871 22.274 77.412 1.00 86.67	AAAA O AAAA C
ATOH 4588 OF FUC 464 ATOH 4590 C5 FUC 464	34.598 23.297 78.115 1.00 87.06 33.921 20.894 78.040 1.00 85.85	AAAA C
ATOI 4593 C6 FUC 464 ATOI 4592 C5 FUC 464	34.279 20.768 79.512 1.00 83.37 35.042 20.150 77.425 1.00 82.43	AAAA C AAAA O
ATOH 4597 C1 HAG 465 ATOH 4599 C2 HAG 465	31.575 19.813 74.940 1.00 64.68 31.267 21.207 74.437 1.00 69.57	AAAA C AAAA C
ATOH 4601 H2 NAG 465 ATOH 4603 C7 NAG 465	32.480 21.642 73.690 1.00 71.25 32.401 21.953 72.381 1.00 73.86	AAAA N AAAA C
ATOM 4604 07 NAG 465 ATOM 4605 C9 MAG 465	31.373 21.835 71.881 1.00 74.80 33.679 22.401 71.787 1.00 76.00	AAAA O
ATOH 4609 C3 NAG 465 ATOH 4611 O3 NAG 465	31.050 22.214 75.546 1.00 72.71 30.713 23.517 75.108 1.00 71.03	AAAA C AAAA C
ATON 4613 C4 NAG 465 ATON 4615 O4 NAG 465	30.035 21.654 76.560 1.00 75.71	AAAA C
ATOM 4617 C5 HAG 465 ATOM 4620 C6 HAG 465	30.498 20.238 76.977 1.00 75.45	AAAA C
22 193	29.461 19.647 77.930 1.00 75.64	AAAA C

AT' 41 4533 116 115/3 28.385 465 1.00 76.25 19.238 77.142 AAAA O ATOM 4619 05 UAG 30.514 465 1.00 71.44 19.425 75.807 AAAA O ATOL 4625 49.927 C1HAG 167 11.058 87.926 1.00 96.51 AAAA C 462 ATOR HAG 467 50.538 89.100 1.00 99.92 AAAA C 4609 49.662 TOTE 110 HAG 467 1.00101.79 12.898 89.458 AAAA N HOTA 4631 C7 HAG 467 49.299 13.021 90.759 1.00103.63 AAAA C HOTA 4632 07 HAG 467 49.541 12.267 91.586 1.00105.48 AAAA O HOTA 4633 C8 HAG 467 48.526 14.239 91.102 1.00105.02 AAAA C 4637 467 **ATOLI** NAG 51.967 12.134. 88.802 1.00101.03 AAAA C 4639 03 HAG 467 52.535 12,761 ATOL 89.949 1.00100.89 AAAA ٥ 4641 HAG 467 10.771 C4 ATOH 52.643 88.506 1.00101.15 AAAA 4643 04 HAG 467 ATO!! 54.967 10.834 88.441 1.00101.35 AAAA O 4545 HAG 467 ATO! **C5** 52.039 10.160 87.218 1.00100.16 AAAA C **ATOII** 4648 26 HAG 467 52.746 8.852 86.934 1.00 99.75 AAAA C 4651 06 HAG 467 52.088 7.704 87.302 1.00101.54 ATOH AAAA O ATOR 4547 05 HAG 467 50.671 9.918 87.503 1.00 98.59 AAAA O ATO! 4653 IIAG 469 Cl 55.375 46.143 66.863 1.00 48.45 AAAA C 46.993 ATOH 4655 HAG 469 56.601 66.861 1.00 50.42 аааа с 4657 HAG 469 57.106 47.015 ATO!! 65.451 1.00 51.50 II AAAA II HOTA 4659 C7 HAG 469 57.235 48.143 64.746 1.00 48.88 AAAA C 4660 07 NAG 469 ATOH 56.849 49.101 65.234 1.00 55.62 AAAA O 4561 C8 HAG HOTA 469 57.838 48.134 63.394 1.00 43.70 AAAA C ATO!! 4665 C3MAG 469 57.608 46.491 67.844 1.00 49.62 AAAA C 4667 11OTA 03 HAG 469 58.640 47.461 68.031 1.00 47.76 AAAA O ATOH 4669 C4 IIAG 469 56.843 46.263 69.172 AAAA C 1.00 48.47 4571 NAG ATCH 04 469 57.826 45,800 70.134 1.00 50.06 AAAA O NOTA 4672 **C5** HAG 469 55.847 AAAA C 45.130 68.959 1.00 50.81 4675 ATOH **C6** NAG 469 55.190 44.720 70.239 1.00 53.92 AAAA C 4678 06 HAG ATOH 469 54.829 45.551 71.193 1.00 56.25 AAAA O **ATOH** 4674 05 HAG 469 54.914 45.599 68.043 1.00 55.45 AAAA O 4579 **ATOH** Cl FUC 470 46.395 53.830 71.203 1.00 61.17 AAAA C HOTA 4681 C2 EUC 470 53.642 47.121 72.534 1.00 59.23 AAAA C 4682 02 FUC 470 ATOH 54.861 46.876 73.241 1.00 55.14 AAAA O 4685 FUC 470 ATO:: C3 53.421 49.429 1.00 58.39 71.757 AAAA 1597 ATOH C3 FUC 470 53.381 49.515 72.637 1.00 56.30 AAAA O ATOI1 4599 C4 FUC 470 52.245 48.255 70.809 1.00 61.24 AAAA 4591 FUC 470 ATOH c: 51.061 47.904 71.544 1.00 63.74 AAAA 0 25 FUC 470 ATOH 4633 52.455 47.086 69.828 1.00 62.20 AAAA 75 FUC ATO 1636 470 51.462 46.723 68.784 1.00 59.15 AAAA 4635 4730 4700 470 ATCL: 05 FUC 52.567 45.889 70.781 1.00 64.68 AAAA 471 ATOH: Cl 112.3 58.034 46.760 71.149 1.00 37.00 AAAA 8855 ATOM HA-3 471 58.977 45.225 72.186 1.00 40.30 AAAA 4704 4706 ATOU HAG 471 58.958 44.787 72.509 1.00 36.82 جحمم ATOU HAG 471 57.956 44.183 72.903 1.00 44.21 EEEE 4767 ATO: ! HAG 471 56.892 44.744 72.885 1.00 51.50 AAAA O **1**−0e C9 471 ATO!! HAG 58.202 42.814 73.323 1.00 46.02 AAAA C €3 471 ATOH NAG 58,901 47,250 73.291 1.00 34.50 aaaa 03 HAG 471 ATO! 59.598 74.385 45.917 1.00 35.84 AAAA 0 1716 4719 C4 471 ATOI: HAG 59.645 43.488 72.694 1.00 38.52 AAAA ō; 471 ATOM: HAG 59.754 49.464 73.694 1.00 37.44 AAAA O 4719 4721 471 ATOH: 112.3 59.056 48.958 71.332 1.00 36.94 AAAA NOTA C6 HAG 471 60.116 49.692 70.525 1.00 36.14 AAAA ATOH 4726 06 HAG 471 61.106 50.390 71.080 1.00 43.49 AAAA O HOTA 4721 05 NAG 471 58.953 47.785 70.530 1.00 34.98 AAAA O 4727 MOTA Cl HAH 472 61.035 49.984 73.959 1.00 53.37 AAAA C HOTA 4729 C2 HAII 472 60.920 51.497 74.260 AAAA C 1.00 56.72 4730 02 HAN NOTA 472 59.924 51.584 75.272 1.00 62.11 AAAA O ATOH! 4733 C3 HAH 472 62.216 52.031 74.840 1.00 60.70 AAAA C 4735 MAN **ATOH** 03 472 62.028 53.337 75.383 1.00 60.70 AAAA O HAH HOTA 4736 C4472 62.787 51.161 75.932 1.00 55.46 AAAA ATOH 4739 04 MAH 472 64.085 51.595 76.171 1.00 57.16 AAAA O HOTA 4740 C5 HAH 472 62.797 49.685 75.511 1.00 52.10 AAAA C ATO!! 4743 C5 MAN 472 63.458 48.905 76.595 1,00 50.32 BAAA C 4746 ATOL Q6 HAN 472 62.990 48.969 77.885 AAAA O 1.00 51.02 HOTA 4742 05 HAH 472 61.443 49.407 1.00 53.33 AAAA C 75,200 ATOH 4748 CI HAN 473 62.594 54.401 74.672 1.00 72.61 AAAA C ATOH 4750 CZ NAH 473 62.417 55.679 75.569 1.00 75.28 AAAA C 4751 HOTA 02 HAN 473 63.378 56.709 75.348 1.00 74.98 AAAA C HOTA 4754 C3MAIL 473 60.977 56.163 75.493 1.00 78.65 AAAA C HOTA 4756 03 MAN 473 60.841 57.447 76.148 1.00 79.16 AAAA O ATO11 4758 C4HAN 473 60.344 56.204 74.114 1.00 78.70 AAAA C HOTA 4760 04 MAII 473 58.983 56.571 74.178 1.00 78.93 AAAA O ATON 4762 C5 HAH 473 60.499 54.802 73.474 1.00 76.89 AAAA ATOH 4765 C6 HAN 473 59.968 54.490 72.091 1.00 74.73 AAAA C 473 ATOU 4768 HAN 60.239 55,469 71.138 1.00 71.39 AAAA O HOTA 1761 05 HAN 473 54.562 61.916 73.463 1.00 74.97 AAAA O 479 **ATOH** 4408 CB ALA 42.462 74.494 -16.374 1.00 82.09 8888 4409 ALA 479 HOTA C 40.017 74.702 17.001 1.00 91.42 BBBB C ATO11 4410 O ALA 179 40.393 75.108 18.103 1.00 96.11 BBBB HOTA 4413 11 ALA 479 40.696 74.461 14.624 1.00 88.43 BBBB N ATOH 4415 CA ALA 479 41.033 74.108 16.033 1.00 88.85 8888 C **ATON** 4416 11 ALA 480 38.749 74.752 16.610 1.00 92.12 8888 N **HOTA** 4418 CA ALA 480 37.684 75.264 17.467 1.00 91.28 8888 C CB ALA 37.925 **ATOH** 4419 190 76.731 17.769 1.00 86.84 PBBB C ALA 480 ATOU 4420 36.306 75.030 16.849 ввве € 1.00 91.39

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AT:41	4421	7. A.J	480	35.413	"4.54"	17.619	1.00 93.79	2888 0
ATH	4422	n gu	1 481	36.135				
ATOH	4424			34.832	75.16			
ATOR	4425	CB GU		34.471	76.19			
ATOH	4426			34.277	77.621			
ATOH	4427	CD GLI		34.067	79.003			
ATOH	4429	OE1 GLI		35.011	79.777			
ATOH	4429			32.792	79.326			
ATOH	4432	C GLI	_	34.755	73.947			
ATOH	4433	o su		33.736	73.508			BBBB C
ATO!	4434	II LYS		35.849	73.188			BBBB O
ATOH	4436	CA LYS		35.982	71.990			BBBB II
ATOH	4437	CB LYS		37.377	71.930			
ATON	4438	OS LYS		38.287	73.128		1.00 76.33	BBBB C
ATOL	4439	CD LYS		39.413	72.968		1.00 80.62	BBBB C
ATOH	4440	CE LYS		39.985	74.310			9888 C
ATOH	4441	HE LYS	_	41.252	74.136		0.01 76.66	BBBB C
ATOH	4445	C LYS		35.779	70.701		0.01 76.20	BBBB N
ATOH	4446	O LYS		35.879	70.744		1.00 67.70	BBBB C
ATOH	4447	II LEU		35.530	69.585		1.00 69.99 1.00 61.47	BBBB O
ATOH	4419	CA LEU		35.193	68.356		1.00 59.03	BBBB N
HOTA	4450	CB LEU		34.256	67.529	13.039	1.00 55.20	BBBB C
ATOH	4451	CG LEU		32.779	67.860		1.00 55.20	BBBB C
ATOH	4453	CD1 LEU		32.405	69.154			BBBB C
ATOH	4453	CD2 LEU		32.433	67.707	13.595 11.385	1.00 44.78	BBBB C
ATOH	4454	C LEU	483	36.421	67.509		1.00 44.63	8888 C
ATOH	4455	O LEU	483	36.465	66.709	14.229	1.00 59.73	BBBB C
ATOH	4456	II ILE	484	37.345	67.543	15.165 13.262	1.00 56.21	BBBB O
ATOH	4459	CA ILE	484	38.597	66.822	13.262	1.00 58.21	BBBB N
ATOH	4459	CB ILE	494	38.480	65.390	12.870		BBBB C
ATOH	4460	CG2 ILE	484	37.769	65.319	11.524	1.00 50.27	BBPB C
ATOH	4461	CG1 ILE	484	39.870	64.766	12.756	1.00 44.85	8888 C
ATOH	4462	CD1 ILE	184	39.888	63.291	12.404	1.00 39.78	8888 C
ATOH	4463	عنڌ ريـ	494	39.623	67.645	12.608	1.00 53.49	8889 C
ATO:	4464	o ILE	484	39.158	68.568	11.942	1.00 48.33	PBBS C
ATOH	4465	II SER	495	40.911	67.499	12.887	1.00 50.85	9889 N
ATOM	4467	CA SER	485	41.898	69.335	12.209	1.00 49.78	2863 C
ATON	4469	TB SER	495	41.969	69.753	12.747	1.00 46.06	3892 C
ATO!!	4459	og ser	425	43.190	70.035	13.376	1.00 63.03	2882 0
ATCM:	4471	T SER	495	43.294	67.711	12.240	1.00 50.57	9BBE C
ATOM	4472	O SER	485	43.510	66.501	12.740	1.00 46.55	2863 0
ATOH:	4473	H BLU	486	44.246	68.389	11.604	1.00 52.16	2282 ::
ATOH	4475	TA SLU	186	45.624	67.974	11.509	1.00 59.12	BBBB C
ATOH	4476	CB GLV	496	46.547	69.683	10.598	1.00 59.71	2322 C
ATOH	4477	og glu	196	46.221	70.162	10.568	1.00 76.75	3352 C
HOTA	11.5	CD GLU	496	47.370	71.045	10.983	1.00 80.53	332B C
ATON	4479	OE1 GLU	196	48.315	70.404	11.472	1.00 91.67	3385 ¢
ATOH	4480	OE2 GLU	495	47.480	72.289	10.997	1.00 86.00	3888 O
ATOH ATOH	4491 4492	0 G10	489 489	46.272	67.773	12.895	1.00 56.50	5855 C
ATOH	4493	U GLU	497	46.768	66.747	13.326	1.00 49.83	3323 0
ATOH	1162	CA GLU	497	45.955 46.129	69.738	13.732	1.00 58.37	2882 11
ATOH	4496	CB GLU	197	45.303	68.736 69.887	15.169 15.729	1.00 59.35	3885 C
HOTA	4497	OG GLU	187			17.159	1.00 61.32 1.00 79.21	8382 C
HOTA	4488	CD GLU	487	46.397	71.545	17.177	1.00 86.09	8888 C
ATOH	4489	OE1 GLU	497	45.768	72.510	17.320	1.00 92.00	BBBB O
ATOH	4490	OE2 GLU	487	47.637	71.452	17.026	1.00 96.51	BBBB O
ATOH:	4491	C GLU	487	45.735	67.436	15.841	1.00 58.84	BBBB C
ATOH:	4492	O GLU	487	46.421	67.018	16.761	1.00 61.93	BBB3 0
ATOH:	4493	II ASP	488	44.748	66.661	15.474	1.00 56.50	8888 11
ATO!	4495	CA ASP	488	44.446	65.347	15.932	1.00 55.61	BBBB C
ATOH	4496	CB ASP	188	42.947	64.977	15.699	1.00 51.22	8988 C
HOTA	4497	CG ASP	488	42.047	66.008	16.267	1.00 45.27	BBBB C
ATOH	4458	OD1 ASP		42.114	66.563	17.387	1.00 56.45	8888 O
INTA	4499	OD2 ASP	488		66.399	15.492	1.00 55.11	BBBB O
ATOH	4500	C ASP	488		64.211	15.238	1.00 58.91	288B C
ATOH	4501	O ASP	488		63.042	15.634	1.00 57.00	3888 O
ATOH	4502	II LEU	499		64.513	14.163	1.00 57.39	988B N
ATOM	4504	CA LEU	489			13.528	1.00 64.93	BBBB C
ATOM	4505	CB TEA	489		63.677	12.024	1.00 62.69	8888 C
ATOH	4506	CG LEU	489			11.226	1.00 53.71	SBBB C
ATOH		CD1 LEU	489		63.243	11.514	1.00 51.88	BBBB C
ATOH ATOH			489		62.967	9.766	1.00 55.20	8888 C
ATOH			489		63.355	14.210	1.00 68.12	8888 C
ATOH		o leu II asn	490 490		62.560	13.838	1.00 71.57	8888 C
ATOM		CA ASN	490		64.318	15.063	1.00 68.24	BBBB N
ATOH		CB ASN	490		64.424 65 910	15.855	1.00 75.04	8888 C
ATOM		CG ASN	490	_	65.910 66.105		1.00 84.46 1.00 98.83	8888 C
ATOH		OD1 ASN	490		65.342		1.00 98.83	8888 C
ATOM		ND2 ASN	490			_	1.00100.47	BBBB O
ATO11		C ASN	490				1.00 80.30	8888 C
ATOH	_	O ASN	490				1.00 80.97	9888 O
ATOH	-	OT ASI	490				1.00 89.51	8888 C
ATOH		S SUL	493				1.00108.87	DDDD S

Atra		9 <u>1</u> 30.		38.45	-7.92	1 56.345	5 1.00112.65	0000 0
ATON ATON	4773	02 SUI	L 493	37.61; 36.53;	3 -6.55			o ddda
ATOL: ATOL:	4775	3 20) 04 20)	494	36.33; 56.567				DDDD O
IOTA IOTA		01 SU1		56.597 57.964			1.00107.98	0 0000
ATOH HOTA		04 SUI		55.749 55.886	21.00	6 66.267	1.00111.35	DDDD O
ATOH ATOH		S SUI	495	34.533 35.274	11.24	0 75.722	1.00114.67	DDDD O DDDD S
ATOH	4782	02 SUI	495	35.476	10.32	9 74.974	1.00113.60	DDDD O
ATOH ATOH	4784	04 20I	495	33.552 33.773				DDDD O
ATOH ATOH		S SUL OI SUL		35.466 35.613			1.00 50.73 1.00 62.59	DDDD S DDDD O
IOTA IOTA		O2 SUL O3 SUL		36.002 35.880	23.583	58.571	1.00 48.59	DDDD O
I IOTA I IOTA	4799	04 SUL S SUL	496	33.958 47.653	24.953	59.034	1.00 59.34	DDDD O
ATOH	4791	Ol SUL	497	47.849	-2.303 -1.058	70.996	1.00 68.98 1.00 68.52	DDDD S DDDD O
ATOH HOTA	4793 (02 SUL 03 SUL	497	48.594 46.187	-2.509 -2.393		1.00 70.94	DDDD O DDDD O
HOTA HOTA		04 SUL S SUL	497 498	47.799 56.527	-3.446 35.758		1.00 71.33 1.00 71.48	DDDD O
HOTA HOTA	_	DI SUL D2 SUL	498 498	55.870 57.759	35.013 34.996	76.621	1.00 72.97	DDDD O
HOTA	4799 (03 SUL 04 SUL	498 498	56.619	37.237	75.785	1.00 72.45	O 0000
11OTA	4800 8	SUL	499	55.623 40.639	35.809 27.365	69.499	1.00 72.74	DDDD O DDDD S
ATOH ATOH	4800 0	01 SUL 02 SUL	499 499	40.218 42.089	26.039 27.608		1.00 76.00	DDDD O
ATOH ATOH		03 SUL 04 SUL	499 499	39.823 40.424	28.467 27.245	70.098 68.018	1.00 77.27	DDDD O
ATOH ATOH	4905 S	SUL SUL	500 500	44.996 45.080	53.229 54.400	20.568	1.00 83.89	DDDD O DDDD S
ATON ATON	480° C	2 SUL 3 SUL	500 500	46.109	52.266	21.461 20.827	1.00 84.79 1.00 90.39	O DDDD O DCDD
ATOH	4803 0	4 SUL	500	45.032 43.762	53.674 52.396	19.135 20.723	1.00 92.23 1.00 91.61	0000 O
ATOM ATOM	4913 0		501 502	29.970 42.522	6.904 18.998	77.713 79.232	1.00 34.84 1.00 55.27	0000 O
ATOH ATOH	4816 0 4919 0		503 504	37.561 50.446	21.003 5.721	67.518 63.485	1.00 41.63	O DDDD
ATOH ATOH	4900 0 4805 0		505 506	56.668 50.605	24.854 57.695	72.729 22.727	1.00 57.34 1.00 54.26	DDDD O
ATOH ATOH	4928 O	TAW W	507 508	55.123	37.781	51.204	1.00 43.71	DDDD O
ATOH ATOH	4934 Of	M MAT	509	17.414 44.263	-9.070 20.985	74.793 63.811	1.00 48.79 1.00 28.64	0000 O
ATOH	4941 0	9 MAT	510 511	45.085 33.537	19.708	94.433 71.115	1.00 49.09 1.00 60.39	0 0000 0 0 000
ATOH ATOH	4946 OI	4 MAT	512 513	19.279 11.502	4.902 -0.835	75.254 68.996	1.00 55.23 1.00 57.51	0 0000 0 0000
ATOH ATOH	4849 OF		514 515	24.591 56.947	17.207 34.914	56.665 62. 55 2	1.00 55.36	O C2GG
ATOH ATOH	4855 OF		516 517	58.092 48.308	39.983 40.726	66.234	1.00 30.34	DDDD O
HOTA HOTA	4861 OF	TAW V	518 519	25.776	2.355	85.630	1.00 66.34	DDDD O
ATOH ATOH	4867 ON	WAT	520	30.644 38.739	68.108 54.257	43.611	1.00 82.28 1.00 43.41	DDDD O DDDD O
ATOH	4973 OW	WAT	521 522	22.886 30.938	4.470 50.249		1.00 48.71 1.00 54.00	DDDD O
ATOH ATOH	4876 OW 4879 OW	WAT	523 524	32.413 41.019	9.061 42.560		1.00 44.45	DDDD O DDDD O
ATOH ATOH	4882 OW 4885 OW		525 526		51.393 13.599	37.513	1.00 55.10	DDDD O
ATOH ATOH	4899 OW 4891 OW		527 528	42.585	10.244	84.472	1.00 35.95	DDDD O
ATOH ATOH	4894 OW 4897 OW	WAT	529 530	27.980	19.862	53.348	1.00 41.05 1.00 54.59	DDDD O
ATOH	4900 OW 4903 OW	WAT	531	22.451		57.437	1.00 37.96 1.00 59.31	DDDD O
ATOM	4906 OW	WAT	532 533	46.835	27.888		1.00 40.39 1.00 52.34	DDDD O
HOTA	4909 OW 4912 OW	WAT WAT	534 535		51.272	50.722 1	1.00 46.05 1.00 52.62	DDDD O DDDD O
ATOH ATOH	4915 OW 4919 OW	yat Taw	536 537	14.263	18.776	73.017 1	1.00 40.61	DDDD O
ATCH ATOM	4921 OW 4924 OW	WAT WAT	538 539	52.469	21.639	73.804 1	1.00 61.98	DDDD O
ATOM ATOM	1927 OW 1930 OW	WAT	540	24.074 -	-1.791	60.077 1	L.00 45.45 L.00 40.40	DDDD O DDDD O
ATOH	4933 OW	WAT	541 542		-1.176		00 51.34 00 48.33	DDDD O DDDD O
ATOH ATOH	4936 OW 4939 OW	WAT WAT	543 544			55.290 1	.00 60.67 .00 71.69	DDDD O
	4942 OW	WAT WAT	216 212		0.030	67.582 1	.00 44.88	DDDD O
				-				2222

ATCH 4948 OW WAT 547 39.459 -14.058 70.554 1.00 84.42 DDDD O ATCH 4951 OW WAT 548 57.310 32.779 60.848 1.00 50.77 DDDD O EHD

Figure 2

:::

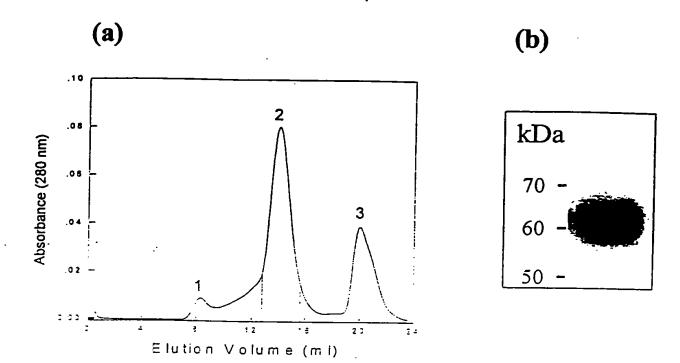


Figure 3

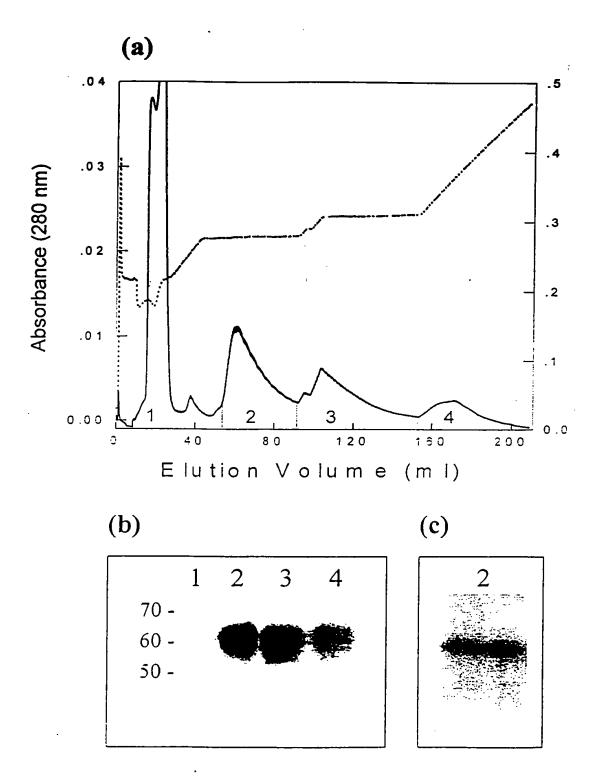


Figure 4

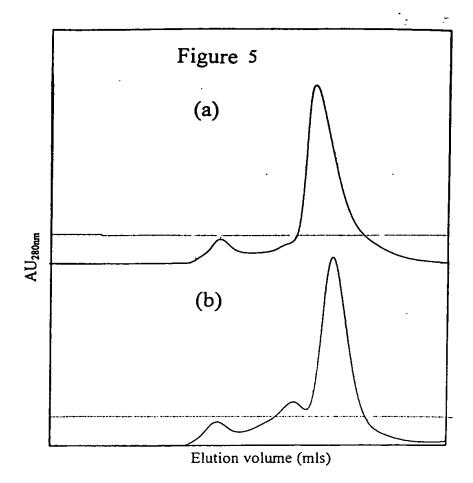
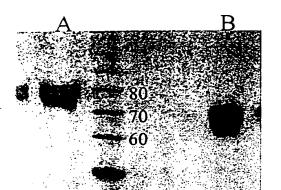
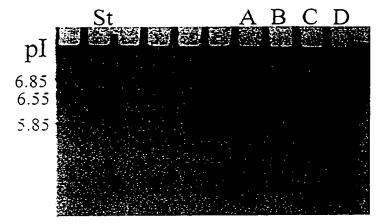


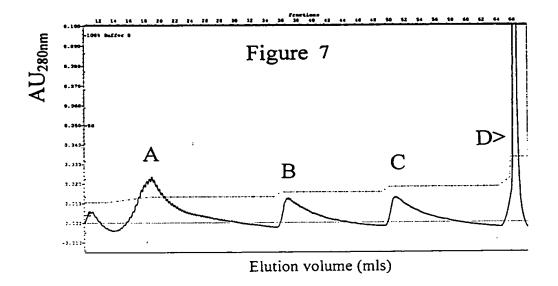
Figure 6

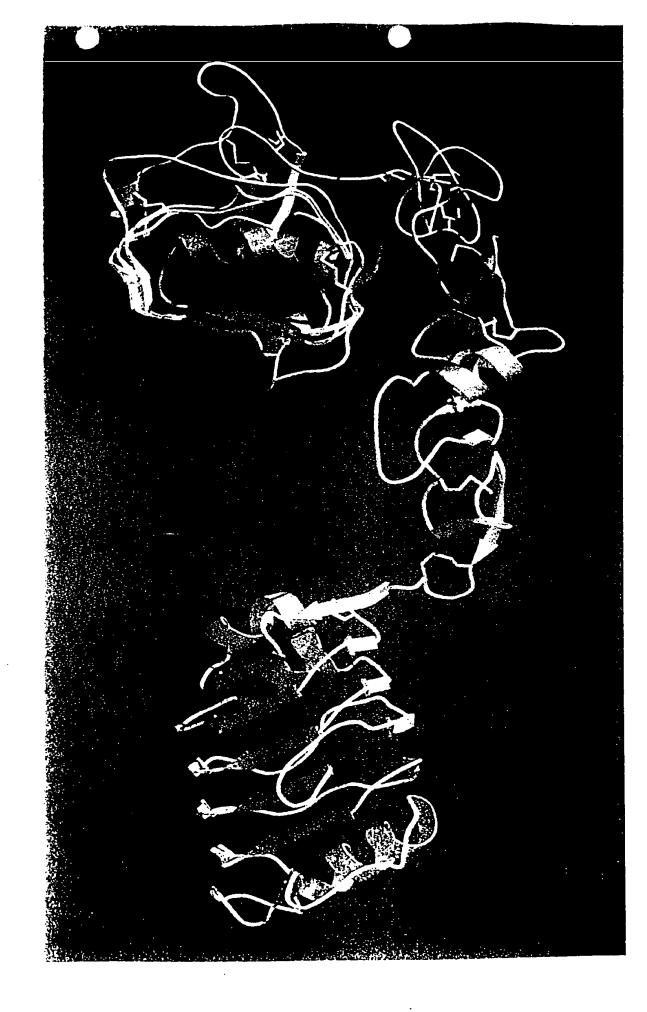
(a) SDS PAGE

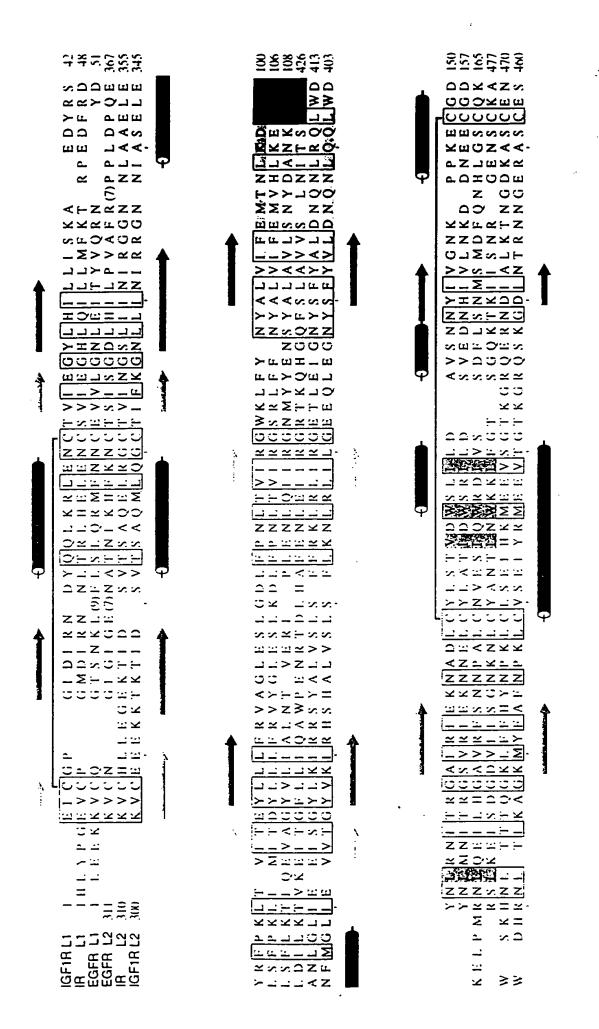


(b) IEF pH3-7

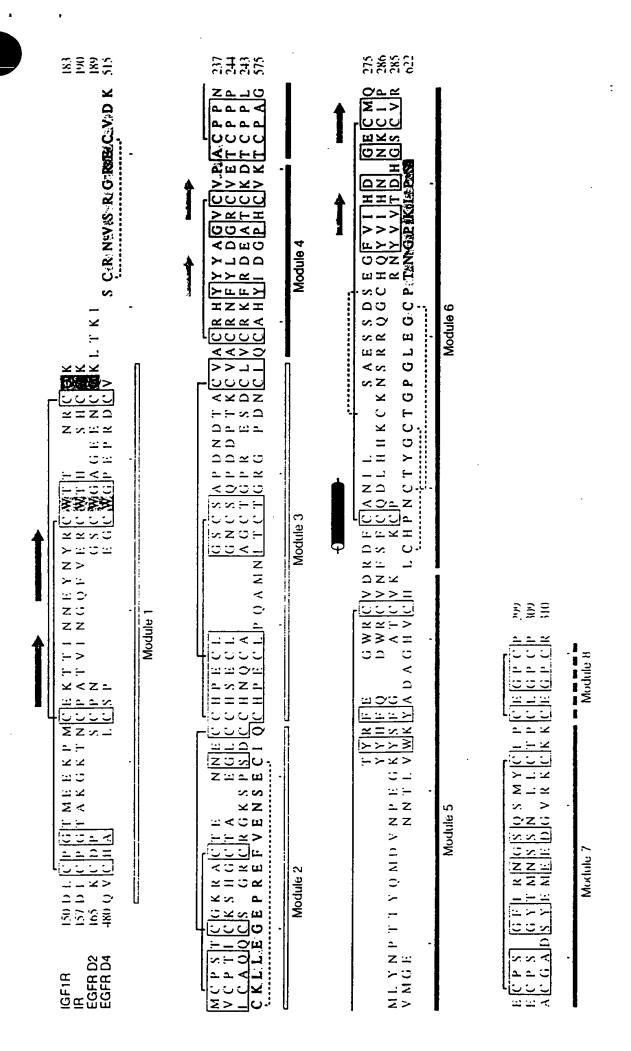








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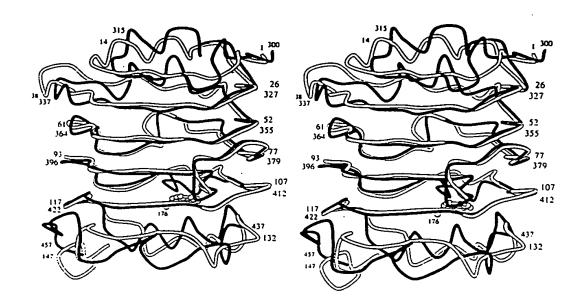
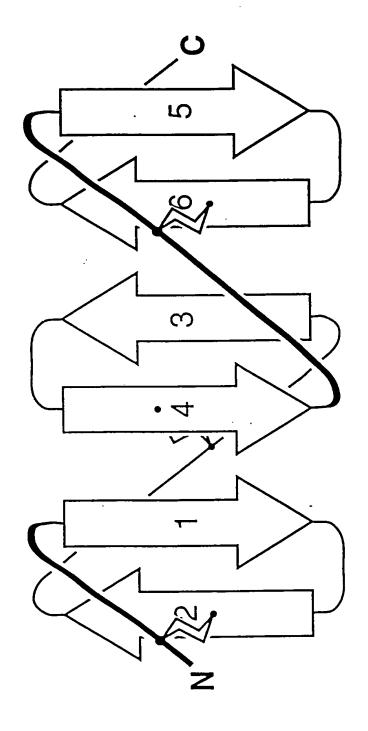
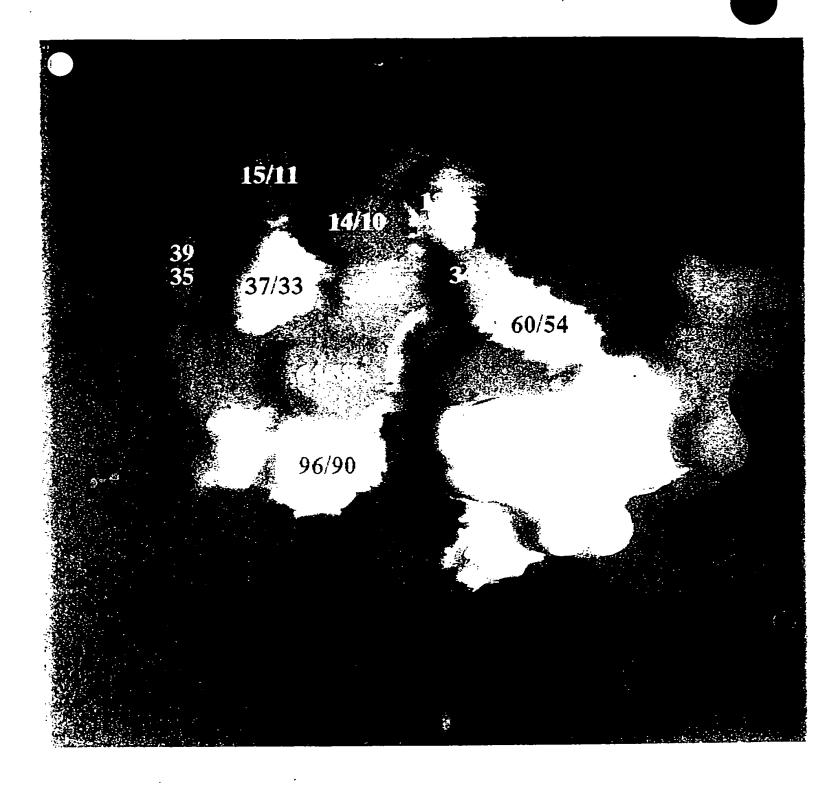


Figure 10





Elgure 12

Figure 13: Sequence Alignment of hIGF-1R, hIR and hIRR ectodomains.

Derived by use of the PileUp program in the software package of the Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA.

Symbol Comparison table: GenRunData:PileUpPep.Cmp CompCheCk: 1254

GapWeight: 3.0 GapLengthWeight: 0.1

Name: Name: Name:		Len:	972 C he	k: 2986 v	Weight: 1.0 Weight: 1.0 Weight: 1.0	0
	<u>.</u>					
Higflr Hir Hirr	EICGP HLYPGEVC.P MNVC.P	GMDIRN <u>NLT</u> R	LHELENCSVI	EGHLQILLM	S KAEDYRS' IF KTRPEDFRDI IF TATGEDFRGI	ւ 49
Higflr Hir Hirr	RFPKLTVITE SFPKLIMITD SFPRLTQVTD	YLLLFRVYGL	ESLKDLFPNL	_TVIRGSRLF	Y NYALVIFEM F NYALVIFEM L GYALVIFEM	7 99
Higflr Hir Hirr	HLKELGLYNL	MNITRGSVRI	EKNNEL CYLA	TIDWSRILD	A VSNNYIVGNI S VEDNYIVLNI A PGANHIVGNI	K 149
	* *		*	*	* * *	
Higflr Hir Hirr	PPK.ECGDLC DDNEECGDIC LG.EECADVC	PGTAKGKTN.	CPATVINGOF	VER CWTHSH	C QKMCPSTCGE C QKVCPTICKS C QRVCPCPHG	198
	* **	* *	* *	*	*	
	ractennecc hgctaeglcc mactargecc	HSECLGNCSQ	PDDPTKCVAC	RNFYLDGR C		248
	*	* *	*	*	*	
Higflr Hir Hirr	EGWR <i>C</i> VDRDF QDWR <i>C</i> V <u>NFS</u> F ESWR <i>C</i> VTAER	CQDLHHKCKN	SRRQGCHQYV	IHNNK CIPE	C PSGFIR <u>NGSC</u> C PSGYTM <u>NSS</u> N C PSGFTR <u>NSS</u> .	1 298
	* *	* *		*		
	SMYCIPCEGP .LLCTPCLGP SIFCHKCEGL	CPKVCHLLEG	EKTIDSVTSA	QELRGCTVI		347
Higflr Hir Hirr	NNLAAELEAN	LGLIEEISGY	LKIRRSYALV	SLSFFRKLR	L ILGEEQLEGN L IRGETLEIGN L IRGDAMVDGN	397
Hir	XSFYVLDNQN XSFYALDNQN YTLYVLDNQN	LRQLWDWSKH	NLTITQGKLF	FHYNPKL CL :	S EIHKMEEVSG	447
	TKGRQSKGDI TKGRQERNDI TRGRQNKAEI	ALKTNGDQAS	CESDV LHF	Y IRTSFDK	III TWHRYRPP	DF 497

						_
Higflr	RDLISFTVYY	KEAPFKNVTE	YDGODA <i>C</i> GSN	SWNMVDVDLP	PNKDV	532
Hir	RDLLGFMLFY	KEAPYONVTE	FDGQDACGSN	SWIVVDIDPP	LRSNDPKSQN	547
Hirr	RDLLSFIVYY	KESPF <u>ONAT</u> E	HVGPDACGTQ	SWNLLDVELP	LSRTQ	530
Higf1r	EPGILLHGLK	PWTQYAVYVK	AVTLTMVEND	HIRGAKSEIL	YIRTNASVPS	582
Hir	HPGWLMRGLK	PWTQYAIFVK	TL.VTFSDER	RTYGAKSDII	YVOTDATNPS	596
Hirr	EPGVTLASLK	PWTQYAVFVR	AITLTTEEDS	PHQGAQSPIV	YLRTLPAAPT	580
Higflr	IPLDVLSAS <u>N</u>	<u>SS</u> SQLIVKWN	PPSLPNG <u>NLS</u>	YYIVRWQRQP	QDGYLYRHNY	632
Hir Hirr	VPLDPISVSN	<u>SS</u> SQIILKWK	PPSDPNGNIT	HYLVFWERQA	EDSELFELDY	646
HILL	APQDAISTSM	222HLLVKWK	PPTORNGNLT	YYLVLWQRLA	EDGDLYLNDY	630
	*			* ** **	*	
Higflr				CGGEKGPCCA		678
Hir Hirr	CHRGLRLPSR CHRGLRLPTS	N NOPPECE	DSQKH <u>NOS</u> E.	YEDSAGE <i>CC</i> SSD <i>CC</i> P	CPKTDSQ	691 673
*****	•	M. MDI MI DOD	DODI LALIE.		egiii i i og v b	075
			α	><β		
Higf1r	KQAEKEEAEY	RKVFENFLHN	SIFVPRPERK	RRDVMQVA <u>NT</u>	TMSSRSRNTT	728
Hir Hirr				RRSLGDVG <u>NV</u> VTSI <u>NKS</u> POR		738 722
HILL	FFUEAQEASE	QAAF ENF DHM	ALITEISPWA	A I STMVZEÓK	D. SGRIRRAA	122
	•				*	
Higf1r Hir				RTVISNLRPF		
Hirr				SLVISGLRHF RAVLSGLRHF		
	<u></u>					
*** = = 1	*	3 C31E11E 3 EM31	D1 501 DD 7 DC		CIPI WIDDE	026
Higflr Hir				PVTWEPRPEN PVTHEIFENN		
Hirr				KVAWEASSKN		
Hiafly	NPNGLILMYE	TRYCS OVED	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	PKACGVKI'VID	I.NIDCNIVTA D T	875
Hir				ALERGCRLRG		
Hirr	DPNGLILKYE	IKYRRLGEEA	TVLCVSRLRY	AKFGGVHLAL	LPPG <u>NYS</u> ARV	864
Higf1r	OATSLSGNGS	WTDPVFFYVO	AKTGYENETH	L		906
Hir	RATSLAG <u>NGS</u>	WTEPTYFYVT	DYLDVPSNIA	K		917
Hirr	RATSLAG <u>NGS</u>	WTDSVAFYIL	GPEEEDAGGL	H		895

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Figure 14: Sequence Alignment of EGFR, ErbB2, ErbB3 and ErbB4 Ectodomains.

[For alignment on the IGF-1R fragment see Fig. 9]

Derived by use of the PileUp program in the software package of the Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA.

Symbol comparison table: GenRunData:Pileuppep.Cmp CompCheck: 1254

GapWeight: 3.000 GapLengthWeight: 0.100

Name: Name: Name:	Erb4	Len Len Len	: 649 Che	eck: 790 teck: 2381	Weight: 1.00 Weight: 1.00 Weight: 1.00 Weight: 1.00
Erb3 Erb4 Egfr Erb2	SDSQSVC	PGTLNGLSVT AGTENKLSSL QGTSNKLTQL TGTDMKLRLP	SDLEQQYRAL GTFEDHFLSL	RKYYENCEVV QRMFNNCEVV	MGNLEITSIE
Erb3 Erb4 Egfr Erb2	51 HNADLSFLQW HNRDLSFLRS RNYDLSFLKT TNASLSFLQD	VREVTGYVLV IQEVAGYVLI	ALNQFRYLPL ALNTVERIPL	ENLRIIRGTK ENLQIIRGNM	100 VYDGKFAIFV LYEDRYALAI YYENSYALAV LFEDNYALAV
Erb3 Erb4 Egfr Erb2		KDGNFG	LKELPMRNLQ	EILNGGVYVD EILHGAVRFS	150 KNDKLCHMDT QNKFLCYADT NNPALCNVES RNPQLCYQDT
Erb3 Erb4 Egfr Erb2	151 IDWRDIVRDR IHWQDIVRNP IQWRDIVSSD ILWKDIFHKN	FLSNMSMDFQ	NGSSGCGRCH NHLGSCQKCD	KSC.TGRCWG PSCPNGSCWG	200 PGSEDCQTLT PTENHCQTLT AGEENCQKLT ESSEDCQSLT
Erb3 Erb4 Egfr Erb2	RTVCAEQCDG KIICAQQCSG	HCFGPNPNQC RCYGPYVSDC RCRGKSPSDC RCKGPLPTDC	CHRECAGGCS CHNQCAAGCT	GPQDTDCFAC GPKDTDCFAC GPRESDCLVC GPKHSDCLAC	250 RHFNDSGACV MNFNDSGACV RKFRDEATCK LHFNHSGICE
Erb3 Erb4 Egfr Erb2	251 PRCPQPLVYN TQCPQTFVYN DTCPPLMLYN LHCPALVTYN	PTTFQLEHNF PTTYQMDVNP	HTKYQYGGVC NAKYTYGAFC EGKYSFGATC EGRYTFGASC	VASCPHNFVV VKKCPHNFVV VKKCPRNYVV VTACPYNYLS	300 .DQTSCVRAC .DSSSCVRAC TDHGSCVRAC TDVGSCTLVC
Erb3 Erb4 Egfr Erb2	PSSKMEV.EE GADSYEM.EE	NGLKMCEPCG NGIKMCKPCT DGVRKCKKCE DGTQRCEKCS	DICPKACDGI GPCRKVCNGI	GTGSLMSAQT GIGEFKDSLS	350 VDSSNIDGFV VDSSNIDKFI INATNIKHFK VTSANIQEFA
Erb3 Erb4 Egfr Erb2	NCTKINGNLI NCTSISGDLH	FLITGLNGDP FLVTGIHGDP ILPVAFRGDS FLPESFDGDP	YNAIEAIDPE FTHTPPLDPQ	KLNVFRTVRE ELDILKTVKE	ITGFLNIQSW
Erb3 Erb4	401 PPHMHNFSVF PPNMTDFSVF		LYNRGFSLLI LYS.GLSLLI	MKNLNVTSLG LKQQGITSLQ	450 FRSLKEISAG FQSLKEISAG

					į	
		•				
Egfr Erb2	PENRTDLHAF PDSLPDLSVF	ENLEIIRGRT QNLQVIRGRI	KQHGQFSLAV LHNGAYSL.T	VS.LNITSLG LQGLGISWLG	LRSLKEISDG LRSLRELGSG	
Erb3 Erb4 Egfr Erb2	NIYITDNSNL DVIISGNKNL	CYHHSLNWTK CYYHTINWKK CYANTINWKK CFVHTVPWDQ	LF.STINQRI LF.GTSGQKT	VIRDNRKAEN KIISNRGENS	CVA EGKVCDP CTA EGMVCNH CKA TGOVCHA	
Erb3 Erb4 Egfr Erb2	501 LCSSGGCWGP LCSSDGCWGP LCSPEGCWGP LCARGHCWGP	GPDQCLSCRR EPRDCVSCRN	FSRGRICIES VSRGRECVDK	CNLYDGEFRE CKLLEGEPRE	550 FAHEAECFSC FENGSICVEC FVENSECIQC YVNARHCLPC	
Erb3 Erb4 Egfr Erb2	DPQCEKMEDG HPECLPQAMN	TATCNGSGSD LLTCHGPGPD I.TCTGRGPD SVTCFGPEAD	NCTKCSHFKD NCIQCAHYID	GPNCVEKCPD GPHCVKTCPA	GLQGA.NSF. GVMGENNTL.	
Erb3 Erb4 Egfr Erb2	IFKYADPDRE VWKYADAGHV	CRPCHENCTQ CHPCHPNCTQ CHLCHPNCTY CQPCPINCTH	GCNGPTSHDC GCTGPGLEGC	IYYPWTGHST PTNGPKIPS.	-	

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Figure 15. Classification of Cys-rich modules
C2-4 denote modules with the 1-3/2-4 double disulphide bond connections.
C1-2 for the single disulphide bonded modules and
C1-2t for stabilised beta turn.

First Cys-rich region C2-4 modules

C2-4 modules				
		1 2 3 4		şi.
•		CPGTHEEK9H-CEKTTINNEYNYRCWTTHRC		(lst)
Hir		CPGTAKGKTH-CPATVINGQEVERCWTHSHC ((lst)
Hicr	154	CPGVLGAAGEPCAKTTFSGHTDYRCWTSSHC ((lst)
Egfr		CDPSCPNG-SCWGAG-EENC QKLTKII	190	(lst)
hErb2		CSPHCKGS-RCWGES-SEDC QSLTRTV	199	(lst)
hErb3		CHEYCKGRCWGPG-SEDC QTLTKTI	190	(Ist)
hErb4	157	CHKSCTGRCWGPT-ENHC QTLTRTV	190	(lst)
Higfir		CPSTOGK-RACTENNEC	200	(2nd)
Hic		CPTICKS-HGCTAEGLC	207	(2nd)
Hicc		CPCPHGMACTARGEC	292	(2nd)
Eg f c		CAQQC3GRCRGKS-2SDC	207	(2nd)
hErb2		CAGGCARCKGPL-PTDC	214	(2nd)
hErb3	191	CYSCCHEHCEGSH-SNGC	207	(2nd)
hErb4	191	CAEQCDGRCYGPY-VSDC	207	(2nd)
Higflr	2:01	CHPECLGSCSAPDNDTAC VA	220	(3rd)
Hir	208	CHSECLGNCSQPDDPTKC VA	227	(3rd)
Hirr	203	CHIECLGGCSQPEDPRAC VA	222	(3rd)
Egfr	209	CHNQCAAGCTGPR-ESDC LV	226	(3rd)
Erb2	215	CHEQCAAGCTGPK-HSSC LA	233	(3:i:
hEsb3	208	CHDECAGGCSGPQ-DTDC FA	225	(354)
hBsb4	2:3	CHRECAGGCSGPK-CTCC FA	226	(3:2
C1-2 modules				
Higfle	221	CRHYY-+-YAGYO YFA	233	.4 1 5
Hir	223	GRMFWLOGRO VET	240	[4th]
Hiss		CRELYFQGAC LWA	235	4th
Esfe-I		CRMFRDEATC MOT	239	(4th-
AErel		CLHFN-+-HSGIC ELH	244	415
nEss 1		CFHFHDSBAC VPR	239	4-5
%Est4		CONFODSEAC NTQ	239	:41%
Higile	234	CPPUTYRFEBWRC WERDF	251	'ātn:
His		CEFFYEHEROWRO TOVESE	253	5 to
Hirr		OFFSTYQYESWRG VTAER	253	(3th;
Eşis		CFFLMLYHETTYONEWHEEKYSEGATO VKK	270	:5th:
nĒrbi		CPALVTYHTOTFESHPHREGRYTEGASC VTA	277	(5th)
hErb3	240	degelvynklteglesnehtkygyggvd vas	270	(5th)
hEsb4	240	CPQTFVVNFTTFQLEHNFNAKYTYGAFC VNK	270	(5th)
Higfle	152	CAMILSAESSOSEGFVIHD.GEC MQE	276	(Sth)
Hi.e	259	CQC.LHHKCKNSRRQGCHQYVIHM.NKC IFE	297	idan.
Hist		CAS. LHSVPGRAST FGIHQ. GSC LAQ	27.5	'Sin'
Eşf:		CPRIVEY/YTOHGSC VRA	295	- 5 t.h.
nEsel		CANTINUSTOWESC TEV	293 293	:6tn.
hErb3		CRESTAL DOTS VRA		: fth' fth'
		CERTFORDSSSC VRA		
		CFFB.FIRNGSQ-SNYC IF	293	โรก
Hit		CPS 3. YTIBISSNLLC TP	303	(7:5)
Hitt		CP33. FTRN3S-+SIFC HK	293	: <u> </u>
E:≤÷		CBADBYEME-EDGYRKC KK	304	755
"Erri		CRIMINESTABOGRANG BH	312 313	Tih: Tia
nZeri -		CPFTRGTEVERTH-JERGTC EP		
15mm (: * .:	C F F B F T TE TY TE EST F F T T T T T T T T T T T T T T T T T	303	ិងស

C1-2t mod	dule			
Hig		4 CEGPC	298	(8th)
Hir		4 CLGPC	308	(8th)
Hir		4 CEGLC	298	(8th)
hEg		5 CEGPC	309	(8th)
hEr		3 CSKPC	317	(8th)
hEr		4 CGGLC	308	(8th)
- hEr		4 CTDIC	308	(8th)
		• • • • • • • • • • • • • • • • • • • •	300	(601)
Second Cys-	rich regi	on.		
C2-4 mod	ules			
hEq		CHALCSPEGCWGPEPRDCVS	501	(1st)
hErl		CHOLCARGHCWGPGPTOCVN	509	(1st)
hErl		CDPLCSSGGCWGPGPGQCLS	500	(1st)
hErl	64 481	CNHLCSSDGCWGPGPDQCLS	500	(1st)
Egfi	534	CHPECLPQAM-NITCTGRGPDNC IQ	557	(4th)
hErl	542	CHPECQPQNG-SVTCFGPEADQC VA	565	(4th)
hErl	533	CHPECOPMEG-TATCNGSGSDTC AQ	556	(4th)
hErl	533	CDPQCEKMEDGLLTCHGPGPDNC TK	557	(4th)
hEgi		CHPNCTYGCTGPGLEGC PTNGPKIPS/	621	(7th)
hEri		CPINCTHSCVDLDDKGC PAEQRAGRASPLTS/	632	(7th)
hErl hErl		CHENCTQGCKGPELQDC LGQT/ CHPNCTQGCNGPTSHDC IYYPWTGHSTLPQHART	614	(7th) (7th)
11611	J. 373	ChristigGendriande Tittwidnaibrenaki	ED 020	(/CII)
C1-2 modu	les :			
hEg:		CRNVSRGREC VDK	514	(2nd)
hErb		CSQFLRGQEC VEE	522	(2nd)
hErb hErb		CRN'SRGGVC VTH CRRFSRGRIC IES	513	(2nd)
ALF	34 301	CRRISRGRIC 125	513	(2nd)
hEgi	fr 515	CKLLEGEPREFVENSEC IQ	533	(3rd)
hErb		CRVLQGLPREYVNARHC LP	541	(3rd)
hErb		CNFLNGEPREFAHEAEC FS	532	(3rd)
hErb	514	CNLYDGEFREFENGSIC VE	532	(3rd)
hEg:		CAHYIDGPHC VKT	570	(5th)
hErb		CAHYKDPPFC V-A	578	(5th)
hErb		CAHFRDGPHC V-S	569	(5th)
hErb	:4 553	CSHFKDGPNC VEK	570	(5th)
hEg i	571	CPAGVMGENNTL-VWKYADAGHVC HL	595	(6th)
hErb		CPSGVKPDLSYMPIWKFPDEEGAC QP	604	(5th)
hErb		CPHGVLGAKGPIYKYPDVONEC RP	593	(6th)
hErb		CPDGLQGANSFIFKYADPDREC HP	594	(6th)
				,,
See Pattern				
IR fami		C2-4, C2-4, C2-4, C1-2, C1-2, C1-2, C1-2,		
EGFR fami.	ly:1st 2nd	C2-4, C2-4, C2-4, C1-2, C1-2, C1-2, C1-2,	C1-2t	
	Znc	C2-4, C1-2, C1-2, C2-4, C1-2, C1-2,		
		C2-4, C1-2, C1-2,		

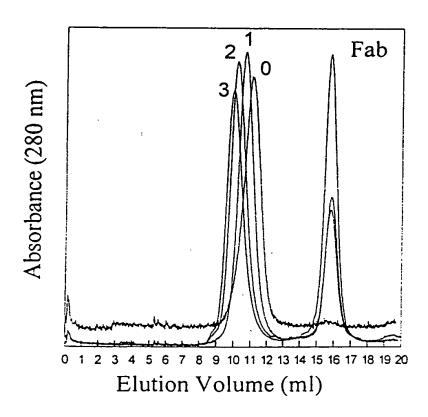
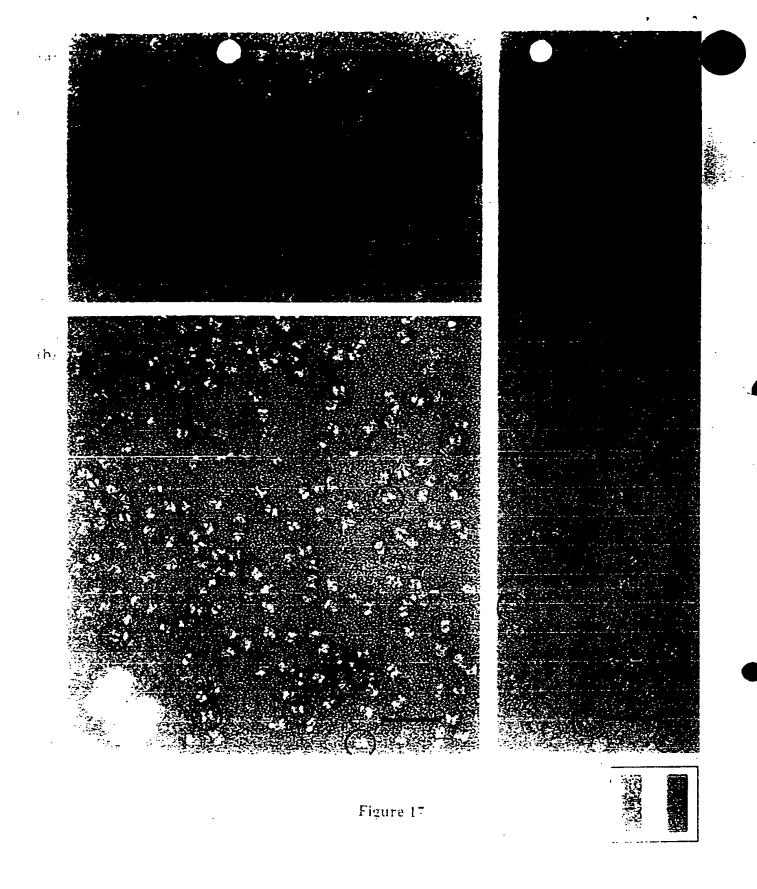


Figure 16



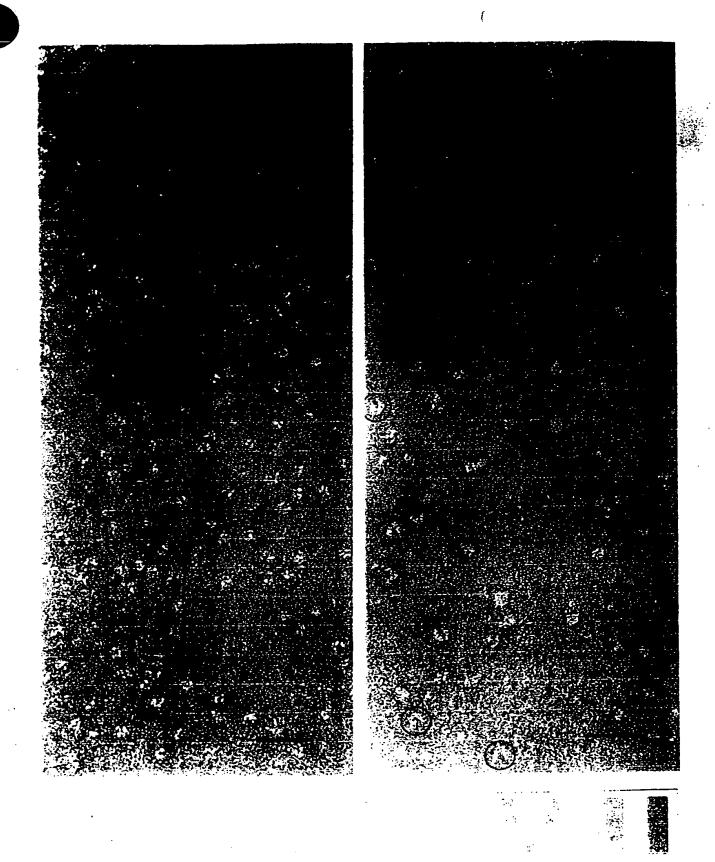


Figure 18

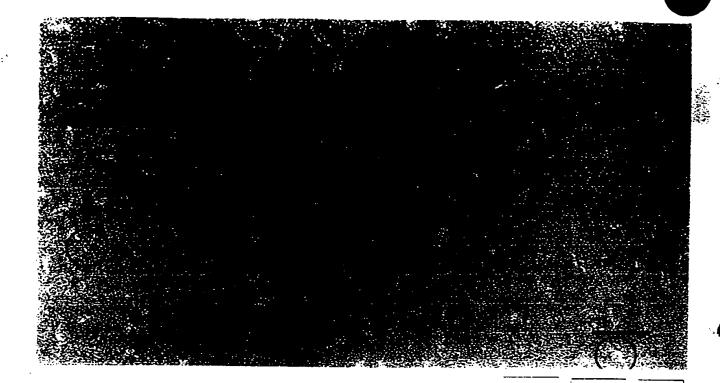


Figure 19

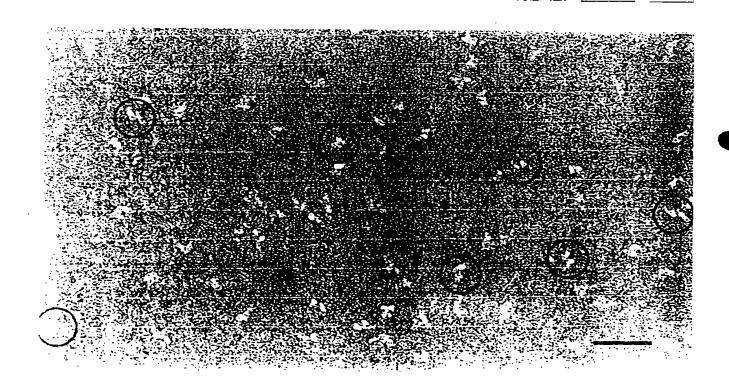


Figure 20

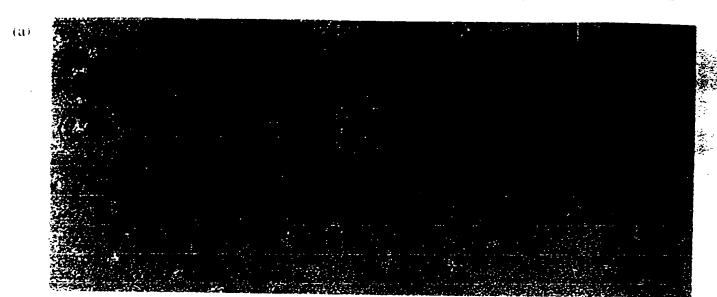




Figure 21

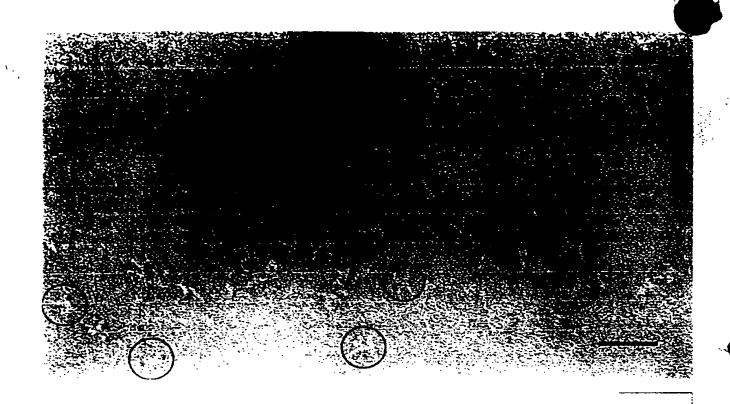


Figure 22

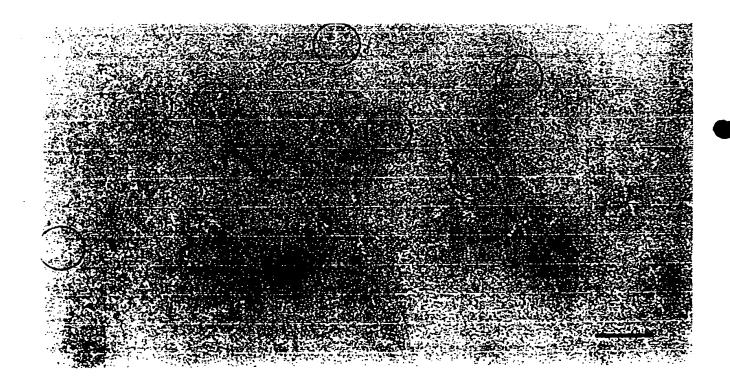


Figure 23